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Spatial and temporal variations of microorganisms in grassland soils – influences of land-use intensity, plants and soil properties

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To my family

for roots to ground and wings to fly.

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1. Summary

Grassland ecosystems provide a wide range of services to human societies (Allan et al., 2015) and plants and soil microorganisms have been identified as key drivers of ecosystem functioning (Soliveres et al., 2016). Therefore, understanding soil microbial distributions and processes in agricultural grassland soils is crucial for characterizing these ecosystems and for predicting how they may shift in a changing environment. Yet we are only beginning to understand these complex ecosystems, which account for about 26% of the world's terrestrial surface (FAOSTATS, 2018), making it especially urgent to gain better insights into the effects of land-use intensity on soil microbial properties and plant-microbe interactions. This thesis was conducted to evaluate the impact land-use intensity has on soil microbial biogeography of grasslands with respect to both spatial patterns and temporal changes in soil microbial abundance, function (in terms of enzyme activities), and community composition. It also investigated the relationships between plants and the spatial and temporal distributions of soil microorganisms. Thereby both, land-use intensity effects and plant-microbe interactions, were assessed in light of ecological niche and neutral theory. This thesis is based on three observational studies conducted on from one to 150 continuously farmed, un-manipulated grassland sites in three regions of Germany within the Biodiversity Exploratories project (DFG priority program 1374).

The first study assessed the effects of land-use intensity and physico-chemical soil properties on the spatial biogeography of soil microbial abundance and function in 18 grasslands sites from two of the three regions, sampled at one time point. The second study analyzed spatial and temporal distributions of alpha- and beta-diversity of arbuscular mycorrhizal fungi in a low land-use intensity grassland with six sampling time points across one season. The third study investigated both legacy and short-term change effects of land-use intensity, soil physico-chemical properties, plant functional traits, and plant biomass properties on temporal changes in soil microbial abundance, function, and community composition in 150 grassland sites across three regions, with particular regard to direct and indirect land-use intensity effects.

Although the three studies used different approaches and assessed different soil microbial properties, general patterns were detectable. Abiotic soil properties, namely pH, nitrogen content, texture, and bulk density played fundamental roles for spatial and temporal microbial biogeography. Since these factors were specific and unique for each investigated

site, they formed the background based on which other processes occurred. In addition to abiotic soil properties, impacts of land-use intensity and plants were detected, though to various degrees in the three studies. Land-use intensity played a much smaller role than anticipated in the first and third study. No influence on the spatial distribution of soil microbial abundance and function could be detected in the first study. In the third study, short-term changes in and legacy effects of land-use intensity played a minor role with respect to short-term changes in soil microbial abundance, function, and community composition. Where detected, changes in land-use intensity had a direct and negative effect on soil microbial properties in structural equation modelling; i.e., increases in land-use intensity reduced, e.g., soil microbial enzyme activities, while legacy effects of land-use intensity were shown to act both directly and indirectly on soil microbial properties. Thereby indirect legacy effects were mediated via plant functional traits. Only one of the three studies detected minor plant diversity effects on soil microbial properties. Instead, functional properties of the plant communities, i.e., plant functional traits, biomass, and nutritional quality, were significantly related to spatial and temporal distributions of soil microorganisms. Finally, the findings of the three studies suggest that processes related to niche and neutral theory both drive spatial and temporal patterns of soil microbial properties at the investigated plot scale (≤ 50 m × 50 m).

This thesis concluded that in order to gain deeper insights into the complex functions and processes occurring in grassland ecosystems, a multidisciplinary approach investigating fundamental physico-chemical site characteristics, microbial soil properties, and plants is necessary. The results of the thesis suggest that focus be turned to functional properties of plant and microbial communities, as they are closely intermingled, provide more detailed insights into plant-microbe interactions, and are able to reflect effects of human impacts on grassland soils better than diversity measures.

2. Zusammenfassung

Grünlandökosysteme stellen menschlichen Gesellschaften eine große Anzahl an Dienstleistungen zur Verfügung (Allan et al., 2015). Dabei wurden Pflanzen und Mikroorganismen als Schlüsselfaktoren für die Funktionen dieser Ökosysteme identifiziert (Soliveres et al., 2016). Um die Vorgänge in diesen Systemen zu verstehen und vorhersagen zu können, wie sie sich unter verändernden Umweltbedingungen entwickeln werden, ist profundes Wissen über bodenmikrobielle Verteilungen und Prozesse in landwirtschaftlichen Grünländern eine Grundvoraussetzung. Dennoch beginnen wir gerade erst diese komplexen Ökosysteme, die ca. 26 % der weltweiten Landfläche ausmachen (FAOSTATS, 2018), zu verstehen. Dafür ist es insbesondere wichtig, die Effekte von Landnutzungsintensität auf bodenmikrobielle Eigenschaften und die Interaktionen zwischen Pflanzen und Bodenmikroben zu verstehen. Die vorliegende Dissertation diente dem Zweck, die Einflüsse der Landnutzungsintensität von Grünländern auf die Biogeographie von Bodenmikroorganismen in Bezug auf die räumliche Verteilung und zeitliche Veränderung von mikrobieller Biomasse, Funktion (im Sinne von Enzymaktivitäten) und Gemeinschaftsstrukturen aufzudecken und die Beziehungen zwischen Pflanzen und den räumlichen und zeitlichen Verteilungsmustern von Bodenmikroorganismen zu untersuchen. Dabei wurde auch betrachtet, inwieweit die Verteilung der Mikroorganismen den Konzepten der ökologischen Nischen- und Neutraltheorie entspricht. Die Dissertation basiert auf drei beobachtenden Studien, die auf einer bis 150 dauerhaft bewirtschafteten und nicht manipulierten Grünlandflächen durchgeführt wurden. Die Flächen sind verteilt auf drei Regionen in Deutschland und Teil des Schwerpunktforschungsprogramms Biodiversitäts-Exploratorien der Deutschen Forschungsgemeinschaft (DFG 1374).

Die erste Studie untersuchte die Effekte von Landnutzungsintensität und physikalisch-chemischen Bodeneigenschaften auf die räumliche Biogeographie von mikrobieller Biomasse und Funktion zu einem einzelnen Zeitpunkt in 18 Grünlandflächen, die auf zwei Regionen verteilt sind. Die zweite Studie analysierte die räumliche und zeitliche Verteilung der Alpha- und Betadiversität arbuskulärer Mykorrhizapilze (AMF) in einem extensiv genutzten Grünland mittels sechs Probennahmezeitpunkten verteilt über die Vegetationsperiode eines Jahres. Die dritte Studie untersuchte sogenannte „Legacy“-Effekte (d. h., der aktuelle Status oder die zukünftige Veränderung von etwas werden

bedingt durch langfristige oder tiefgreifende Vorgänge in der Vergangenheit (James, 2015)) und kurzfristige Effekte von veränderter Landnutzungsintensität, physikalisch-chemischen Bodeneigenschaften, funktionellen Pflanzeneigenschaften und Charakteristika der pflanzlichen Biomasse auf zeitliche Veränderungen von mikrobieller Biomasse, Funktion und Gemeinschaftsstruktur in 150 Grünlandböden verteilt auf drei Regionen. Dabei waren direkte und indirekte Effekte der Landnutzungsintensität von besonderem Interesse.

Obwohl alle drei Studien unterschiedliche Ansätze verfolgten und verschiedene bodenmikrobielle Eigenschaften untersuchten, sind generelle Muster erkennbar: abiotische Bodeneigenschaften, namentlich pH-Wert, Stickstoffgehalt, Textur und Lagerungsdichte, waren für die räumliche und zeitliche Biogeographie der Bodenmikroorganismen von fundamentaler Bedeutung. Sie waren spezifisch für jede der untersuchten Flächen und bildeten den Hintergrund, vor dem sich andere Prozesse abspielten. Zusätzlich zu den abiotischen Bodeneigenschaften wurden, wenn auch in unterschiedlichem Maße, Einflüsse von Landnutzungsintensität und Pflanzen in den drei Studien detektiert. Die Landnutzungsintensität spielte dabei eine wesentlich geringere Rolle als ursprünglich in der ersten und dritten Studie angenommen. Sie hatte keinen Einfluss auf die räumliche Verteilung der bodenmikrobiellen Biomasse oder Funktion in der ersten Studie. In der dritten Studie waren kurzfristige Veränderungen und Legacy-Effekte nur in geringem Maße mit kurzfristigen Veränderungen von bodenmikrobieller Biomasse, Funktion und Gemeinschaftsstruktur assoziiert. Die Strukturgleichungsmodelle zeigen, dass sich die Effekte von kurzfristigen Veränderung der Landnutzungsintensität, dort wo sie auftraten, direkt und negative auf die kurzfristigen Veränderungen bodenmikrobieller Eigenschaften auswirkten. Das heißt, Steigerungen der Landnutzungsintensität waren zum Beispiel mit Verringerungen von mikrobiellen Enzymaktivitäten verbunden. Dahingegen wirkten sich Legacy-Effekte der Landnutzungsintensität sowohl direkt als auch indirekt auf bodenmikrobielle Eigenschaften aus. Die indirekten Legacy-Effekte wurden dabei über funktionelle Pflanzeneigenschaften auf die Mikroorganismen übertragen. Nur eine der drei Studien fand einen, wenn auch geringen, Einfluss der Pflanzendiversität auf die bodenmikrobiellen Eigenschaften. Stattdessen waren funktionelle Eigenschaften der Pflanzengemeinschaften sowie deren Biomasse und Futterqualität signifikant mit der räumlichen und zeitlichen Verteilung von Bodenmikroorganismen verbunden. In Bezug auf die Nischen- und Neutraltheorie sprechen die Ergebnisse der drei Studien dafür, dass sowohl Prozesse, die mit der Nischentheorie zusammenhängen, als auch solche, die mit der Neutraltheorie in Verbindung stehen, die räumliche und zeitliche Verteilung von bodenmikrobiellen Eigenschaften auf der untersuchten Plotskala (≤ 50 m × 50 m) steuern.

Diese Dissertation zieht die Schlussfolgerung, dass multidisziplinäre Forschung notwendig ist, um die komplexen Funktionen und Prozesse von Grünlandökosystemen zu erforschen. Diese müssen sowohl die fundamentalen physikalischen und chemischen Eigenschaften der Böden, als auch die Eigenschaften der Bodenmikroorganismen und Pflanzengemeinschaften umfassen. Dabei sprechen die Ergebnisse dieser Arbeit dafür, dass ein besonderes Augenmerk auf die funktionellen Eigenschaften von Pflanzen- und Mikrobengemeinschaften gelegt werden sollte, da diese eng miteinander verflochten sind und bessere Einblicke in die Interaktionen zwischen Pflanzen und Mikroorganismen gewähren sowie besser in der Lage sind die Effekte von menschlichen Einflüssen auf Grünlandböden wieder zu spiegeln, als die bisher oft üblichen Diversitätsmessungen.

3. Introduction

Agriculturally managed grasslands are, in the first place, determined to provide fodder for livestock. As permanent meadows and pastures they cover approximately 3331 million hectare worldwide (≈ 26%) (FAOSTATS, 2018) and 13% of the surface of Germany (Statistisches Bundesamt (Destatis), 2017). Grasslands are among the most productive ecosystems, with highly intensive biotic nutrient cycling (Titlyanova, 2007). While net primary production by grasslands is modest in relation to forests, belowground biomass production through root growth is much higher in grassland soils, as is bioturbation (Mason and Zanner, 2005). Underground plant biomass can exceed aboveground biomass by a factor of five, leading to high organic matter inputs into grassland soils. In meadow steppes, 60% of the nitrogen taken up by plants is re-transferred into the soil via dead roots (Bazilevich and Semenyuk, 1986 in Titlyanova, 2007) and 50% to 90% of the net primary production of grassy vegetation is translocated belowground (Titlyanova, 2007). Grassland ecosystems are, therefore, generally considered to be carbon (C)-sinks (Jones and Donnelly, 2004) and on an annual basis, decomposition of fine roots in grasslands is an important source of soil organic matter (Mason and Zanner, 2005).

Worldwide, grassland distribution is closely linked to regional climatic conditions (Mason and Zanner, 2005). Most grasslands in temperate regions are situated on sites too marginal for cropping, e.g., due to limited accessibility with cultivation equipment caused by high groundwater levels and/or reduced percolation of rain water, steep slopes or very shallow soils (Ernst and Rieder, 2000). These site specific conditions also determine whether a grassland site is used intensively or marginally, and whether it is preferably used as grazed pasture, mown meadow or at intermediate management forms. Sites situated on steep slopes, e.g., are prone to be grazed, as machinery use is difficult. The use of a grassland, such as whether it is mowed or grazed, affects the nutrient withdrawal rate from the site. In Germany, e.g., from a herb-rich meadow mowed three times per year and with about 85 dt dry matter (DM) ha^{-1} yield, approximately 210 kg nitrogen (N), 44 kg phosphorus (P), and 216 kg potassium (K) are removed per hectare (Ernst and Rieder, 2000). In contrast, grazing removes 0% to 30% of these nutrients through digestion of fodder by animals, depending on the species of an animal, its age, and use (DLG, 2005). This equates to a removal of approximately 25 kg N, 4 kg P, and 5 kg K in 85 dt DM of grass across all grazer types (sheep, horses, and cows of various age and use); the rest re-enters the soil as patchy distributions of feces and urine. Atmospheric N deposition in Germany on a transect from south-west to north-east ranges from ≈ 9 kg ha^{-1} a^{-1} in Münsingen (Schwäbische Alb), to ≈ 11 kg ha^{-1} a^{-1} in Kammerforst (Hainich-Dün), and to ≈ 10 kg ha^{-1} a^{-1} in Chorin (Brandenburg) on meadows and pastures (UBA, 2018); levels that are negligible in terms of fertilization. It is therefore crucial for farmers to fertilize meadows with organic or mineral fertilizer and to harrow/level pastures to distribute feces more homogeneously and prevent rank patches for sward conservation to ensure long-term productivity of the sites. Intensively managed meadows are mowed up to five times a year in Germany and fertilized with up to ≈ 400 kg N ha^{-1} a^{-1} (Ernst and Rieder, 2000). On pastures, continuous grazing ranges from < 1 livestock unit ha^{-1} a^{-1} (1 livestock unit = 500 kg live weight) on marginally used pastures to up to 3 livestock units ha^{-1} a^{-1} on intensively used sites (LAZBW, 2018). Land management can be characterized by its land-use practices and categorized into the three classes: "pasture" (pure grazing), "mown pasture" (mown and grazed) and "meadow" (pure mowing), or by the intensity of land-use as described by Blüthgen et al. (2012). They used mowing frequency and livestock density together with the N fertilization rate of a site to calculate a land-use intensity index (LUI index):

$$LUI_i = \sqrt{\frac{F_i}{F_{mean,R}} + \frac{M_i}{M_{mean,R}} + \frac{G_i}{G_{mean,R}}}$$

where *i* the site, *F* is fertilization intensity in kg N ha^{-1} $year^{-1}$, *M* is mowing frequency per year, *G* is livestock density for grazing in livestock unit $days^{-1}$ ha^{-1} a^{-1}, and *R* is region. Due to its standardization by mean values within a region, the LUI index is dimensionless. A third option to describe land-use intensity on a grassland site is the nutrient balance of inputs and outputs of the macronutrients N, P, and K by utilization of growth and fertilization.

3.1. Land-use intensity effects on plant communities in grasslands

Land management influences the plant communities of grassland sites. With increasing fertilization, plant communities decline in species number and shift towards species characterized by high biomass production (Milton, 1940; Klaus et al., 2011; Weiner et al., 2011; Socher et al., 2012). Mowing ideally selects for high yield top grasses such as false oat-grass (*Arrhenatherum elatius* (L.) P.Beauv. ex J.Presl & C.Presl), meadow fescue (*Festuca pratensis* Huds.) or Timothy-grass (*Phleum pratense* L.), while grazing promotes leaf-rich bottom grasses with often annual life forms and rosette or stoloniferous life forms such as Kentucky bluegrass (*Poa pratensis* L.) or perennial ryegrass (*Lolium perenne* L.) (Ernst and Rieder, 2000; Pakeman, 2004). Large herbivores tend to preferentially graze on dicotyledons and legumes instead of grasses, while mowing selects for grass rich plant communities. In fact, several studies have found shifts in plant communities towards fast growing species with high leaf P and N content, low leaf dry matter and high specific leaf area (SLA), i.e., the ratio of leaf area to leaf dry weight, with increasing grassland fertilization and use by grazers and mowing (e.g., Pfestorf et al., 2013 and Busch et al., 2018). The aforementioned measures of functional characteristics of plants are termed plant functional traits. According to Garnier et al. (2016) "a trait is any morphological, physiological, or phenological heritable feature measurable at the individual level, from the cell to the whole organism, without reference to the environment or any other level of organization". The functional trait values of individuals can be aggregated across the plant community of a site as community abundance weighted means (CWM). These measures can be used as integrative functional markers of the plant community life strategy (Garnier et al., 2004), as they indicate the adaptation of a plant community to long-term site conditions. The traits leaf N, leaf P, and SLA are part of the leaf economics spectrum (Wright et al., 2004), in which high values of the traits represent fast growing plant species with high biomass turnover, preferentially growing under nutrient-rich site conditions (Reich, 2014). Specific leaf area was, e.g., found to be negatively related to leaf age (Garnier et al., 2016). Therefore, plant communities with high SLA have a high leaf turnover, leading to more litter inputs into the soil. At the same time, they show faster growth rates, which increases rhizodeposition (Aulakh et al., 2001; Herz et al., 2018). Rhizodeposition was also shown to increase due to defoliation by Paterson and Sim (1999). They also detected increased root growth and exudation under low N supply. Garibaldi et al. (2007) found higher litter decomposition rates and N concentrations in plant litter under grazed compared to ungrazed sites. Fertilization, and by that higher availability of nutrients, also increases the amount of nutrients such as N and P in a plant's biomass (Haumann and Dietzsch, 2000; Klaus et al., 2011). Together these processes accelerate the nutrient cycling in soils and provide resources for soil microorganisms.

3.2. Effects of land-use intensity on soil microorganisms and plant-microbe interactions

The microbial communities in soils play a key role in nutrient cycling. They are largely responsible for the decomposition of organic matter and the transformation of organically bound nutrients into mineral forms, e.g., via ammonification, which can be directly utilized by plants. Nitrifying bacteria and archaea facilitate the transformation of ammonium into nitrate, which is the preferred N source of plants, while denitrifiers are cause for gaseous N losses in the forms of N_2 and N_2O from soils (Daims et al., 2016). Microbes also act as nutrient sinks while capturing nutrients in their living or dead biomass, making them temporarily unavailable for plants. The vast majority of extracellular enzymes in soils, such as those involved in degradation of lignin or organic P, are of microbial origin (Das and Varma, 2011; Baldrian, 2014). For example, the microbial function to mineralize organic P compounds by excreting acid and alkaline phosphatase is crucial to make the vast pool of organic P available for plant nutrition. This is especially important at grassland sites with low mineral phosphate fertilization, and crucial to facilitate plant-available P in organically fertilized soils or sites with low phosphate availability. Several studies have shown an increase in microbial biomass and enzyme activity, i.e., microbial functions, in response to increased land-use in terms of fertilization and grazing (Kandeler and Eder, 1993; Bardgett et al., 1998; Wang et al., 2006; Robson et al., 2007), or a decrease with cessation of grazing (Bardgett and Leemans, 1995). It has also been shown that land management can affect microbial community composition (Donnison et al., 2000b). Studying microbial community composition with respect to N and P levels in soils, Leff et al. (2015) found a decrease in mycorrhizae and oligotrophic bacteria with increasing nutrient levels in soils accompanied by an increase in copiotrophic bacteria. Similarly, Bardgett et al. (1999a) found higher fungal:bacterial ratios in unfertilized grasslands compared to intensively managed ones. Addition of N also caused a reduction in fungal biomass in forest soils, without impacting bacterial biomass (Frey et al., 2004). The stronger reaction of fungi compared with bacteria towards soil nutrient concentrations was also shown by Lauber et al. (2008). In contrast, Rousk et al. (2011) described decreases in overall phospholipid fatty acid (PLFA) biomass markers with increasing N fertilization together with strong impacts of pH levels, i.e., reduction in bacterial growth and increase in fungal growth, with decreases in soil pH. This reduction in microbial biomass was also observed as a reaction to urine addition by Orwin et al. (2010), but the effect was context dependent on soil moisture content, thereby indicating that impacts of animal feces on soil microorganisms depend on the environmental conditions of a soil. Denef et al. (2009) did not find significant effects of mowing on soil microbial communities or on their activity, but observed a reduction in fungi due to fertilization. The contradictions between the aforementioned studies may be explained by the differing reactions of microbial species to fertilization, in which, e.g., some fungal species' abundances increase with fertilizer addition, while others are detrimentally affected (Donnison et al., 2000a). In addition, land-use intensity effects may be obscured by plant-microbe interactions at a site. The aforementioned shift in plant community composition towards fast growing species with more easily degradable litter and higher root exudates under increased grassland land-use intensity, results in higher resource availability, especially of more easily degradable resources for soil microorganisms. De Vries et al. (2012), e.g., could show an association of plant functional traits of the "fast" end of the fast-slow life history strategy with bacterial dominated soil microbial communities. Rhizodeposition, which is closely related to root growth and plant nutrient acquisition, has been found to be a major source of C and N for soil microorganisms (Liliensiek et al., 2012). Butenschoen et al. (2008) suggested that an increase in available C was the reason for the observed enhancement of microbial biomass after plant defoliation. The close coupling of soil microorganisms with plants through rhizodeposition was, e.g., reviewed by Paterson (2003). As plants react towards land-use management and they are closely linked to soil microorganism, it is very likely that indirect pathways of land-use intensity effects via plants on soil microorganisms exist. Bardgett and Wardle (2003) reviewed the effects of foliar and root herbivory on soil microorganisms and depicted a wide variety of positive, negative or neutral effects on soil microorganisms depended on the study, methods, and investigated organismal processes. Based on the reviewed studies, they expected higher available resource quantities for soil microorganisms by, e.g., increased root exudation in combination with high amounts of labile nutrients from large animal's urine and feces together with higher proportions of easily degradable litter due to shifts in plant communities towards fast life-history-strategies in nutrient rich ecosystems (see Figure 3-1). In contrast, they proposed negative herbivory effects in nutrient poor systems, where grazing of large animals induces shifts in plant communities towards species with lower litter quality and higher content of secondary plant compounds which in turn reduce decomposition rates.

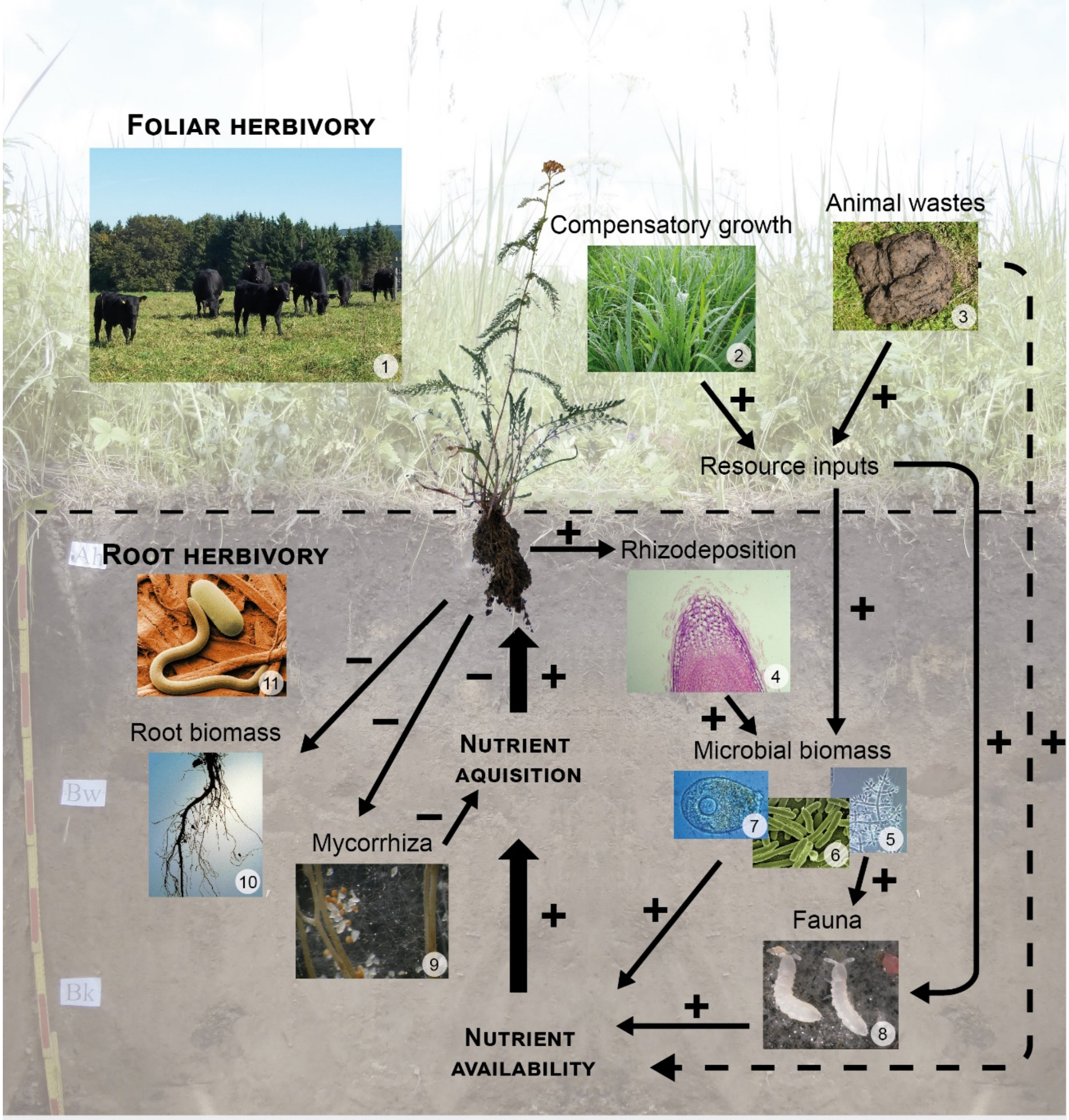

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Figure 3-1: Display of plant-microbe-interactions as feedbacks to foliar and root herbivory in nutrient-rich grassland soils (based on Bardgett and Wardle, 2003). Aboveground defoliation induces compensatory growth as well as increased rhizodeposition and animal feces which together increase the available resources for soil microbial (bacteria, fungi, protozoa) and faunal (e.g., Collembola) organisms. Their activity, in turn, fuels mineralization and thereby nutrient availability for plants. At the same time, mycorrhizal fungi and root biomass are reduced, which negatively impacts nutrient acquisition by plants.

Generally, interactions between plants and soil microorganisms can have positive or negative effects in both directions (Lynch, 1990; Walker et al., 2003; Bais et al., 2006).

Negative effects can, e.g., occur through microbial plant pathogens, or exudation of antibiotic substances by plants as well as increases in tannin content of plant tissues which reduces resource availability for microbes. On the other hand, there are multiple examples of positive plant-microbe interactions. Amongst the most prominent ones are the symbioses between rhizobia and legumes and those between mycorrhizal fungi and plants.

Mycorrhizal fungi play a significant role in the global nutrient cycle as they form symbiotic relationships with almost all plants across multiple ecosystem types: from arable soils to deserts to tropical forests (van der Heijden et al., 2015). Four main types of mycorrhizal fungi have been described up to date, depending on their growth behavior and their symbiotic partners: arbuscular mycorrhizal (AMF), ectomycorrhizal (EMF), ericoid and orchid mycorrhizal fungi. Of these, AMF are the most important type of mycorrhizae in grassland soils. Arbuscular mycorrhizal fungi form tree-like arbuscules inside cortical plant root cells and their hyphae run parallel to the endodermis. An estimated 80% of all plant species live in symbioses with mycorrhizae, of which AMF are the dominant symbionts (Wang and Qiu, 2006), forming symbioses with 74% of angiosperms (Brundrett, 2009). Thereby host-specificity of mycorrhizal fungi appears to be low: the estimated 300 to 1600 AMF taxa form symbioses with approximately 200000 plant species (Brundrett, 2009) and most plants are associated with more than one AMF taxon (Brundrett, 2009; van der Heijden et al., 2015) while a number of them even host more than one type of mycorrhiza, e.g., AMF and EMF (Egerton-Warburton and Allen, 2001). All arbuscular mycorrhizae described to date are obligate mutualists (van der Heijden et al., 2015). By extending the rooting zone of plants, mycorrhizae forage for nutrients such as N and P and supply these to their host plants in return for carbohydrates (Smith and Read, 2008). Up to 90% of plant P demands are supplied by AMF while N supply ranges between 0% and 20%. In return, plants reallocate 10% to 20% of their photosynthates to AMF (van der Heijden et al., 2015). Altogether, the properties of mycorrhizal fungi underscore the importance of soil microorganisms in nutrient cycling and the interconnectivity of plants with soil microorganisms. Some studies have investigated land-use management effects on AMF, with differing results. Gehring and Whitham (1994) showed that in most studies of AMF and EMF, aboveground herbivory reduced the amount of mycorrhizae, likely due to photosynthate limitations, confirming the effect described by Bardgett and Wardle (2003) shown in Figure 3-1. This was challenged by Barto and Rillig (2010), whose meta-data analysis also showed positive effects of herbivory on mycorrhizal colonization in various studies, especially from recent years. In a tallgrass prairie, N fertilization and P amendment increased extraradical arbuscular mycorrhizal hyphae and N addition also increased root colonization (Eom et al., 1999), while opposite effects occurred in a wet oligotrophic meadow (Titus and Lepš, 2000). These differing study outcomes indicate the need for more research on this behalf in the future.

3.3. Spatial and temporal variability of soil microorganisms

Biogeography is the study of distribution patterns of organisms across various spatial and temporal dimensions (Lomolino et al., 2010; Hanson et al., 2012). Thereby spatial variation can occur at local (Regan et al., 2014), regional (Griffiths et al., 2011), and global (Fierer et al., 2009) as well as microscales (Grundmann, 2004), and over depths scales (Fierer et al., 2003), while temporal fluctuations are measurable within a day or season or between different seasons and years (Ramette and Tiedje, 2007; Hanson et al., 2012).

In ecology, two fundamental theories are used to describe the biogeography of organisms: niche theory (Vandermeer, 1972), which assumes environmental causes, i.e., deterministic processes, of species distribution and neutral theory, which assumes that stochastic processes, i.e., probabilistic or random occurrence, drive species distribution (Hubbell, 2001 in Chase, 2014). These fundamental concepts of organismal distribution are broadened in this thesis, following Keil et al. (2011), to include the functions of organisms, e.g., in case of enzyme activities of soil microorganisms. Studies of spatial biogeography most often assess distance-decay relationships of similarity which assume a decrease in organismal community composition similarity with increasing distance between measurement locations as a fundamental pattern of biodiversity (Ramette and Tiedje, 2007; Green et al., 2008; Hanson et al., 2012; Bahram et al., 2013). These distance-decay relationships can, e.g., be determined by measuring spatial autocorrelation, e.g., using variogram analyses, of the members of a community or of community diversity measures (Legendre, 1993; Bahram et al., 2013). Thereby autocorrelation describes the amount of non-randomness in data (Legendre, 1993). Most often, studies of microbial biogeography focus on species distributions of prokaryotes and fungal eukaryotes. The underlying species definition is often based on detected operational taxonomic units (OTUs) to classify microbial taxa. These OTUs are defined by the sequence similarity of nucleotides from one or more regions of a genome; usually 97% similarity thresholds are used (Rousk et al., 2010; Hanson et al., 2012; Prober et al., 2015). The resulting display of spatially explicit distribution patterns is based on four basic ecological processes: selection, drift, dispersal, and mutation (Hanson et al., 2012), of which dispersal is relevant in the context of this thesis. Many studies by now have shown biogeographical patterns of soil microorganisms (for review see Martiny et al., 2006), amongst them distance-decay relationships (e.g., Davison et al., 2015) as well as niche related distribution patterns dependent, e.g., on soil pH (Fierer and Jackson, 2006; Rousk et al., 2010), texture, and organic C (Dequiedt et al., 2011), or moisture content (Lennon et al., 2012). The latter providing evidence for the second part of the theory of Baas Becking (1934) that “everything is everywhere, but the environment selects”. Aside the many studies on the biogeography of soil microbial community composition, the spatial biogeography of microbial biomass and functions, i.e., enzymatic activities, has been assessed (e.g., Berner et al., 2011; for review see Baldrian, 2014). Sinsabaugh et al. (2008) identified soil pH and organic matter content as major influences on soil enzyme activities. Baldrian (2014) specified the environmental influences on soil enzyme activities in his review according to the level of investigated spatial scales, with land-use type and pH, e.g., being important at large scales >1 km^2, while, e.g., soil moisture and tree species were more relevant at the intermediate m^2 scale, followed by, e.g., patches of microbial biomass, nutrients, and roots at the small cm^2 scale. At these small scales, microbial hotspots play an important role in microbial biogeography and have been identified in the resource rich rhizosphere (Spohn and Kuzyakov, 2014), detritusphere (Rønn et al., 1996; Wachinger et al., 2000), and drilosphere (Kuzyakov and Blagodatskaya, 2015; Hoang et al., 2016). Especially the occurrence in the rhizosphere and detritusphere underscore the importance of soil microorganisms in nutrient cycling. At the microscale, microbial associations with organic particles, e.g., plant debris, aggregate surfaces and the formation of bacterial micro-aggregates consisting of bacteria, extracellular polysaccharides, and clay minerals, have been shown (Chenu and Sotzky, 2002) as well as different PLFA distributions among pore size classes (Ruamps et al., 2011).

Apart from spatial variation, soil microorganisms show temporal fluctuations. These are generally regarded to be induced by changes in environmental properties, such as soil moisture and temperature or nutrient availability (Wardle, 1998), but it is still challenging to determine the underlying environmental factors. Temporal fluctuations can occur as relatively short “hot moments” with sudden increases in microbial abundance and activity at a certain spot (Kuzyakov and Blagodatskaya, 2015) and can happen independently of their less variable physico-chemical soil environment (Görres et al., 1998; Stoyan et al., 2000). Pereira e Silva et al. (2012), e.g., showed that temporal changes in bacterial and fungal diversity were not explained by environmental changes, whereas temporal changes in archaeal diversity were correlated to soil pH and nitrate content, indicating greater susceptibility of archaea towards changing environmental conditions than of bacterial or fungal communities. Microbial abundance and activity have been shown to vary across seasons in relation to soil N and moisture content, with highest PLFA content in spring and lowest in autumn, while microbial biomass C and N showed maximum values in summer and minima in winter (Bardgett et al., 1999a). Studies of temporal fluctuations in soil microbial properties vary in their time scales from days (Cruz-Martínez et al., 2012) over months/seasons (Regan et al., 2014) to years (Waldrop and Firestone, 2006). Temporal instability of phosphatase activities within one year was shown by Piotrowska-Długosz et al. (2016). Waldrop and Firestone (2006) observed microclimatic influences on temporal variations in microbial properties in Mediterranean grassland and oak forest soils of California over a period of two years.

Fluctuations in plant and microbial properties also occur due to land-use changes in grasslands. Changes in land-use intensity of wet meadows, for example, led to long-term successional changes in plant diversity and functional composition (Velbert et al., 2017). In addition, Robson et al. (2007) found a reduction in N transformation processes and corresponding microbial enzyme activities due to abandonment of mowing and manuring in subalpine grasslands. In many cases, chronosequence studies of land-use effects (reviewed in Maharning et al., 2009) on soil microorganisms have been carried out on parallel sites with different land-use in the past (e.g., Van Der Wal et al., 2006), often with multiple samplings within one year (e.g., Lauber et al., 2013; Robson et al., 2007), but little is known about the temporal effects of changing land-use intensity on soil microbial properties measured at the same site over several years. Additionally, even though multiple ecosystems have been studied to date, many studies are constrained to a limited number of investigated environmental properties.

With regard to temporal dynamics, an important influence on the current developments of soil microorganisms resolves from past events (Kulmatiski and Beard, 2011). The so called “legacy effects” refer to inherited conditions and describe the development of the current status of a system or its future changes due to effects of the long-term history of a site; in a strict sense the latter is related to anthropogenic influences (James, 2015). The study of legacy effects has gained increasing interest in ecological sciences in recent decades (Foster et al., 2003; Perring et al., 2016), but so far they have rarely been investigated with respect to soil microorganisms. Existing studies have focused, e.g., on climate change greenhouse experiments (Kaisermann et al., 2017) or forest (Janssen et al., 2018) and arable soils (Crotty et al., 2016), but no literature could be found on studies about legacy effects of land-use intensity on changes in soil microorganisms at grassland field sites.

4. Objectives of the thesis

Understanding ecosystem processes and how they drive microbial distribution and function is crucial to gain insights into to be expected changes in nutrient cycles and ecosystem services as a consequence of, e.g., direct human impact or climate change. Much of the aforementioned knowledge of plant-microbe interaction and effects of land-use management on soil microbial processes has been derived from laboratory experiments (e.g., Bardgett et al. 1998), or experimental field studies, such as the Jena Experiment (Marquard et al., 2009). This thesis investigated the effects of land-use intensity on soil microbial processes as well as plant-microbe interactions in "real-world" ecosystems within three observational studies in continuously farmed, un-manipulated grasslands under the temperate climate of Germany. The framework of the German Biodiversity Exploratories project (DFG priority program 1374) with its three regions Schwäbische Alb, Hainich-Dün, and Schorfheide Chorin (see Figure 4-1) provided the unique opportunity to investigate different spatial patterns and temporal fluctuations in soil microbial properties in an interdisciplinary approach with a large number of environmental properties. A detailed description of the three regions is given in Chapter 7.3.

Based on the three studies incorporated in this thesis, the following research questions were investigated: 1) How does land management, especially its intensity, influence the biogeography, i.e., the spatial distribution and temporal changes, of microbial abundance, function, and community composition in grassland soils? and 2) Which relationships exist between plants and the spatial and temporal distribution of soil microorganisms? Thereby it was also considered to which extend the study results speak in favor of a microbial distribution according to niche or neutral theory. It was expected that the same principles would apply in the observational "real-world" studies included in this thesis as in experimentally designed studies, i.e., land-use intensity due to nutrient inputs and plant defoliation was expected to have a strong influence on soil microbial biomass, function, and community patterns with increases in microbial activity and abundance corresponding to increasing land-use intensity, i.e., grazing, mowing and fertilization (Kandeler and Eder, 1993; Hamilton III and Frank, 2001). It was further expected that a close relationship between plant species richness and soil microbes would be detectable (Zak et al., 2003; Eisenhauer et al., 2010), explaining temporal and spatial distribution patterns.

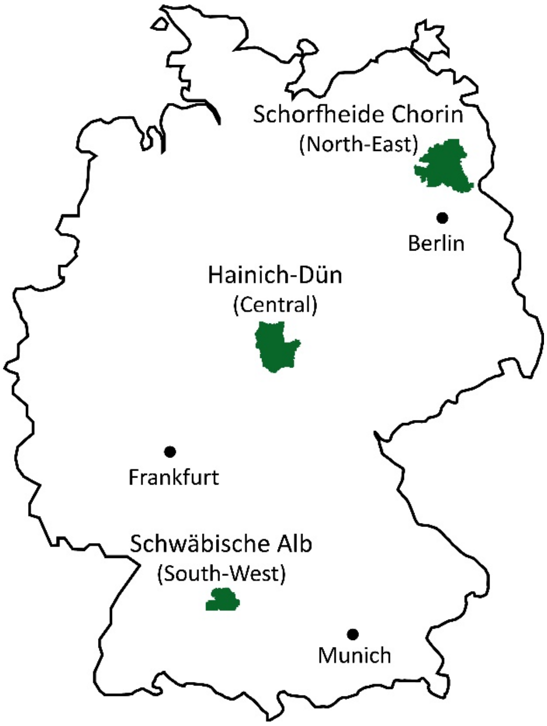

Figure 4-1: The three regions of the Biodiversity Exploratories in Germany. Synonyms used in the presented studies: Schwäbische Alb: Swabian Alb, South-West; Hainich-Dün: Hainich National Park, Central; Schorfheide Chorin: North-East.

The project from which the first study of this thesis (Chapter 5) originated began in 2008, when studies on microbial biogeography at the plot scale of grasslands were scarce and debates on the ecology of soil microorganisms were uprising (Prosser et al., 2007). Its goal was to investigate the impacts of different land-use intensities at 18 grassland sites in two regions, Schwäbische Alb and Hainich-Dün, on the spatial distributions of soil microbial biomass and enzyme activities and to determine other environmental drivers of microbial distribution patterns at a single time point.

The second study arose from the *SCALEMIC Experiment* project starting in 2011, which used a broad interdisciplinary approach to detect temporal fluctuations in spatial patterns of bacterial, fungal, and protozoal communities as well as functions in relation to environmental properties on a single grassland site in the Schwäbische Alb (Regan et al., 2014; Regan et al., 2015; Klaus et al., 2016; Stempfhuber et al., 2016; Regan et al., 2017). The study presented in Chapter 6 investigated distribution patterns of alpha- and beta-diversity of AMF across six sampling time points within one year to clarify whether they are driven by niche-related processes and if so, which environmental properties have the greatest impact on their spatio-temporal distribution patterns.

The third study, presented in Chapter 7, used the platform of the interdisciplinary soil sampling campaigns of the Biodiversity Exploratories in 2011 and 2014 in all three regions, Schwäbische Alb, Hainich-Dün, and Schorfheide Chorin, to gain deeper insights into drivers of temporal variation in soil microbial abundance, community composition, and function across three regions and 150 grassland sites. Thereby the differing impacts of legacy effects and changes in land-use intensity, soil physico-chemical properties, plant functional traits, and plant biomass properties on observed changes in soil microbes were determined.

5. Do general spatial relationships for microbial biomass and soil enzyme activities exist in temperate grassland soils?

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5.1. Abstract

In heterogeneous environments such as soil it is imperative to understand the spatial relationships between microbial communities, microbial functioning and microbial habitats in order to predict microbial services in managed grasslands. Grassland land-use intensity has been shown to affect the spatial distribution of soil microorganisms, but so far it is unknown whether this is transferable from one geographic region to another. This study evaluated the spatial distribution of soil microbial biomass and enzyme activities involved in C-, N- and P-cycling, together with physico-chemical soil properties in 18 grassland sites differing in their land-use intensity in two geographic regions: the Hainich National Park in the middle of Germany and the Swabian Alb in south-west Germany. Enzyme activities associated with the C- and N-cycles, namely β-glucosidase, xylosidase and chitinase, organic carbon (C_{org}), total nitrogen (N_t), extractable organic carbon, and mineral nitrogen (N_{min}) were higher in the Swabian Alb (Leptosols) than in the Hainich National Park (primarily Stagnosols). There was a negative relationship between bulk density and soil properties such as microbial biomass (C_{mic}, N_{mic}), urease, C_{org}, and N_t. The drivers (local abiotic soil properties, spatial separation) of the enzyme profiles (β-glucosidase, chitinase, xylosidase, phosphatase, and urease) were determined through a spatial analysis of the within site variation of enzyme profiles and abiotic

properties, using the Procrustes rotation test. The test revealed that physical and chemical properties showed more spatial pattern than the enzyme profiles. β-glucosidase, chitinase, xylosidase, phosphatase, and urease activities were related to local abiotic soil properties, but showed little spatial correlation. Semivariogram modeling revealed that the ranges of spatial autocorrelation of all measured variables were site specific and not related to region or to land-use intensity. Nevertheless, land-use intensity changed the occurrence of spatial patterns measurable at the plot scale: increasing land-use intensity led to an increase in detectable spatial patterns for abiotic soil properties on Leptosols. The conclusion of this study is that microbial biomass and functions in grassland soils do not follow general spatial distribution patterns, but that the spatial distribution is site-specific and mainly related to the abiotic properties of the soils.

5.2. Introduction

The characterization of spatial relationships of soil microorganisms and their functions in terrestrial ecosystems is a pre-requisite to our understanding of ecosystem function (Ettema and Wardle, 2002). Currently, ecological theories suggest that microbial biogeography is more influenced by local short-term habitat conditions than by dispersal barriers or historical events (Lindström and Langenheder, 2012). Therefore, ecological biogeography suggests that differences in microbial abundance and function are driven mainly by interactions among organisms as well as with their immediate physical and biotic environments. Generally, microbial abundance and function can be determined by local (within habitat) as well as regional factors that operate at scales larger than the habitat. Recent studies have addressed the distribution of soil microorganisms at continental (Fierer and Jackson, 2006), regional (Dequiedt et al., 2011; Griffiths et al., 2011), plot (Ritz et al., 2004; Berner et al., 2011; Keil et al., 2011; Regan et al., 2014), and micro scales (Ruamps et al., 2011). Some of the large scale studies identified a strong influence of soil pH on the biogeography of microbial communities (Fierer and Jackson, 2006; Griffiths et al., 2011). The study of Liu et al. (2015) revealed that the biogeographical distribution of fungal communities was driven mainly by the carbon content of black soils in northeast China. There is also evidence that regional, inter- and intra-site properties might differ in their influence on abundance, diversity and functioning of the soil microbial community (Aşkin and Kizilkaya, 2006; Šnajdr et al., 2008; Berner et al., 2011; Piotrowska et al., 2011).

Long-term nutrient management practices may also have long-lasting effects on the spatial distribution of soil microorganisms as well as on abiotic soil properties (Dao 2014, Lauber et al., 2008; Millard and Singh, 2010; Steenwerth et al., 2006). These studies include the history of land-use which affects the nutrient status of the soil and the composition of plants. Only a limited number of studies have focused on the interactions between site specific soil management and chemical as well as physical soil properties, despite the fact that understanding the spatial organization of microbial functions improves predictions of agro-ecosystem services (Berner et al., 2011; Keil et al., 2011). Prober et al. (2015) and Aşkin and Kizilkaya (2006) found that above-below ground interactions in grassland soils subjected to different management practices may influence the composition and function of soil microorganisms.

To our knowledge no study has investigated the spatial variability of microbial biomass, soil enzyme activities and physico-chemical soil characteristics in grassland soils at four scales: different regions, various land-use intensities, between (inter-site) and within (intra-site) single grassland sites. More importantly, only a few studies on microbial biogeography have used variance partitioning or similar approaches to compare the relative importance of regional versus local factors (Lindström and Langenheder, 2012).

The aim of the present study was to determine whether general spatial relationships of microbial biomass and soil enzyme activities between regions and land-use intensities exist and how they may be affected by physico-chemical soil properties. We selected nine grassland sites in the region of the Hainich National Park, Germany, that differ in their land-use intensity, and analysed them for a number of soil chemical and microbiological properties. These results were compared with an equivalent data set from a second region, the Swabian Alb, published by Berner et al. (2011). The two selected regions differ in their climatic and topographic conditions as well as their soil types. We hypothesized that 1) higher land-use intensity would result in greater spatial homogeneity of both physico-chemical and biological soil properties, due to a more homogenous treatment of the site in terms of mowing and fertilizing. In addition we wanted to test whether 2) spatial dependence was more important for the distribution of soil enzyme activities than physico-chemical soil properties and whether 3) land-use intensity was the strongest driver of microbial biomass and soil enzyme activities, independent of region and site.

5.3. Materials and Methods

5.3.1. Sampling sites

For the present study, nine grassland sites from the Hainich National Park region (HEG sites) were compared with nine sites from the Swabian Alb region (AEG sites) in an on-farm research approach. All the study sites belong to the German Biodiversity Exploratories (www.biodiversity-exploratories.de). At the time of sampling, the sites had been managed by farmers as continuous grasslands for more than 16 years under three different land-use intensity regimes, ranging from hardly managed, grazed pastures to frequently mowed and fertilized pastures and meadows (LUI classes as defined by Fischer et al. (2010)). In each region, samples were taken from three unfertilized pastures (low LUI class), three moderately fertilized and mowed pastures (intermediate LUI class) and three highly fertilized and mowed meadows (high LUI class) (Table 5-1). Although the overall management of the sites was grouped into three LUI classes, the grazing, mowing and fertilization intensities were specific to each site (Blüthgen et al., 2012). For a detailed description see Table S5-1. The Hainich National Park is located in the centre of Germany, at an altitude of between 285 and 450 m above sea level and the Swabian Alb is located in southwestern Germany at an altitude of 660 to 808 m above sea level (Fischer et al., 2010). Although mean annual temperatures are comparable (6.5–8.0 °C in the Hainich National Park, 6.0–7.0 °C in the Swabian Alb), they differ in annual precipitation: 500–800 mm in the Hainich National Park and 700–1000 mm in the Swabian Alb (Fischer et al., 2010). The regions are characterized by different geological formations and soil types: calcareous bedrock is found underneath Stagnosols in the Hainich National Park, while calcareous bedrock with karst phenomena lay underneath Leptosols in the Swabian Alb (Fischer et al., 2010).

Table 5-1: Soil and land use characteristics for the nine investigated grassland sites at the Hainich National Park (HEG sites) and the Swabian Alb (AEG sites). Soil classification according to the World Reference Base of Soil Resources, LUI = land-use intensity, v. = vertic, l. = luvic, r. = rendzic, eu = eutric, si = siltic, Camb. = Cambisol, Stagn. = Stagnosol. HEG7 was fertilized with manure once in 2006.

Site[b]	Elevation m a.s.l.[c]	Slope %[c]	Longitude[c]	Latitude[c]	Soil type[d]	Land use type[b]	Animals[b]	# Cuts[b]	Fertilization[b]	LUI class[b]	LUI index 2006-2008[a]	Shannon Diversity[e]
HEG1	292	5	10°24‘19.3“	50°58'17.9“	v. Camb. (eu)	Meadow	-	2	yes	high	2.65	2.5
HEG2	288	4	10°25‘48“	51°0‘2.7“	v. Stagn. (eu)	Meadow	-	3	yes	high	2.74	2.1
HEG3	286	4	10°25‘58.6“	50°59‘53.1“	v. Stagn. (eu)	Meadow	-	3	yes	high	2.74	2.5
HEG4	285	4	10°26‘10.2“	51°6‘48.1“	v. Stagn. (eu)	Mown Pasture	Cattle	1	yes	intermediate	1.96	1.8
HEG5	450	5	10°19‘21.1“	51°12‘57.2“	v. Stagn. (eu)	Mown Pasture	Cattle	2	yes	intermediate	2.42	1.7
HEG6	299	3	10°23‘28.4“	51°12‘53.8“	l. Stagn. (si)	Mown Pasture	Cattle	1	yes	intermediate	2.07	2.2
HEG7	290	3	10°24‘37.5“	51°16‘24.9“	v. Stagn. (eu)	Pasture	Cattle	-	yes	low	1.89	2.9
HEG8	296	4	10°25‘4.6“	51°16‘16.5“	v. Stagn. (eu)	Pasture	Cattle	-	no	low	1.86	2.5
HEG9	325	2	10°22‘50.8“	51°13‘26“	v. Stagn. (eu)	Pasture	Cattle	-	no	low	0.78	2.5
AEG1	691	3	9°20‘31.2“	48°23‘52.8“	r. Leptosol	Meadow	-	2	yes	high	1.81	1.0
AEG2	753	6	9°28‘22“	48°22‘36.7“	r. Leptosol	Meadow	-	3	yes	high	2.55	1.4
AEG3	808	3	9°31‘56.6“	48°24‘32“	r. Leptosol	Meadow	-	2	yes	high	2.19	1.3
AEG4	660	11	9°25‘8“	48°22‘51.2“	r. Leptosol	Mown Pasture	Cattle	1	yes	intermediate	1.85	2.1
AEG5	718	3	9°26‘21.1“	48°23‘45.2“	r. Leptosol	Mown Pasture	Cattle/Horses	1	yes	intermediate	1.99	1.4
AEG6	711	7	9°26‘30“	48°24‘4.5“	r. Leptosol	Mown Pasture	Cattle/Horses	1	yes	intermediate	2.89	2.0
AEG7	795	10	9°22‘36.6“	48°23‘29.1“	r. Leptosol	Pasture	Sheep	-	no	low	0.53	2.1
AEG8	760	4	9°29‘31.6“	48°25‘21.5“	r. Leptosol	Pasture	Sheep	-	no	low	1.27	1.9
AEG9	743	13	9°30‘10.1“	48°23‘40.8“	r. Leptosol	Pasture	Sheep	-	no	low	0.58	2.7

[a] Blüthgen et al., 2012; [b] Fischer et al., 2010; [c] Nieschulze, 2010; [d] Herold et al., 2014; [e] Socher et al., 2012

5.3.2. Soil sampling

Soil sampling and analyses were similar in both regions. Sampling in the Hainich National Park took place in April 2008, one week after sampling in the Swabian Alb, at the start of the vegetation period, using a spatially explicit sampling regime: a raster of nine grid points, 2.5 m apart one from the other, was placed in the middle of a 10 x 10 m site. Starting from each grid point, samples were taken along a spatially randomized spiral with decreasing inter-sample distances: 1.5 m, 1 m, 0.5 m, 0.25 m, and 0.125 m as described by Keil et al. (2011). In total, 54 spatially referenced samples were taken per site, resulting in a total of 486 samples in each of the two regions. Soil samples were taken using core augers (internal diameter of 5.8 cm) from the top 10 cm depth and cooled immediately to 4 °C. Two intact cores were taken from each sampling location; the first was used to determine the bulk density and the second for chemical and biological analyses. The latter sample was sieved to 2 mm. Stones and plant material were removed as was the litter layer (top 1 cm). The samples were stored at -20 °C until use.

5.3.3. Analyses

Bulk density (BD) was determined after drying the soil core at 105 °C for three days. The soil water content (SWC) was determined gravimetrically by drying the samples until constant weight was reached (105 °C for 24 hours). The SWC used for calculations in this paper was related to the water holding capacity (WHC), published by Birkhofer et al. (2012), of each site. Soil organic C (C_{org}) and total N (N_t) were measured with the MACRO CNS Elemental Analyzer (Elementar Analysensysteme GmbH, Hanau, Germany) according to ISO 10694:1995 (1996) and DIN ISO 13878 (1998), respectively. The soil pH was analysed with a pH-meter (ProfiLabph 597, WTW Wissenschaftlich-Technische Werkstätten GmbH, Weilheim, Germany) in 0.01 M $CaCl_2$ (1:2.5 soil:$CaCl_2$). Mineral nitrogen (NH_4^+ and NO_3^-) was determined following DIN ISO 14256-2 (2006) using an AutoAnalyzer 3 (Bran & Luebbe, Norderstedt, Germany).

Microbial biomass carbon (C_{mic}) and nitrogen (N_{mic}) were measured using the chloroform-fumigation-extraction method (CFE) according to Vance et al. (1987). C and N were extracted from each fumigated and non-fumigated replicate (10 g) with 40 ml 0.5 M K_2SO_4 as described by Keil et al. (2011). C and N concentrations in extracts were measured with a TOC/TN analyzer (Multi N/C 2100S, Analytik Jena AG, Jena, Germany). Microbial C and N were calculated using the k_{EC} factor given by Joergensen

(1996) and the k_{EN} factor of Brookes et al. (1985), respectively. Extractable organic carbon (EOC) and extractable nitrogen (EN) were determined from the non-fumigated samples.

The following soil enzyme activities were determined: β-glucosidase (EC 3.2.1.21), xylosidase (EC 3.2.1.37), chitinase (β-N-acetylglucosaminidase, EC 3.2.1.52), phosphatase (EC 3.1.3.1), and urease (EC 3.5.1.5). With the exception of urease, all enzymes were determined according to the method of Marx et al. (2001) using fluorescent 4-methylumbelliferone substrates (4-MUF; Sigma-Aldrich, St. Louis, USA) and a buffered solution of pH 6.1, as described in detail by Berner et al. (2011). Urease activity was measured photometrically after Schinner et al. (1996), using 1 g of fresh soil that was incubated for 2 hours at 37 °C with 1.5 ml 0.08 M urea solution. As the majority of soil enzymes are of microbiological origin (Das and Varma, 2011), they are used as a proxy for microbial functions in this study.

5.3.4. Statistical analyses

All statistical analyses were carried out in R version 3.0. (R Core Team, 2013). Kriging was performed with ArcGIS 10 (ESRI 2011. ArcGIS Desktop: Release 10. Redlands, CA: Environmental Systems Research Institute). Multivariate analyses were carried out on abiotic soil properties (C_{org}, N_t, NH_4^+, NO_3^-, EN, EOC, pH, BD and SWC) and on enzyme profiles (β-glucosidase, chitinase, xylosidase, phosphatase, and urease).

The relationships among variables were tested by Spearman's rank correlation using a Bonferroni adjusted *P*-value (confidence interval 95%, level of significance = $P < 0.05$). Correlations among variables were computed for all samples within a region. To determine how the different variables of interest were affected by land-use intensity, both the LUI index developed by Blüthgen et al. (2012) and the LUI classes (Fischer et al., 2010) were used. While the LUI classes account categorically for sites being mowed, grazed or fertilized, the LUI index (Blüthgen et al., 2012) accounts numerically for the intensities of mowing, nitrogen fertilization and grazing and is, therefore, a metric that reflects the specific management practices at each site. The details of how to calculate the LUI index can be found in Blüthgen et al. (2012).

One way ANOVAs were used to determine significant differences between the two regions and the three LUI classes, separately as independent factors. ANOVAs were performed with the R package "stats" (R Core Team, 2013) after the data were checked for normality of distribution and homogeneity of variance. Tukey's HSD test (package "agricolae" by de Mendiburu (2013)) was performed separately for the LUI classes and sites to evaluate significant differences ($P < 0.05$) between the mean values of all measured variables.

The association between enzyme profiles and abiotic soil property matrices (subdivided into groups of abiotic-C [C_{org}, EOC], abiotic-N [N_t, NH_4^+, NO_3^-, EN] and other abiotic properties [pH, BD, and SWC]) and the spatial coordinates matrix was determined by Procrustes rotation using the "protest" function in "vegan" (Oksanen et al., 2013). The Procrustes rotation is a method for determining the similarity between multivariate datasets (Peres-Neto and Jackson, 2001). The relationships between enzyme profiles and abiotic property matrices were determined to identify how local soil properties affect profiles of enzymes activities. The relationship between enzyme profiles and the spatial coordinates matrix was used to identify spatial autocorrelation in the enzyme profiles. One way ANOVAs and pairwise t-tests were used to identify significant differences between the Procrustes rotation results.

The spatial structure of each of the variables was determined by semivariance analyses, after transforming data where necessary, using the R package "gstat" (Pebesma, 2004). The analysis involves computing the semivariance of a variable as a function of inter-sample separation distance (empirical semivariograms). The semivariograms are characterised by three parameters (Ettema and Wardle, 2002; Regan et al., 2014): the semivariance increases as a function of inter-sample distance until it reaches a plateau. This plateau is the sill and represents the total variability in the dataset. The distance at which the sill is reached is called the range. The range indicates the distance over which a variable is spatially autocorrelated. At the origin, semivariograms often show a discontinuity, the nugget effect, which reflects measurement error or the variation present at scales below the scale of sampling (i.e. minimum inter-sample separation distance). The partial sill (psill) is calculated by subtracting the nugget from the sill. Empirical semivariograms were computed for all variables measured at each of the sites. In order to determine the characteristic parameters of the semivariograms, different models (exponential (Exp), spherical (Sph) and linear (Lin), according to McBratney and Webster (1986) and Goovaerts (1998)) were fitted to the empirical semivariograms using the "automap" R package (Hiemstra et al., 2009). The model that resulted in the smallest residual sum of squares was chosen to characterize the semivariograms. The empirical semivariograms that displayed no spatial structure (i.e. no trend in semivariance as a function of inter-sample separation distance) were termed pure nugget semivariograms. In cases where a model could be reasonably fitted to an empirical semivariogram, this was defined as a detected spatial pattern. The percent structural variance, which describes how much of the variance is spatially correlated, was calculated as the psill to sill variance ratio multiplied by 100.

Variance components analysis was used to determine which factors (LUI class, inter-site, and intra-site) explained most of the variance in each of the variables using the "lme" and "VarCorr" functions in R from the "nlme" package (Pinheiro et al., 2013). Principal component analyses were carried out on enzyme profiles and abiotic soil properties in order to determine how biotic and abiotic properties varied overall as a function of regional and land-use intensity differences. This was done using the R package "vegan" (Oksanen et al., 2013). The PCA site scores were then treated as variables in univariate analyses of variance using the using the "lme" and "anova" functions from the "nlme" package (Pinheiro et al., 2013) to determine if the enzyme profiles or abiotic variables were significantly separated by regions or LUI classes.

5.4. Results

5.4.1. Abiotic and biotic soil properties in the Hainich National Park

In the Hainich National Park, the highest amounts of total nitrogen and organic carbon were found in the lowest LUI class, especially in the HEG7 and HEG8 sites (Figure 5-1a-b, Table S5-2a). Similar trends were observed for many of the other variables, namely, N_{min}, EOC, EN, C_{mic}, N_{mic}, and the activities of β-glucosidase, xylosidase, chitinase and urease (Figure 5-1 and Figure 5-2, Table S5-2a). The HEG6 site (intermediate LUI class) had the highest bulk density of all the Hainich sites and the lowest values for most of the other variables.

The correlation analysis, which was performed to determine the relationships between variables, revealed that only EOC showed a strong (negative) correlation with the LUI index (Table S5-3a). We also found strong positive correlations of C_{org} with N_t, N_{min}, EN, C_{mic}, N_{mic}, and urease activity. Urease was more closely correlated with C_{mic} than the enzymes involved in C- and P-cycling. Urease, xylosidase, and β-glucosidase activities were strongly correlated with each other. Phosphatase activity showed a strong negative correlation with soil pH. The water holding capacity of each site (Birkhofer et al., 2012) had a stronger influence on the biological soil properties than the soil water content at the time of sampling (Table S5-3a). There were negative relationships between the sand content, measured by Herold et al. (2014), and a number of biological properties, i.e. C_{mic}, N_{mic}, β-glucosidase, xylosidase and urease. Clay was positively correlated with urease and negatively correlated with phosphatase. The latter was positively correlated with silt, as was pH.

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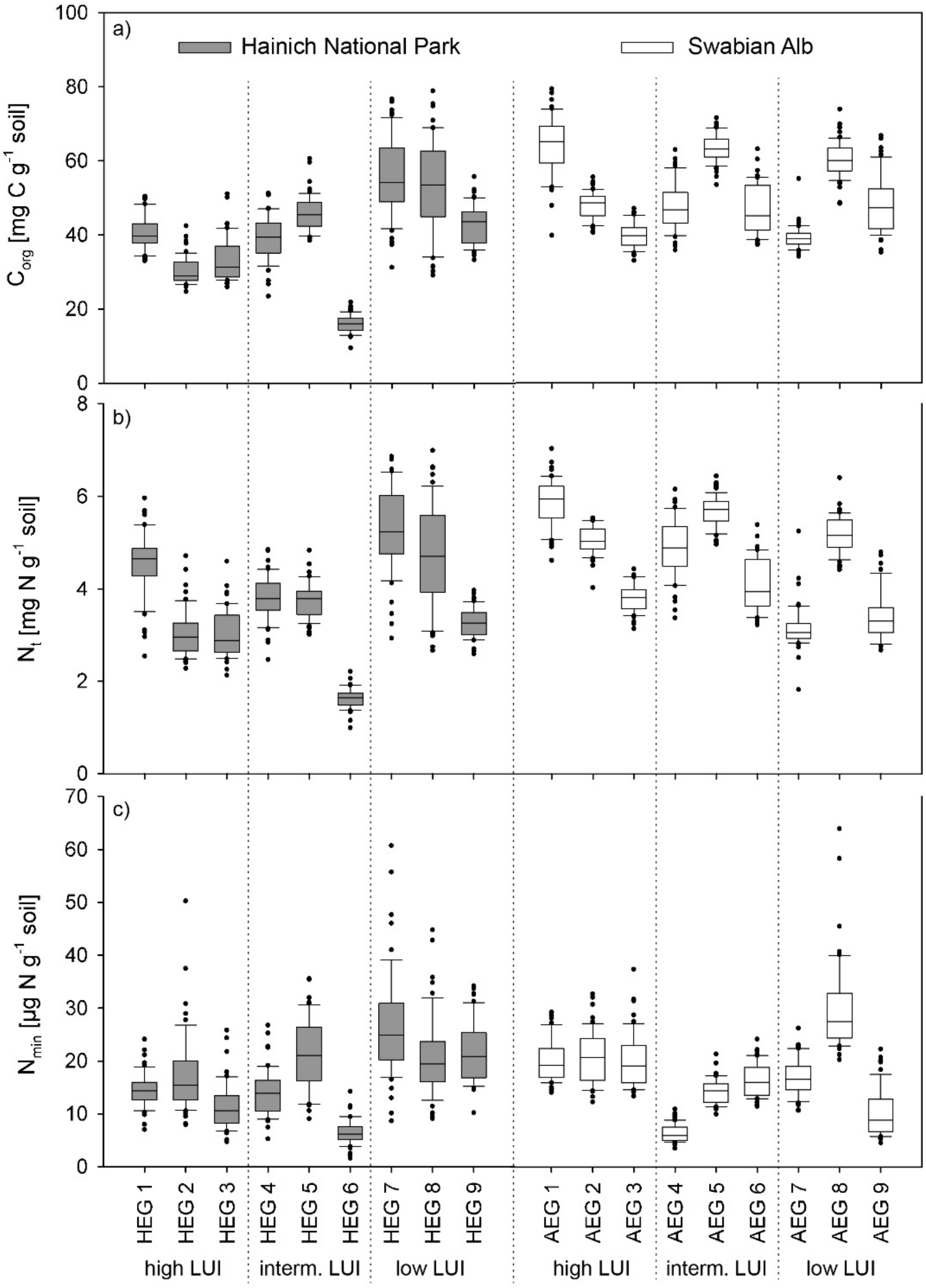

Figure 5-1: a) organic carbon (C_{org}), b) total nitrogen (N_t) and c) mineral nitrogen (N_{min}) content of all 18 sites from the Hainich National Park (HEG1–9) and the Swabian Alb (AEG1–9). The boxes show the median surrounded by the 25th and 75th percentiles, error bars indicate the 90th and 10th percentiles.

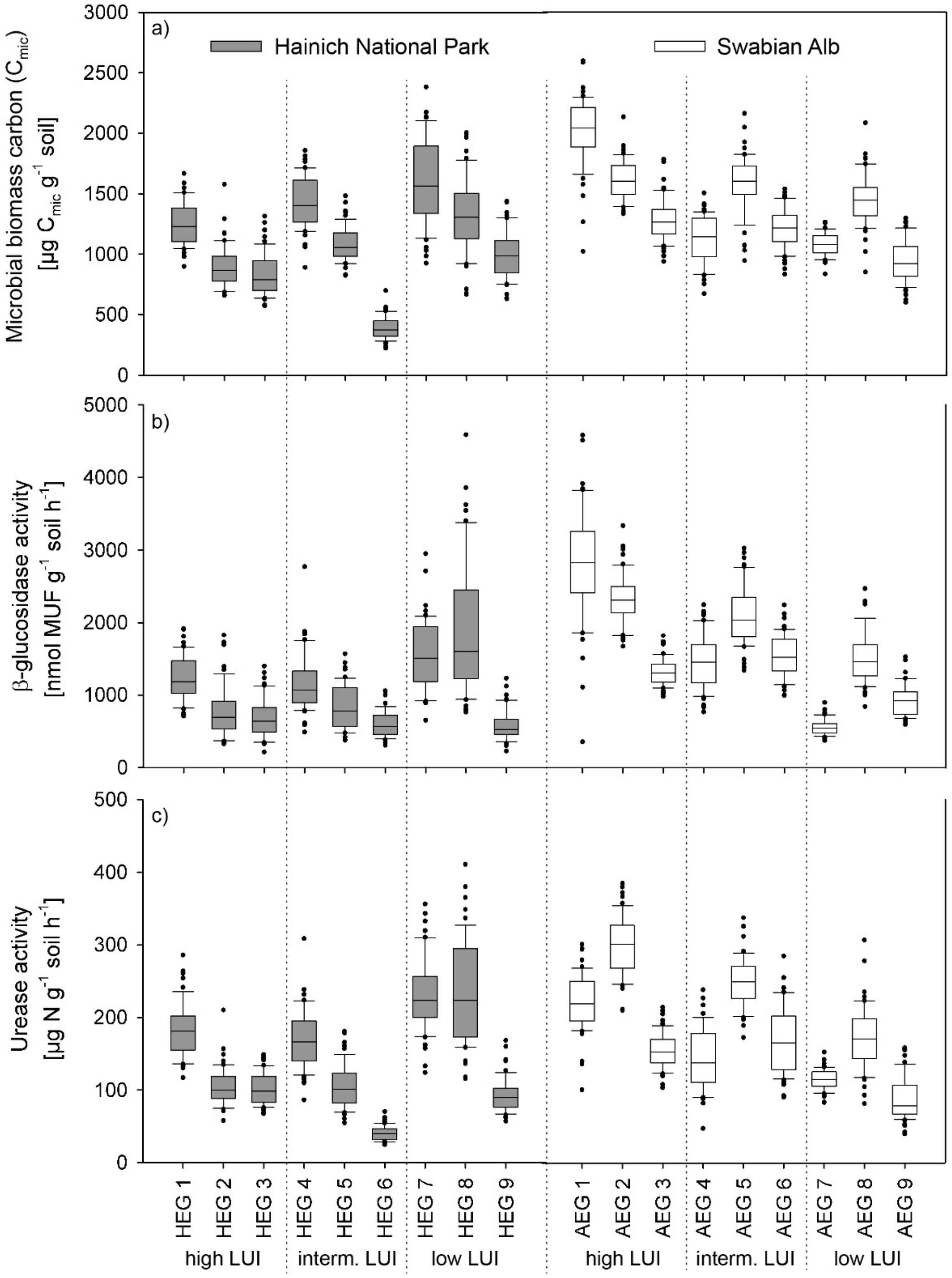

Figure 5-2: a) microbial biomass carbon (C_{mic}), b) β-glucosidase activity and c) urease activity of all 18 sites from the Hainich National Park (HEG1–9) and the Swabian Alb (AEG1–9). The boxes show the median surrounded by the 25th and 75th percentiles, error bars indicate the 90th and 10th percentiles.

5.4.2. Spatial variability of soil properties

In order to evaluate the relationship between soil enzyme activities and their environment, the Procrustes rotation test was used. It showed that the enzyme profiles were generally more strongly significantly correlated with the abiotic soil properties in both regions, and less frequently significantly correlated with the spatial coordinate data (Table 5-2). We found that the relationship between enzymes and the group of SWC, BD and pH was strongest (15 out of 18 sites showed a significant correlation and the strongest correlations were found here), followed by that of enzymes and abiotic-N (14 out of 18 sites showed a significant correlation). Significant correlations between the spatial matrix and the enzyme matrix were found in only nine out of the 18 sites. Pairwise t-tests on the Procrustes rotation results revealed that the abiotic-N group and the group of SWC, BD and pH, were more significantly related to the soil enzyme activity profiles than was the spatial data ($P = 0.04$ and $P = 0.001$, respectively). One way ANOVAs showed that the significance level was only significantly affected by region in the case of the group of SWC, BD and pH versus spatial coordinate's data ($F_{1,\,18} = 11$; $P = 0.004$), where more significant correlations were found in the Swabian Alb than in the Hainich National Park. Of the abiotic-C variables, the interaction between region and land-use intensity had a significant effect on the number of significant correlations ($F_{5,\,18} = 5.6$; $P = 0.007$).

Semivariogram models were used to determine the influence of land-use intensity on the plot scale spatial distribution (10 x 10 m scale) of chemical and biological properties at each site. The number of spatially structured variables at each site varied considerably (Table S5-4), e.g., only three variables were spatially structured in HEG2, but 16 were in AEG5; pH showed a spatial pattern at 14 sites, phosphatase at four. Over all sites the percentage of spatially structured variables was higher for the abiotic than for the biotic variables (Figure 5-3).

Table 5-2: Correlations between all enzymes (Enz.), abiotic-N (N_t, NH_4^+, NO_3^-, EN), abiotic-C (C_t, EOC), other abiotic factors (o. abiotic factors = SWC, pH, BD) and space as derived from the Procrustes test. Numbers give the correlation coefficient of rotation (CoR); significance levels: $^{*} = P \leq 0.05$; $^{**} = P \leq 0.01$; $^{***} = P \leq 0.001$; correlations are considered weak if $0.3 < \mathrm{CoR} < 0.5$ and strong if $\mathrm{CoR} > 0.5$.

Site	Enz.vs. space	abiotic-N vs. Enz.	abiotic-C vs. Enz.	o. abiotic factors vs. Enz.	Site	Enz.vs. space	abiotic-N vs. Enz.	abiotic-C vs. Enz.	o. abiotic factors vs. Enz.
HEG1	0.276^{*}	0.310^{*}	0.406^{**}	0.463^{**}	AEG1	0.330^{*}	0.228	0.191	0.575^{***}
HEG2	0.249	0.275^{*}	0.501^{***}	0.514^{**}	AEG2	0.240	0.285^{*}	0.233	0.420^{**}
HEG3	0.350^{**}	0.382^{**}	0.396^{**}	0.562^{***}	AEG3	0.207	0.236	0.168	0.220
HEG4	0.285^{*}	0.442^{***}	0.208	0.571^{***}	AEG4	0.305^{*}	0.637^{***}	0.588^{***}	0.701^{***}
HEG5	0.186	0.285^{*}	0.334^{**}	0.283^{*}	AEG5	0.274^{*}	0.439^{***}	0.374^{**}	0.525^{***}
HEG6	0.177	0.127	0.184	0.196	AEG6	0.362^{**}	0.517^{***}	0.529^{***}	0.493^{***}
HEG7	0.199	0.319^{**}	0.154	0.390^{**}	AEG7	0.315^{**}	0.183	0.227	0.216
HEG8	0.145	0.468^{***}	0.446^{**}	0.502^{***}	AEG8	0.166	0.373^{**}	0.162	0.378^{**}
HEG9	0.213	0.286^{*}	0.090	0.348^{**}	AEG9	0.291^{*}	0.382^{**}	0.162	0.387^{**}

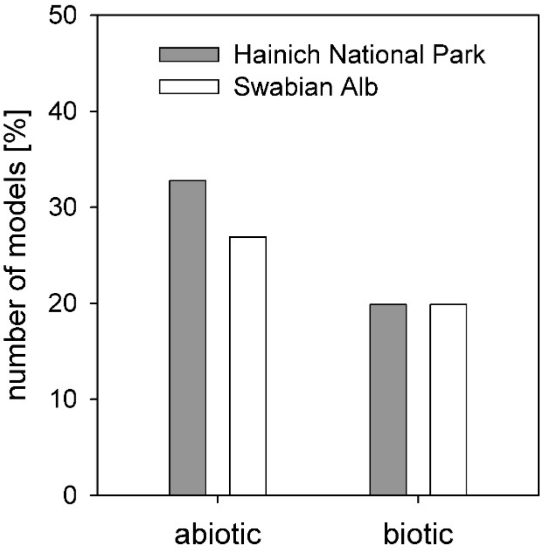

Figure 5-3: Number of semivariogram models (exponential, spherical and linear) in the Hainich National Park and the Swabian Alb that could be fit for abiotic (C_{org}, N_t, C_{org}:N_t ratio, NH_4^+, NO_3^-, N_{min}, extractable nitrogen (EN), extractable organic carbon (EOC), pH, bulk density (BD), and soil water content (SWC)) and biotic (C_{mic}, N_{mic}, β-glucosidase, chitinase, xylosidase, phosphatase, and urease) soil properties.

The ranges varied among enzymes: most ranges were below 2 m with single outliers (Table S5-4). Urease was the most spatially structured enzyme activity. The spatial patterns of the different enzymes were not similar. Exemplary distributions (urease and xylosidase at the HEG1 site) showing differences are displayed in Figure 5-4. With increasing land-use intensity, abiotic properties tended to become less spatially structured in the Hainich National Park, but more so in the Swabian Alb. Spatial structure decreased in the enzyme data as land-use intensity increased. This was true in both regions, though the decline was greater in the Hainich National Park than in the Swabian Alb.

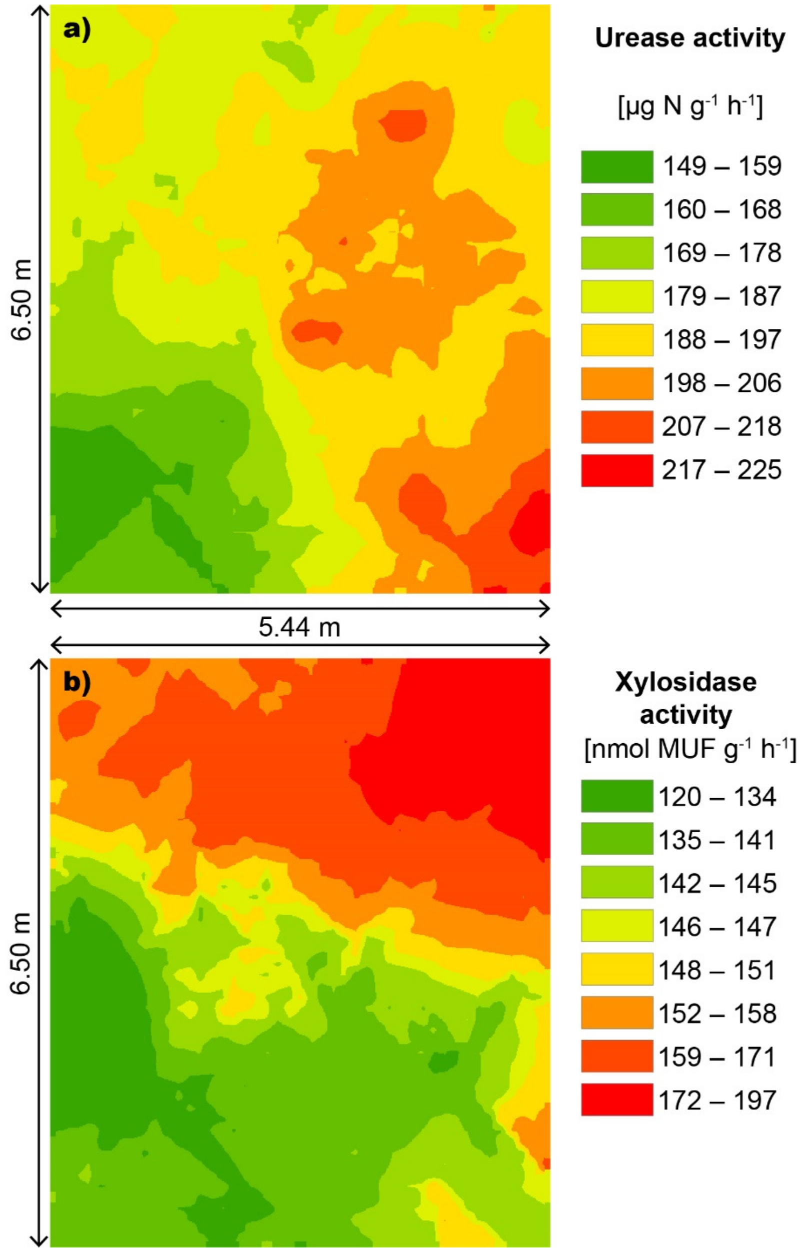

Figure 5-4: Kriging maps of a) urease activity and b) xylosidase activity of the Hainich National Park site HEG1.

5.4.3. Land-use intensity effects in relation to regional and site specific variations

The one way ANOVAs on data from both regions, Hainich National Park and Swabian Alb, indicated that the variables were principally affected by regional variations (Figure 5-1 and Figure 5-2). The grassland sites of the Swabian Alb showed significantly higher C_{org} ($F_{1,\,927}$ = 635.6; $P < 0.001$) and EOC ($F_{1,\,927}$ = 846.9; $P < 0.001$) values together with significantly higher urease activities ($F_{1,\,927}$ = 62,6; $P < 0.001$) and significantly lower C_{mic}/N_{mic} ratios ($F_{1,\,927}$ = 1227; $P < 0.001$) than the Hainich National Park; although similar trends were observed for N_t, N_{min} and microbial biomass content as well as other enzyme activities, these were not significant. The C_{org}/N_t ratio of both regions ($F_{2, 926} = 111$; $P < 0.001$) was significantly affected by LUI classes and ranked them high LUI < intermediate LUI < low LUI. Urease activity ($F_{2, 926} = 13.9$; $P < 0.001$) was significantly higher in the high LUI class than in low and intermediate LUI classes.

Principal component analyses (PCA) were carried out in order to identify overall patterns in abiotic soil properties and enzyme profiles related to regional or land-use intensity differences. These tended to confirm the results of the ANOVAs. There was a pronounced ($F_{1, 12} = 55.1$; $P < 0.001$) regional effect, visible along the first PC axis (which accounted for 61% of the total variance; Figure 5-5a) of the ordination of abiotic properties. No significant land-use intensity effect was visible along either the first or second (explaining 13% of the total variance) ordination axes. The regional separation was due to the fact that all variables had higher values in the Swabian Alb region, apart from pH and bulk density, which were highest in the Hainich National Park (Figure 5-5a). Samples with high bulk density from one site (HEG6) were different from all the other sites. A similar picture emerged from the analysis of the enzyme profiles in that the regional effect ($F_{1, 12} = 32.67$; $P < 0.001$) was seen along the first PC axis (which accounted for 74% of the total variation in the data; Figure 5-5b). The separation between regions was due to overall higher enzyme activities in the Swabian Alb region compared to the Hainich National Park. Additionally, a slightly significant interaction ($F_{2, 12} = 4.21$; $P = 0.041$) was found between region and LUI class on the first ordination axis. Along the second PC axis (17% of the total variance) land-use intensity ($F_{2, 12} = 3.05$; $P = 0.085$) did not clearly affect the distribution, while the regional effect was significant ($F_{1, 12} = 7.35$; $P = 0.019$).

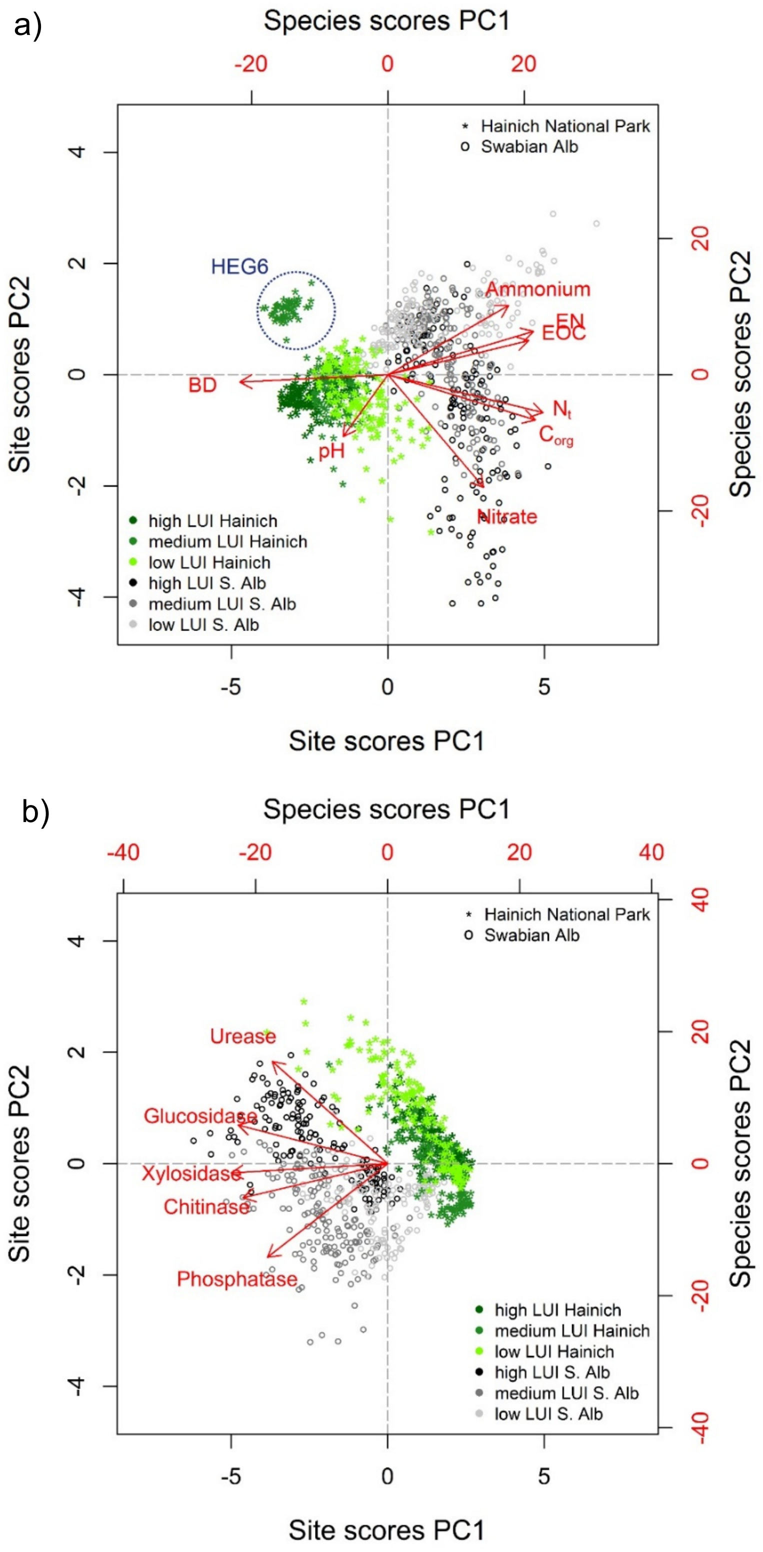

Figure 5-5: PCA-results for a) abiotic (C_{org}, N_t, ammonium, nitrate, EN, EOC, pH, BD, and SWC) variables, PC1 explains 61%, PC2 13% of the variance; and b) enzymatic variables (activities of β-glucosidase, chitinase, xylosidase, phosphatase, and urease), PC1 explains 74%, PC2 17% of the variance. Printed are the site scores for the regions and LUI classes as dots and the species scores in form of arrows with variable names.

Variance components analysis was used to determine the scale at which the soil properties varied in the two regions: LUI class, inter-site, or intra-site variation. Most of the variance in both regions was explained by inter-site variation, followed by intra-site variation and LUI class (Figure 5-6a and b). The proportion of variation explained by the three factors differed between the regions, however. In the Hainich National Park LUI class was dominant for EOC, EN and C_{mic}/N_{mic} (54%, 50% and 54%, respectively), while in the Swabian Alb, LUI class explained most of the variance for pH, C_{org}/N_t, nitrate, xylosidase, and phosphatase (54%, 49%, 48%, 45%, and 77%, respectively). Intra-site variation was

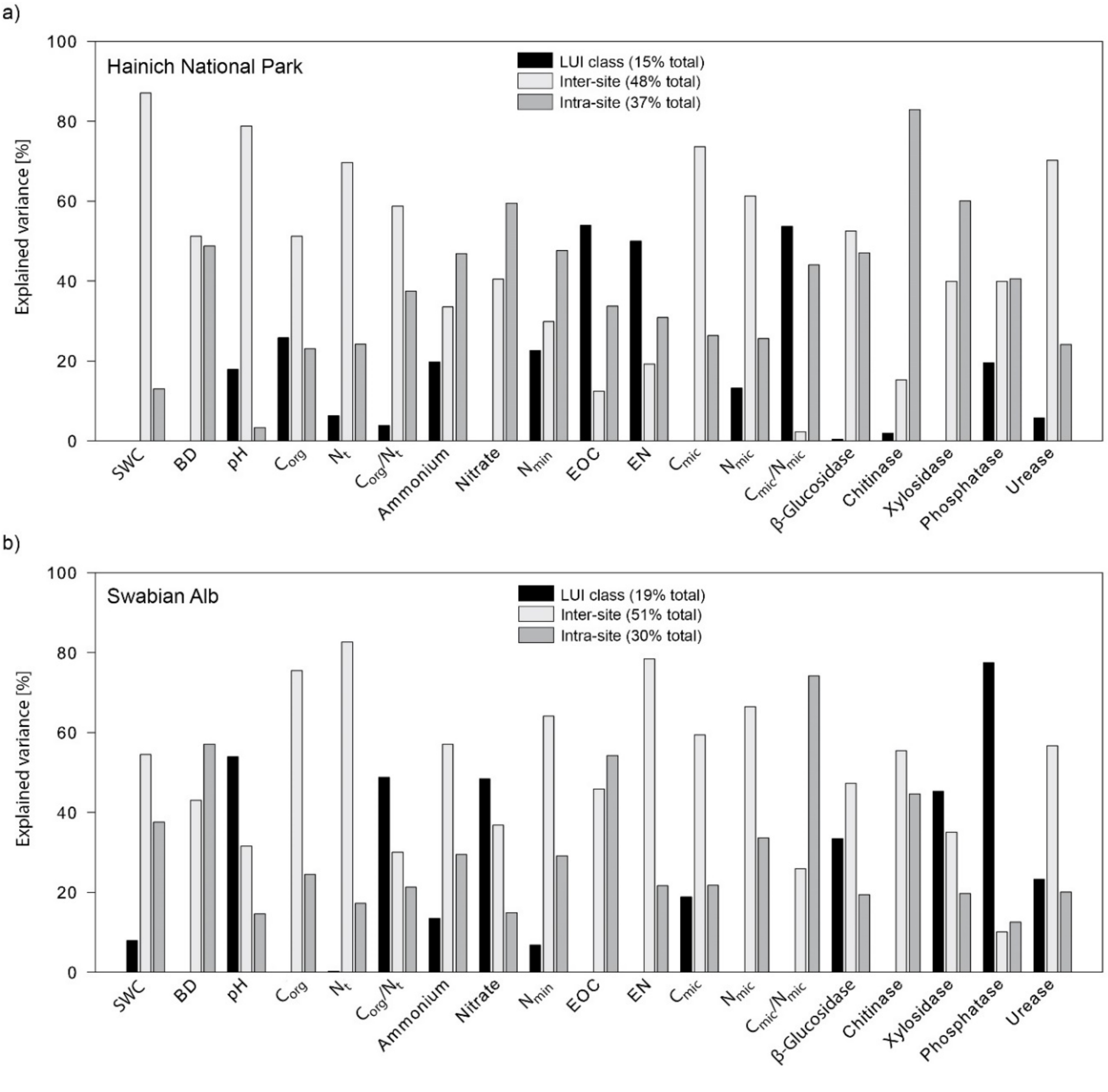

Figure 5-6: Variance components analysis showing the percent explained variance for LUI class, inter-site, and intra-site for all measured variables in a) the Hainich National Park and b) the Swabian Alb.

dominant for BD, EOC and C_{mic}/N_{mic} in the Swabian Alb, while in the Hainich it was most important for ammonium, nitrate, N_{min}, chitinase, xylosidase, and phosphatase.

5.5. Discussion

The 18 independent grassland sites which were compared in this study differed in mowing and grazing practices as well as fertilizer application, resulting in three land-use intensity classes. They belong to two regions differing in climate, especially precipitation, elevation and soil type (Leptosols in the Swabian Alb, mostly Stagnosols in the Hainich National Park). This was the framework within which the spatial and environmental relationships of soil microbial biomass and function were analysed. The set up made it possible to investigate whether there were general underlying mechanisms determining these relationships or whether they were context dependent and, therefore, site specific.

5.5.1. Regional and land-use intensity effects on spatial distributions of soil properties

We observed that the ranges of autocorrelation for biological as well as physico-chemical soil properties were not similar over the different sites or land-use intensities. Furthermore, we did not find spatial trends within or between regions. This suggests that the spatial patterns of the measured soil properties were site specific at the scale of measurement. In his recent review, Baldrian (2014) summarized that in contrast to abiotic soil properties, which are often influenced by large scale variations (e.g. type of plant cover, geology, climate), microbial activities vary mainly at smaller scales. He emphasized the importance of soil water content for enzyme activities. Depending on their abundance and activity, soil macrofauna can also influence the spatial distribution of soil properties. At the small scale, bioturbation and excrement of macrofauna can lead to the homogenization of chemical and biological soil properties (Beare et al., 1995; Bruneau et al., 2005). Nevertheless the abundances of Lumbricidae and also that of Enchytraeidae, as soil burrowing fauna, both studied by Birkhofer et al. (2012), did not correlate with the calculated ranges at the investigated sites. Grazing intensity as well as faeces distribution may explain the spatial distribution of enzyme activities at the plot scale. Ritz et al. (2004) suggested a strong influence of patchy nitrogen deposition via urine of grazing animals on the spatial distribution of microbes. Different animal species (sheep, cows and horses) grazed with varying intensities on the investigated sites in our study (Gockel et al., 2013). This may have led to a very heterogeneous distribution of faeces between sites with little relevance to land-use intensity. In turn, this could have affected individual spatial patterns of microbial soil properties at the grazed sites. We found that soil enzyme activities showed no spatial dependence (i.e. only nugget effect) or a linear model structure at many different sites, suggesting that the sampling scale of this study did not cover parts of the true spatial autocorrelation variability. Schmidt et al. (2007) and Purcell (1977) pointed out that the microbial world is more closely associated with the molecular scale than with the scale of action of macro organisms such as plants or animals. Bruneau et al. (2005) found differences in bacterial colonization dependent on faunal faeces at < 1 mm scale. Therefore, it is possible that more spatial patterns would be detected at finer scales than at the scales of analysis of the present study.

Land-use intensity had different effects in the two regions on the number of abiotic variables and enzymes that were spatially structured. While an increase in the LUI index resulted in more abiotic properties exhibiting spatial structure in the Swabian Alb, it decreased the number in the Hainich National Park. With increasing land-use intensity, field traffic of agricultural machinery usually also increases, and with it, traffic frequency and vehicle loads. Machinery use could have had different effects on the two prevailing soil types in this study, due to differences in soil depth (shallow in the Swabian Alb, deeper in the Hainich National Park) and soil water content, resulting in changes in pore structure as well as water and oxygen availability. It may, therefore, be that there is an interaction between land-use intensity and soil type that has an influence on spatial patterns as well. The increasing number of variables that were spatially structured with increasing LUI index may indicate that the agricultural machinery used on the sites of the Swabian Alb led to a spatial structure of abiotic properties that was measurable at the centimetre to meter scale. This effect was not visible for enzyme activities, for which the number of spatially structured variables declined with increasing LUI index in both regions. The functional and phylogenetic diversities of plants are known to influence microbial populations (Bolton Jr et al., 1993; Bardgett et al., 1999; Reynolds et al., 2003; Zak et al., 2003; Wardle et al., 2004) and it is therefore likely that they also affect soil enzyme activities. Plant community richness in terms of the Shannon/Wiener index as well as plant functional groups in terms of grasses, herbs and legumes (Socher et al., 2012), were ruled out as drivers, as they were not correlated with the calculated ranges. This suggests that management practices, which are known to affect plant community richness, e.g. the number of vascular plant species, in grasslands (Klaus et al., 2011), do not necessarily have the same effects on the spatial organisation of abiotic and biotic soil characteristics. We concluded that there were no general spatial patterns found across the two regions or across land-use intensities. A transfer of spatial characteristics found at one site to another site for interpolation purposes is hence questionable. We therefore rejected our first hypothesis that increasing land-use intensity would always result in an increase in spatial homogeneity of microbial biomass and enzyme activities.

5.5.2. Relationship between enzyme activity, local soil properties and space

The Procrustes rotation test revealed that soil enzyme activities measured in this study were more significantly correlated with abiotic soil properties than with geographic distances at the plot scale. Even though this has been seen in microbial community studies (Hossain and Sugiyama, 2011), to our knowledge we are the first to show this for soil enzyme activities. Soil enzyme activities depend on various environmental factors, such as substrate and oxygen availability, soil moisture, temperature, soil texture, and the presence of humic substances (Linn and Doran, 1984; Wallenstein and Weintraub, 2008; Ruamps et al., 2011; Baldrian, 2014), all of which are unlikely to vary simultaneously in space. Soil water content, pH and bulk density had the strongest relationships with the analysed enzymes, followed by abiotic-N properties. Other studies have shown the importance of nitrogen, pH and soil water content (which is influenced by bulk density) on enzyme activities, e.g. phosphatase, urease and sulphatase (Speir et al., 1980; Amador et al., 1997; Vahed et al., 2011). The data obtained here indicate that the spatial distributions of enzyme activities are more related to the abiotic properties of soil than geographic distance, which contradicts our second hypothesis.

5.5.3. Influence of regions and land-use intensities on soil properties

The principal component analyses revealed that geographic region had a strong influence on the investigated soil properties, while land-use intensity did not significantly influence those properties. We found that apart from higher carbon and nitrogen content in the Swabian Alb compared to the Hainich National Park, soil pH and bulk density distinguished the regions. A negative effect of increasing bulk density on all enzyme activities and on microbial biomass was observed, perhaps caused by oxygen limitation in soils of high bulk density. High bulk density affects the moisture regime and aeration of soils (Scheffer, 2002; Lebert, 2010) and, therefore, plays an important role in many chemical and biological soil processes (Parkin, 1993). The strong regional separation observed in principal component analyses suggests that climate and soil type are strong drivers for biological and physico-chemical soil properties in grasslands and that land-use intensity is secondary. Soil type has previously been shown to influence microbial biomass and activity more strongly than plant species (Groffman et al., 1996; Bossio et al., 1998). In the Stagnosols of the Hainich National Park, the periodical occurrence of waterlogging could have reduced microbial activity (Waldrop and Firestone, 2004), possibly explaining the significantly lower values found for some variables here compared to the Swabian Alb. According to Tscherko (1999), soil type influence on microbial abundance and function is a reflection of long-term climatic, topographic and land-use effects. Parkin (1993) identified soil type, surface topography and water distribution as the main influences on microbial properties at the landscape scale. The number of soil types within this study was not sufficient to draw conclusions regarding different spatial patterns according to soil type, but we assume that the differences between soil types between the two study regions influenced the differences in physico-chemical and biological soil properties, such as C_{org}, EOC, C_{mic}/N_{mic} ratio and urease activity.

As the principal component analysis indicated a dominant influence of region on the measured soil properties, we took a closer look at the data within region using variance component analysis. This analysis revealed, for both regions, an overall ranking of influences by inter-site > intra-site > LUI class, even though the single variables were not always influenced in the same way. The influence of LUI class was higher in the Swabian Alb (total 19% explained variance) than in the Hainich National Park (total 15% explained variance), probably due to a little more homogeneous site management within the LUI classes in the Swabian Alb. The effect of land-use intensity on pH, phosphatase, nitrate, xylosidase, and the C_{org}/N_t ratio was dominant in the Swabian Alb, but not in the Hainich National Park. It is possible that fertilization of the shallow soils together with higher C_{org} values and an overall higher soil water content at the time of sampling had stronger effects on soil chemical properties and enzyme activities in the Swabian Alb than in the Hainich National Park with its deeper mineral soils. In the Hainich National Park LUI class variation had a strong effect on the extractable fractions of nitrogen and organic carbon of the soil as well as the C_{mic}/N_{mic} ratio, but not on the C_{org}/N_t ratio. Higher C_{mic}/N_{mic} ratios are indicative of microbial communities with proportionally more fungi relative to bacteria (Ottow, 2011). Therefore, land-use intensity may have changed the microbial community structure in the Hainich National Park, without affecting soil enzyme activity.

We saw that in both regions inter-site variation explained about 50% of the variance. Due to the on-farm research approach, the investigated sites were not identical replicates and it is likely that individual fertilization and grazing regimes at the sites, especially grazing intensity and resulting input of animal faeces and urine, contributed to this effect. This would be comparable to the influence already discussed on the spatial distribution of the analysed soil properties. Van Eekeren et al. (2009) showed higher bacterial biomass with cattle manure fertilization compared to a control and mineral fertilizer treatment. Higher concentrations of dissolved organic carbon were also found in urine-treated compared to water-treated plots by Singh et al. (2009). Two sites in the Hainich National Park, HEG7 and HEG8 (low LUI class), had nutrient and carbon inputs in the form of winter-fodder given to the cows grazing at the sites (Gockel et al., 2013) and both showed high carbon content and β-glucosidase activity. Together with the overall higher grazing intensity in the Hainich National Park (Blüthgen et al., 2012), this could also have contributed to the observed different results in the Swabian Alb, where no additional fodder was provided on the investigated sites. The variation in grazing intensities and feeding strategies between sites is likely to have increased the inter-site effect. The intra-site effect was stronger in the Hainich National Park (37%) than in the Swabian Alb (30%). We suspect the strong effects of inter- and intra-site variations on the soil properties to be related to site specific spatial patterns that were observed in the spatial data analyses. The results did not support our third hypothesis that land-use intensity has a stronger influence on soil enzyme activities than region or site.

5.6. Conclusion

At our sampling scale, spatial patterns were site specific for the analysed soil properties. This could indicate that a simple up-scaling from plot to regional scales in terms of distribution patterns is not necessarily reliable and that nested sampling designs need to be considered. Instead of the expected clear spatial patterns for enzyme activities, we found that enzyme activities were related to abiotic soil properties, regardless of geographic distribution. The study showed that even though land-use intensity affects the spatial structure of enzymes, its influence on microbial biomass and soil enzyme activity was not as large as expected and that individual site characteristics were more important in grassland soils.

5.7. Acknowledgement

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6. Unraveling spatio-temporal variability of arbuscular mycorrhiza fungi in a temperate grassland plot

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6.1. Summary

Soils provide a heterogeneous environment varying in space and time; consequently, the biodiversity of soil microorganisms also differs spatially and temporally. For soil microbes tightly associated with plant roots, such as arbuscular mycorrhiza fungi (AMF), the diversity of plant partners and seasonal variability in trophic exchanges between the symbionts introduce additional heterogeneity. To clarify the impact of such heterogeneity, we investigated spatio-temporal variation in AMF diversity on a plot-scale (10 × 10 m) in a grassland managed at low intensity in southwest Germany. AMF diversity was determined using 18S rDNA pyrosequencing analysis of 360 soil samples taken at six time points within a year. We observed high AMF alpha- and beta-diversity across the plot and at all investigated time points. Relationships were detected between spatio-temporal variation in AMF OTU richness and plant species richness, root biomass, minimal changes in soil texture, and pH. The plot was characterized by high AMF turnover rates with a positive spatio-temporal relationship for AMF beta-diversity.

However, environmental variables explained only ≈ 20% of the variation in AMF communities. This indicates that the observed spatio-temporal richness and community variability of AMF was largely independent of the abiotic environment, but related to plant properties and the co-occurring microbiome.

6.2. Introduction

Understanding spatial and temporal patterns in species diversity is one of the fundamental goals of biodiversity research (Gaston and Spicer, 2013). Soil microbial communities exhibit spatial patterns at scales from sub-millimeter to hundreds of meters, determined by heterogeneous environmental conditions at respective scale-dependencies (Grundmann et al., 2001; Ettema and Wardle, 2002; Nunan et al., 2003; Bahram et al., 2015). Simultaneously, dynamic variations in abiotic soil conditions lead to fluctuating soil microbial abundances and functions over time, documented in agricultural (Kandeler and Böhm, 1996; Kandeler et al., 1999), tundra (Björk et al., 2008), and forest ecosystems (Görres et al., 1998; Nacke et al., 2016). Moreover, plant growth and development or changes in vegetation within a year are able to shift soil microbial communities (Chaparro et al., 2014; Nacke et al., 2016). This is especially relevant for obligate biotrophic plant mutualists such as arbuscular mycorrhizal fungi (AMF; Smith and Read, 2008).

Recent studies have aimed to identify general patterns of and major influences on AMF community composition. Some findings have included, for instance, high impacts of land-use intensity (Bouffaud et al., 2017), soil properties (Kivlin et al., 2011; Lekberg et al., 2012), plant community composition (van der Heijden et al., 1998; König et al., 2010; Neuenkamp et al., 2018), and/or host plant identity (Sanders, 2003). Since AMF are obligate root mutualists, most studies have focused on fungus-plant-relationships. Conflicting results have been observed, however, regarding the interactions between plant community composition and AMF communities, ranging from enhanced (Wu et al., 2007; Hiiesalu et al., 2014) to reduced plant diversity in the presence of AMF (Antoninka et al., 2011) to no relationship between plant and AMF diversity (Öpik et al., 2008). These contradictory findings may be related in part to study scales (Hempel, 2018), since different environmental forces work at different scales (Chase, 2014); this also applies to AMF (Vályi et al., 2016).

According to ecological theory, niche-related (environmental/deterministic; MacArthur and Wilson, 1967) and neutral (stochastic; Hubbell, 2001) processes in particular shape community composition and habitat colonization. But these processes appear to have different strengths at various scales: niche-related effects are more common at larger (e.g. regional or global) scales, while neutral processes operate mainly at small spatial scales (Chase, 2014). Many studies have been conducted at broad geographical scales (Öpik et al., 2006; Hazard et al., 2013; Davison et al., 2015; Bouffaud et al., 2016; Bouffaud et al., 2017), but to date little is known about richness and occurrence patterns of AMF at or within plot scales (≤ 50 m × 50 m) in grassland ecosystems (Lekberg et al., 2012; Horn et al., 2014). One advantage of such small-scale study designs is the focus on environmental conditions and variations in plant communities within a specific habitat, thereby excluding overriding effects of large-scale heterogeneity at the landscape level (Berner et al., 2011; Regan et al., 2017). Thus, fundamental influences on AMF communities can be studied at such plot or subplot scales, ranging from centimeter to meter. Repeating such sampling scales at one plot adds information on temporal autocorrelations (Tobler, 1970), providing an opportunity to investigate spatial hot spots and temporal hot moments simultaneously.

To understand temporal influences and to identify hot moments (Kuzyakov and Blagodatskaya, 2015) in changing AMF communities (Dumbrell et al., 2011), a study would need to cover the entire vegetation period by sampling soils at several time points. To date, few of the studies focused on temporal variation have sampled AMF communities more than twice during the growing season (Bainard et al., 2014; Liu et al., 2014). Repeated sampling is necessary, however, to account for seasonal variations in plant cover, which is likely coupled with changes in soil moisture, temperature, and nutrient fluxes (e.g. phosphate and nitrate), and thus reflected in dynamic soil microbial communities (Bardgett et al., 2005). Even though a direct connection between AMF diversity, its abundance, and changes in plant diversity is not always apparent: Dumbrell et al. (2011) showed that during spring and summer, when plant growth is strong, environmental conditions and AMF distribution patterns are not constant. However, even fewer studies have investigated both spatial and temporal variations in AMF communities (Davison et al., 2012; Koorem et al., 2014; Barnes et al., 2016), and these studies have mainly been done on forest sites. Davison et al. (2012) found seasonal differences in AMF richness as well as distance decay in community similarity at three 10 m × 10 m forest plots sampled four times within one year, while Koorem et al. (2014) confirmed the seasonal variability in AMF by fatty acid analyses at small spatial scales

(1.05 m × 1.05 m) sampled twice during one summer. Combining spatial and temporal sampling also makes it possible to quantify the beta-diversity of AMF communities, which describes how species composition changes over spatial scales and over time. However, analyses of beta-diversity have only rarely included microorganisms (e.g. Gossner et al., 2016).

Within the research platform "Biodiversity Exploratories" (Fischer et al., 2010) the project *SCALEMIC Experiment* established a spatio-temporal sampling design in a low land-use intensity grassland at the plot scale (10 m × 10 m) and assigned six sampling dates from spring to autumn in one vegetation season. Through an interdisciplinary approach, it was previously clarified that plant growth changes plot-scale spatial heterogeneity of soil microorganisms during the vegetation period, and elucidated driving forces behind this observed microbial heterogeneity (Regan et al., 2014). We linked existing measures of seasonal and spatial changes in plant diversity, abiotic soil properties, and general microbial community composition (Regan et al., 2014; Regan et al., 2015; Klaus et al., 2016; Regan et al., 2017) to AMF diversity and community patterns. Using high-throughput sequencing technology, this study aimed to answer the following questions: (a) how much variability in AMF alpha- and beta-diversity exists on a spatial scale of 10 m × 10 m and a temporal scale of one season?; (b) are spatial and temporal AMF patterns coupled?; and (c) which environmental drivers are responsible for the observed patterns? We expected a strong relationship between the AMF community and its changing environment, primarily vegetation and phosphate availability.

6.3. Results

6.3.1. Taxonomical distribution of AMF

We recovered 1,088,162 AMF SSU rDNA gene reads from all 360 soil samples. After a quality filtering step that included removal of 22,042 potential chimera and non-AMF reads, we had a total of 562,320 AMF reads representing 1,562 reads per sample, and which were clustered into 155 abundant operational taxonomical units (OTUs). As described in detail in the "experimental procedures" section, the removal of rare OTUs (OTUs represented by ≤ 3 reads) had no significant effect on AMF beta-diversity. Thus, the AMF matrix including only abundant OTUs was used for further analyses.

The 155 abundant AMF OTUs were assigned to seven genera: *Acaulospora* (2 OTUs), *Ambispora* (2), *Archaeospora* (3), *Claroideoglomus* (20), *Diversispora* (9), *Glomus* (117), and

Paraglomus (2). Taxonomical distribution based on the number of observed AMF OTUs differed slightly between sampling dates. The genus *Glomus* was most abundant throughout the entire growing season, ranging from 69% in April to 77% in November (Figure 6-1, Table S1) with the highest diversity (a total of 106 OTUs) detected in October. Besides *Glomus*, other AMF genera displayed temporal peaks; e.g., *Claroideoglomus* in June (16.4%) and *Diversispora* in April (8%).

6.3.2. Spatio-temporal variation in AMF richness

The OTU richness of total AMF was spatially modeled and checked for autocorrelation. Kriged maps were generated for all sampling dates except October, at which date the empirical variogram model was a pure nugget, indicating no spatial autocorrelation at the measured scale (Figure 6-2a–e). The observed patterns occurred and were distributed throughout the entire AMF community over the entire sampling season. In April and May (Figure 6-2a and b), AMF diversity was homogeneous with low OTU richness across the plot. An increase in AMF OTU richness was detected in June (yellow areas in Figure 6-2c). Moreover, first patches developed in June, and became more pronounced in August and November (Figure 6-2d and e). In general, total AMF OTU richness decreased at the end of the growing season (increase of dark green in the kriged maps), but discrete hot spots and cold spots with high or low AMF OTU richness appeared.

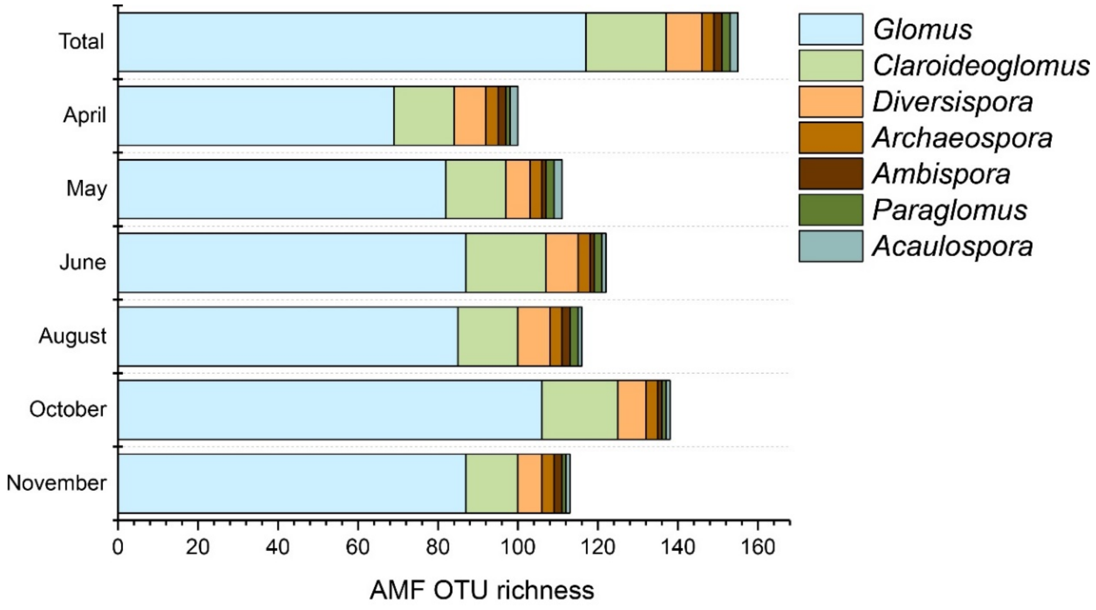

Figure 6-1: Bar graphs representing the temporal distribution of AMF OTUs of Glomeromycota genera detected across the entire plot.

For the two most abundant AMF genera, *Glomus* and *Claroideoglomus*, OTU richness was also spatially modeled and could be visualized through kriged maps (Figures S6-1 and S6-2). Spatial distribution of *Glomus* could be modelled in May, June, August and November, while the spatial distribution of *Claroideoglomus* could only be modelled in August and November. As was the case for all AMF OTUs, *Glomus* OTU richness was low to medium in May and June (Figures S6-1a, b), tending toward spatial patches of low or high richness. Heterogeneity of distribution became more pronounced in August with two spots of high OTU richness (Figure S6-1c). However, a shift in OTU richness

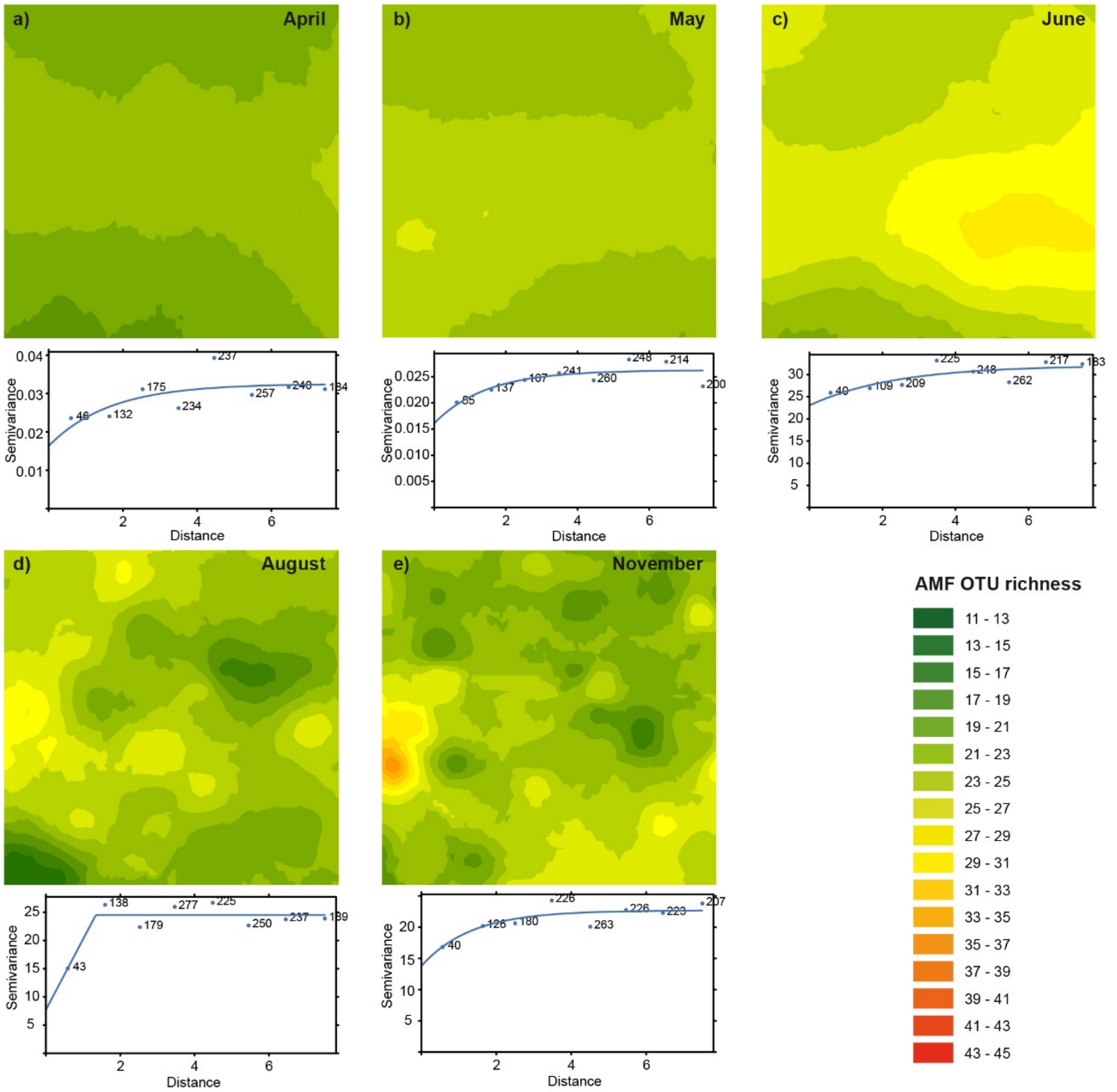

Figure 6-2: Geostatistical data analysis of AMF OTU richness with all AMF OTUs grouped together per sampling date: a) April, b) May, c) June, d) August and e) November. Spatial patterns within the data were analyzed and calculated as semivariogram models (lower panels in figure) and visualized as kriged maps using these models (corresponding upper panels in figure). Dimensions of all maps are 10 m x 10 m.

occurred in November (Figure S6-1d) with areas of low and high OTU richness of *Glomus*. *Claroideoglomus* OTUs exhibited similar spatial patterns in August with areas of low and intermediate richness (Figure S6-2a) and in November generally lower richness but more heterogeneous distribution across the plot (Figure S6-2b).

The effect of sampling date on AMF richness, assessed by linear mixed effect models (LMEM), was plotted for all OTUs and additionally for the OTUs of the two most abundant genera, *Glomus* and *Claroideoglomus* (Figure S6-3). Sampling date significantly influenced richness of both total AMF and *Glomus* OTUs ($p < 0.0001$), but not *Claroideoglomus* OTUs. OTU richness significantly increased in all AMF OTUs from April to June, dropping in August. Total AMF OTU richness peaked in October and dropped significantly in November. The richness of *Glomus* OTUs was similar with significantly lower richness in April and a peak in October. The OTU richness of *Claroideoglomus* did not change over the sampling season.

6.3.3. Environmental impacts on AMF richness

Linear mixed effect models, taking into account the impact of all available environmental factors (n = 34) on total AMF OTU richness, revealed significant effects of soil- and plant-related parameters in 21 cases, as well as 23 significant effects of environmental variables on *Glomus* OTU richness. *Claroideoglomus* OTU richness was significantly affected by soil carbon content, but this explained only 3% of its variance. To detect those environmental variables most closely associated with the observed temporal effect on total AMF and *Glomus* OTU richness, we combined environmental variables and sampling date as fixed effects in LMEMs. This combination indicated that the measured environmental variables explained less unique variance in total AMF and *Glomus* OTU richness than did sampling date. The final LMEM (Table 6-1) for total AMF OTU richness pointed to plant species richness, percent silt content and sampling date as the three main drivers at the investigated site, which, taken together, explained 36% of the variance. Silt content had a positive effect, while plant species richness was slightly negatively associated with total AMF OTU richness. Temporal variation was reflected by the significant effects of sampling time and indicated by the different intercepts of the single months (Table 6-1). *Glomus* richness was driven by plant species richness, root biomass, percent silt content, pH, and sampling date, which together explained 38% of the variance in *Glomus*. Here, we found a slightly negative impact of plant species richness, while root biomass, silt content and pH positively affected the OTU richness of *Glomus*.

For both total AMF and *Glomus* OTU richness, sampling date explained large proportions of the variance; 27% and 28%, respectively. As plant species richness was only assessed at three sampling dates, we additionally fitted models without this variable for total AMF and *Glomus* OTU richness to determine the best predictor variables across the whole season. When all six sampling dates were analyzed, total AMF OTU richness was not influenced by plant variables; instead there was a slight negative association with soil NH_4^+ content. *Glomus* OTU richness was best predicted by legume and root biomass, NH_4^+, silt content, pH, the fungal to bacterial ratio, and sampling date over the entire season (see Table 6-1).

Table 6-1: LMEM results for richness of entire AMF, *Glomus*, and *Claroideoglomus* for three and six sampling dates. Given are significant environmental variables with their coefficients (data z-transformed for comparison between coefficients), number of samples in the model as well as explained variances. Subplot number was used as random effect (intercepts not displayed). n = number of samples.

Sampling dates	**Target**		**Model coefficients of fixed effects**	**n**	**Percentage explained variance**		
					Random effects	**Fixed effects**	
						Environmental variables	**Sampling time**
3	all AMF OTU	=	-0.57 * plant species no. + 1.7 * silt content + 23.39 (for sampling time May) + 25.47 (for sampling time June) + 30.95 (for sampling time October)	180	48	9	27
6	all AMF OTU	=	-0.7 * NH_4^+ + 1.3 * silt content + 22.25 (for sampling time April) + 22.81 (for sampling time May) + 25.3 (for sampling time June) + 22.82 (for sampling time August) + 30.5 (for sampling time October) + 22.96 (for sampling time November)	360	45	6	27
3	*Glomus* OTU	=	-0.41 * plant species no. + 0.5 * root biomass + 1.5 * silt content + 0.75 * pH + 15.78 (for sampling time May) + 16.73 (for sampling time June) + 22.9 (for sampling time October)	180	60	10	28
6	*Glomus* OTU	=	0.37 * legume biomass + 0.34 * root biomass – 0.65 * NH_4^+ + 1.25 * silt content + 0.35 * pH – 12.73 * fungi:bacteria ratio + 15.46 (for sampling time April) + 16.73 (for sampling time May) + 18.06 (for sampling time June) + 17.41 (for sampling time August) + 23.82 (for sampling time October) + 17.96 (for sampling time November)	360	54	7	14
6	*Claroideoglomus* OTU	=	0.57 * C_{total}	360	11	3	—

6.3.4. Spatio-temporal variation in AMF community composition

AMF beta-diversity (β_{SOR}) was lower within time points and within subplots than between these groups (ANOSIM *p*-value = 0.001). When the data set was stratified by sampling date, silt content, pH, microbial biomass, soil C content, and K_2SO_4-extractable organic N significantly explained variation in β_{SOR}. However, these variables together explained less than 10% of the variation in β_{SOR}. No relationship between AMF β_{SOR} and any plant variable could be detected. Additionally, a spatial gradient explaining 4% of the variability was observed (Tables S6-2 and S6-3).

The AMF β_{SOR} of the subplots between one time point and the one immediately following varied slightly (Figure S6-4). However, there was no stronger correlation between subplots near each other in comparison to those subplots further distant (Figure S6-5; for data on *Glomus* and *Claroideoglomus* see Figures S6-6 and S6-7, respectively). No significant correlations between the temporal development of β_{SOR} and environmental variables were observed. Turnover (β_{SIM}), meaning OTU replacement between time points, and nestedness (β_{SNE}), meaning OTU gain and loss from one time point to the next, are summarized in Figure 6-3 (for data on *Glomus* and *Claroideoglomus* see Figure S6-8). The turnover in AMF community composition appeared to be constant between 0.3 and 0.4 during the sampling season. The highest AMF β_{SIM} was detected between June and August, which is likely linked to the fact that this difference represented a duration of two months. β_{SNE} peaked later in the season, particularly between August and October, but also between October and November. However, kriged maps revealed hot spots of turnover from April to May as well as from October to November (Figure S6-9).

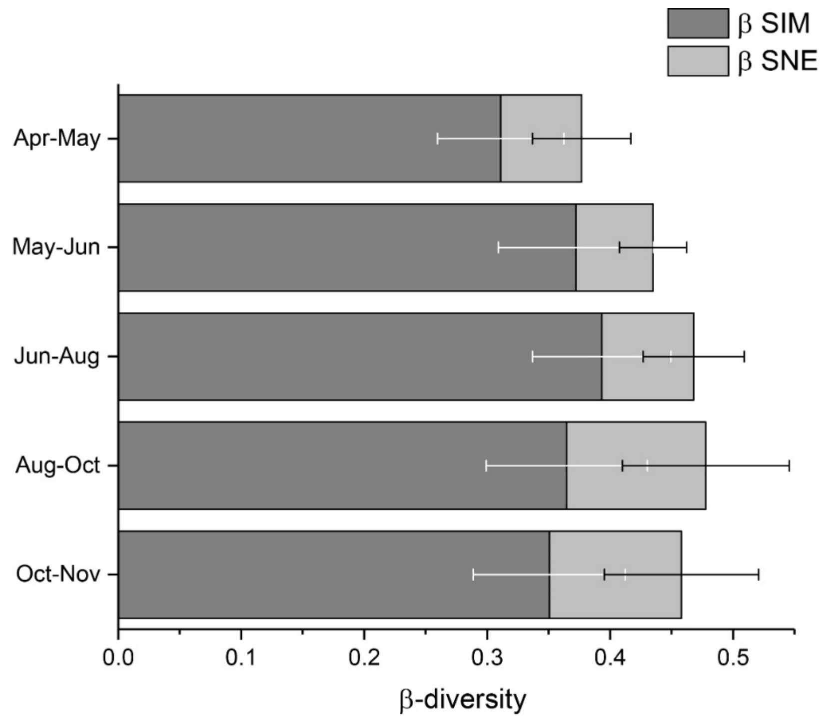

Figure 6-3: Patterns of variability within AMF assemblages across the studied plot from one time point to the next. Stacked bars represent overall beta-diversity (β_{SOR}) observed in the partial data sets, computed using the R-package betapart (Baselga and Orme, 2012); dark grey sections of the bars represent the contribution of the turnover of AMF (β_{SIM}), light grey sections account for the nestedness of AMF (β_{SNE}); error bars represent variability between SCALEMIC subplots.

Analysis of spatial AMF β_{SOR} demonstrated some continuity within subplots early in the growing season (see supplemental material for more details; Figure S6-10 and Figure S6-11). The relationship between temporal β_{SOR} (the average β_{SOR} over time) and spatial β_{SOR} (the average AMF β_{SOR} with the neighboring subplots) of each subplot displayed a positive trend (Figure 6-4), indicating that subplots with AMF communities that differed strongly from neighboring subplots also changed more over time. The positive relationship was significantly stronger than the relationship observed in null-models of β_{SOR}, which were based on random community permutations that maintained each sample's richness and the overall or sampling date point-specific probability of OTU occurrence (Figure S6-12). Concurrently, no significant relationships between OTU

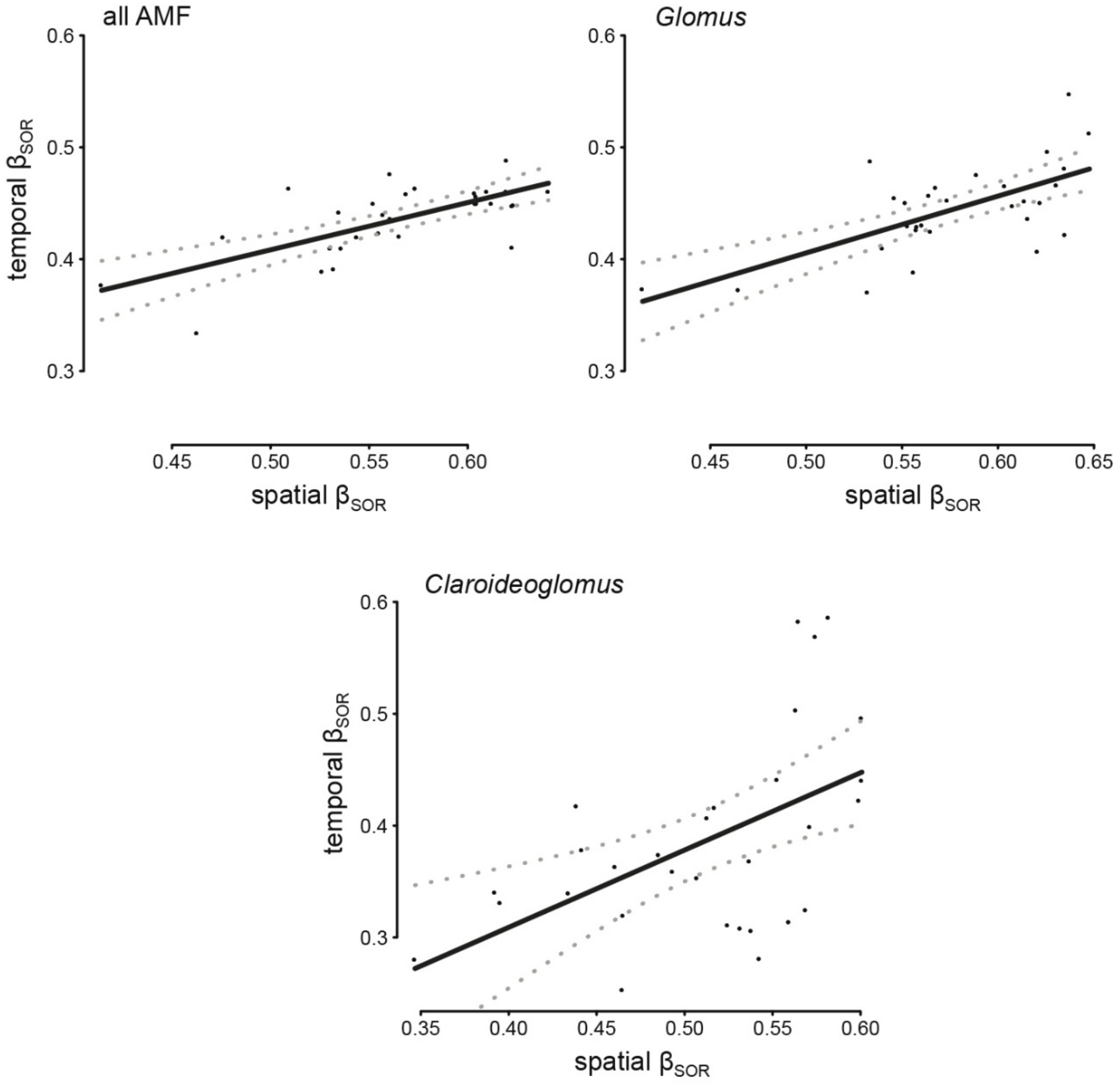

Figure 6-4: Relationship between spatial and temporal β_{SOR} of total AMF, *Glomus* or *Claroideoglomus*, respectively. Spatial indices of AMF turnover (x-axis) represent the AMF turnover between each subplot and its neighbors averaged over all sampling dates. Temporal indices (y-axis) represent the mean delta (turnover from one time point to the subsequent time point). Regression lines (black) are based on linear models and 95% confidence intervals (grey dotted lines).

richness or changes in alpha-diversity with spatial or temporal β_{SOR} were observed. The same pattern was observed for the β_{SOR} of *Glomus* OTUs, while *Claroideoglomus* β_{SOR} did not differ significantly from the null-models (Figure S6-12). No explanatory power was gained by adding environmental variables to the linear model explaining temporal β_{SOR} with spatial β_{SOR}. Among the environmental variables, the mean grass biomass best explained spatial β_{SOR} of all OTUs (p-value 0.01, adjusted $R^2 = 0.43$).

6.4. Discussion

6.4.1. General characterization of AMF

AMF form a multispecies mutualism with over 80% of terrestrial plants, i.e. with more than one fungus per host plant (Smith and Read, 2008). With a total of 155 abundant AMF OTUs on a 10 m × 10 m plot over a vegetation period that extended from April to November, our study found relatively high AMF richness compared to recent studies (Dumbrell et al., 2010; Davison et al., 2012; Horn et al., 2014).

All four orders of the phylum Glomeromycota and seven genera were represented in the observed OTUs. Dominant at all time points was the AMF genus *Glomus*. This dominance is in agreement with previously published studies in grasslands, forests, and agricultural ecosystems (Daniell et al., 2001; Gai et al., 2009; Öpik et al., 2009). Although AMF OTU richness was high, genera such as *Rhizophagus* or *Funneliformis*, which have often been observed in a comparable German grassland of low land-use intensity (Horn et al., 2014), were not detected in our dataset.

6.4.2. Spatio-temporal variation in AMF alpha-diversity

Our current study determined whether AMF richness exhibits spatio-temporal variation at a small spatial scale in a grassland soil, and which environmental variables shape differences in AMF alpha-diversity. Studies in which other results of the *SCALEMIC Experiment* have been published observed an increase in biomass of grasses and forbs until June and additionally a gain in biomass of legumes in October as well as significant shifts in mineral nitrogen content of soils over time (Regan et al., 2014). Moreover, temporal shifts in plant biomass and nutrient availability were detected (Klaus et al., 2016). Results of our spatial analyses illustrate clearly how AMF OTU richness varied across the sampled plot and also over the season. The appearance of hot or cold spots of AMF richness showed a dynamic process that developed during the vegetation period. The detected spatial autocorrelation of AMF OTUs with ranges below 10 m across our plot for five of six time points is in accordance with previous studies, e.g., by Bahram et al. (2015), who reported autocorrelation ranges around 9 m. Richness of AMF OTUs therefore shows distance-decay relationships at the investigated plot scale.

Interestingly, although more than 100 OTUs were detected on the entire 10 m × 10 m plot at each sampling date, many of these AMF appeared in patches of 20–30 OTUs per sampling point. This discrepancy between total observed OTU richness across the plot and OTU richness per individual sampling point may be related to carrying capacity (Allen, 1989). We define carrying capacity as the maximum number of AMF OTUs the studied *SCALEMIC* grassland plot can sustainably support. Accordingly, the local AMF carrying capacity appears to have been patchy but potentially dynamic over time. The observed temporal dynamic could be connected to changes in resource availability. This could be related to asynchronous growth of plants across the site (Yachi and Loreau, 1999). For instance, a changing supply of photo-assimilates could be accompanied by dense AMF population sizes at one sampling point (hot spot), but reduced AMF richness at another point (cold spot) on the plot within or across sampled time points. This is in line with findings of the linear mixed effect models, which found a connection between AMF richness and changing environmental variables such as plant species richness, root biomass, pH and NH_4^+. To our knowledge, this has not been shown previously and underscores the need for more temporal investigations.

6.4.3. Restricted impact of environmental variables on AMF richness

Linear mixed effect model analyses revealed a significant effect of soil texture on the total richness of both AMF and the genus *Glomus* across the plot. The heterogeneous distribution of silt in our soil modified important habitat conditions. Hot spots of high silt content are characterized by larger volumes of medium sized pore space and improved aeration in the surrounding micro-environment (Horn et al., 2010), resulting in favorable habitat conditions for AMF, which lead to increased AMF OTU richness. Although the dependence of AMF on soil texture in grassland soils was shown in a large scale study (Oehl et al., 2017), no studies have yet demonstrated that this effect occurs with small textural changes (changes in silt content < 10%) at the plot scale. Soil texture significantly affected temporal variations in AMF OTU richness even though it was temporally stable. We suggest that this is because soil texture influences a number of habitat conditions such as nutrient availability, pore space distribution and thereby also the hydrological budget and oxygen supply (Horn et al., 2010), which themselves vary over time. That soil texture was a better measure than single effects, e.g., soil water content, indicates its value as a measurement that captures a range of temporal variations in texture-dependent habitat conditions. This result emphasizes the importance of microhabitat conditions for AMF.

In addition to soil texture, plant species richness was a significant driver of OTU richness for both total AMF and *Glomus* in the months of May, June and October. Interestingly, a reduction in plant species richness led to an increase in total AMF and *Glomus* OTU richness. Argüello et al. (2016) described a positive feedback mechanism for AMF-plant mutualism, leading to stronger cooperation between AMF and plants under the condition of high AMF diversity per plant. In addition, newly emerging plant species over the season may have had different root architectures such as less root biomass, leading to a reduction in AMF OTU richness, as higher root biomass significantly increased the OTU richness of the genus *Glomus*. It has also been suggested that both AMF and plants actively control their associated symbiotic partners (van der Heijden et al., 2015), in which case changes that resulted in a more cooperative plant community could influence AMF OTU richness. Similarly, the newly emerging plant species may have had more acidic root exudates, which would have reduced the OTU richness of *Glomus*, as *Glomus* OTU richness decreased with decreasing soil pH. A similar effect of pH on AMF OTU richness in grassland ecosystems was also observed by Heyburn et al. (2017). Even when they were evaluated over all six sampling dates throughout the season, the effects of soil texture, pH, and sampling date remained significant. Over the longer time, the impact of plants on total AMF OTU richness was not significant; instead, a negative effect of NH_4^+ was detected. The same was true for OTU richness of *Glomus*. As NH_4^+ reduces soil pH, this was likely a combined effect of the two soil properties. In addition, an increase in legume biomass led to an increase in *Glomus* OTU richness, which may have been due to increased coverage of the mycorrhizal plant partners such as *Trifolium pratense* (L.) (van der Heijden et al., 1998) and *Vicia sepium* (L.) (Closa and Goicoechea, 2011) over time. The negative relationship between the fungal:bacterial ratio of phospholipid fatty acids and *Glomus* richness was related to an overall increase in saprotrophic fungi at the site (Regan et al., 2014), which was accompanied by a reduction in *Glomus* richness, indicating both competition for resources (Hodge et al., 2001) and interactions due to fungal community composition (Tiunov and Scheu, 2005) at the study site. However, not all AMF genera reacted in the same way. *Claroideoglomus* was affected neither by soil texture nor by any of the above mentioned environmental properties; instead, a small but significant effect of soil carbon content on this genus was detected.

Even though environmental soil properties explained a portion of the variance in AMF alpha-diversity, sampling date was the most important driver of total AMF and *Glomus* OTU richness. Previous studies have reported an increase in AMF OTU richness during the growing season with a decrease in autumn, which could be explained by changing weather conditions within a sampling year (i.e. temperature and precipitation; Kabir et al., 1998; Staddon et al., 2003). In our study, there were significantly fewer AMF OTUs in November than in June or October. This phenomenon may have been related to cold temperatures and less precipitation at this sampling date (see supplemental Figure A1 of Regan et al. (2014)). Also, the observed decline in AMF OTU richness in August may have been associated with a suppression of plant growth and reduced carbon supply from plant to fungus after the mowing event (Gehring and Whitham, 2002). This mowing event and the subsequent regrowth of plants could have led to the high number of AMF OTUs detected in October. It was shown recently that more AMF propagules are present in mown than in unmown soils (Binet et al., 2013), benefiting new AMF infections after mowing. In addition, this is likely connected to increasing root exudation following aboveground plant biomass removal (Waters and Borowicz, 1994). More diverse exudates are likely to recruit a greater AMF diversity (Hugoni et al., 2018). Consequently, mowing leads to emerging micro-niches, which favor a higher variability in AMF. Thereby, AMF can be considered as stress tolerant since they can cope with partition and destruction of their hyphae (Buscot, 2015). Since up to only 10% of the explained variance was directly attributable to measured environmental effects (see Table 6-1), our results could indicate that neutral processes, stochasticity, or randomness due to natural variability may play a role in the formation of unpredictable AMF patchiness in addition to the contribution from deterministic processes. This applied to both total AMF OTUs and OTUs of the genera *Glomus* and *Claroideoglomus*.

6.4.4. Pronounced spatio-temporal relationships in AMF beta-diversity

In addition to alpha-diversity, this study sought to understand whether or not beta-diversity in AMF exhibited similar spatio-temporal patterns. With respect to OTU richness, AMF beta-diversity expressed as Sørenson index indicated spatio-temporal relationships. Theoretically, local AMF communities should be of a common and predictable composition since the species pool at the plot scale is limited; thus, beta-diversity in both spatial and temporal senses should be low according to Powell and Bennett (2016). However, in our study AMF beta-diversity appeared high, with a particularly high turnover rate from one observed time point to the next. Although the turnover rates were high (consistently ≈ 40% of the AMF community changed from one time point to the subsequent one), a certain spatio-temporal stability of AMF communities was observed. Our results suggest that AMF community composition at the first three time points (April–June) was determined by prior communities. It is possible that DNA measures either detected defective and dead cells (Carini et al., 2016), or dormant AMF stages, such as spores from the previous year, which impacted the observed AMF community at the beginning of the vegetation period. This effect was lost during the summer, which suggests that either legacy effects due to the cyclic character of seasons in temperate regions (Bahram et al., 2015) or the appearance of priority effects (Viana et al., 2016) shaped AMF community composition, as has been shown for soil bacteria (Francioli et al., 2016; Francioli et al., 2018). The plant-AMF interaction may have been set back to zero during winter, resulting in a random start of plant growth and fungal infections during spring. These priority effects could have resulted in high heterogeneity within subplots, which decreases over the season. Coupled with this is the fact that competition amongst AMF emerges only over time (Maherali and Klironomos, 2012). Alternatively, AMF detected from spores in our analyses transformed from spores while colonizing growing plant roots during the second half of the vegetation period. In the second half of the year these AMF may have dropped below the molecular detection limit. Also, the mowing event before sampling in August shuffled AMF community composition, since mowing is known to multiply AMF propagule numbers (Binet et al., 2013). However, we could not identify a direct link between either the plant community taken together or between single plant species and the AMF community. This missing link between these two communities (Hart et al., 2001) supports the “independence hypothesis” which suggests that neither plants nor AMF express any co-variation at all in this mutualism (Zobel and Öpik, 2014).

Recent studies mention dispersal limitation of AMF (Davison et al., 2015) as one reason for patchiness in community composition at small scales. This results in “unpredictable assembly” (Powell and Bennett, 2016) of AMF, which corresponds well with our findings that approximately 80% of variation in β_{SOR} could not be explained by environmental variables. This could indicate that stochastic rather than niche related processes shape AMF β_{SOR}. However, one general pattern could be identified: over time, AMF community composition differed less within than between subplots. More similar environmental conditions found within a subplot appeared to result in significantly lower beta-diversity over time. This indicates that even small environmental differences between two subplots affected AMF community composition. Indeed, it has previously been shown that pH, C, N, P, and soil water content shape AMF grassland communities (Horn et al., 2014). In our study, around 20% of the observed variation in AMF beta-diversity could be explained by measured environmental factors. Nevertheless, it is possible that the low variance explained by environmental variables in our study indicates the influence of important but unmeasured variables, and not stochastic processes as such. To confirm that neutral processes shape spatio-temporal AMF beta-diversity, future studies should consider microscale effects such as root exudates and pore space to identify currently unidentifiable drivers.

6.5. Conclusions

Our study of AMF alpha- and beta-diversity found spatio-temporal distribution patterns at the observed plot scale of 10 m × 10 m. We were able to illustrate well both the dynamism of AMF OTU richness, and community development across one vegetation season. Thereby, we demonstrated, albeit indirectly, that stochastic recruitment processes largely shaped our observed patterns of AMF OTU richness and community composition. If seasonal variations in carrying capacity are considered, then shifts in plant growth, diversity, and dominance are likely to favor AMF species already engaged in the symbioses. However, our results revealed high AMF turnover over time, suggesting ongoing recruitment of AMF from formerly dormant propagules. We acknowledge that the detection of niche-based processes could have been limited by the choice of our measured environmental parameters, which were either unable to detect them or wrongly selected for this purpose. Nonetheless, both the scale and spatio-temporal approach of the *SCALEMIC Experiment* have expanded our understanding of biotic and abiotic interactions at scales that had heretofore not been examined in such detail. Further research, ideally on more than one site, is needed for a deeper and more comprehensive understanding of the spatio-temporal assembly of soil microbes at small scales by assessing and linking functions of bacteria and fungi with plant traits. Likewise, and within the frame of an emerging discussion as to whether AM fungal communities are more structured by the abiotic or biotic environment (Hempel, 2018), future studies should incorporate balanced consideration of environmental variables.

6.6. Experimental procedures

6.6.1. Study site and soil sampling

The studied grassland plot (48°27’31.37”N, 9°27’36.26”E) is one of 300 experimental plots in the large and long-term interdisciplinary research project *“Biodiversity Exploratories”*, which aims to understand relationships between land-use, multi-trophic biodiversity and ecosystem functioning across Germany (Fischer et al., 2010). The grassland plot is located in the Schwäbische Alb in southwest Germany. The plot has never received mineral fertilizers and has never been plowed. Characterized by a rather nutrient-poor substrate, this plot's soil type is a Rendzic Leptosol (FAO classification). The plot is dominated by *Plantago lanceolata* L., *Festuca rubra* L and *Helictotrichon pubescens* (Huds.) Pilg. and belongs to the phytosociological class of Festuco-Brometea (Oberdorfer et al., 2001; Klaus et al., 2016). Furthermore, the grassland is usually mown once per year, and grazed briefly by sheep for 1–2 weeks in late summer or early autumn. In 2011, the year of investigation, mowing took place on July 30th and sheep herds grazed on this site in May for five days, in September for seven days and in October for one day.

The *SCALEMIC Experiment* (Regan et al., 2014) encompasses a 10 m × 10 m plot divided into 30 subplots, each 2 m × 1.67 m (see Figure S6-13). Within each subplot six pairs of sampling locations (each 20 cm × 20 cm) were randomly assigned, with one pair sampled at each of six dates over one growing season. This provided a randomized complete block design for temporal data analysis with sampling date as "treatment" factor, subplots as complete blocks, and pair of sampling locations as randomization unit. Sample pairs were separated by 50 cm to provide appropriate lag distances for geostatistical analyses. Sampling dates were chosen along a seasonal gradient with the following characterization: 1) beginning of vegetation (April 5th), 2) stage of main plant growth (May 17th), 3) peak of plant biomass (June 27th), 4) two weeks after mowing (August 16th), 5) nine weeks after mowing (October 5th) and 6) after the first frost (November 21st). Accordingly, a total of 360 soil samples were collected (60 per date × 6 dates) in the year 2011.

Soil samples were collected with core augers (diameter 58 mm). The upper 10 cm layer was taken at each sampling point (see Figure S6-13) after vegetation was removed and the top one cm, consisting of litter, was discarded from the sample. Subsequently, the soil was immediately stored at 4 °C and sieved (< 5 mm) within 24 h after sampling to remove stones, roots and macrofauna. An aliquot for molecular analyses was stored at -20 °C before processing in the laboratory. A detailed description of the sampling design and procedure can also be found in Regan et al. (2014).

6.6.2. DNA extraction and pyrosequencing of AMF amplicons

DNA was extracted from two replicates of each homogenized soil subsample (300 mg each) according to the manufacturer's protocol using the FastDNA® SPIN Kit for Soil (MP Biomedicals, Solon, OH, USA) as described in Stempfhuber et al. (2016). Independent measurements of DNA concentration from both sample replicates were made on a NanoDrop® ND-1000 spectrophotometer (Thermo Scientific, Wilmington, DE, USA). The replicates were subsequently pooled and re-measured, confirming the final DNA concentration of each sample, which was diluted to a PCR template concentration of 5 ng DNA ml^{-1} with ultra-pure water. A semi-nested PCR protocol was used to amplify the ≈ 630 bp-long small subunit (SSU) region of the AMF 18S rDNA via pyrosequencing analysis (454 GS FLX, Roche). In the first PCR run (PCR I) a Glomeromycota-specific region was amplified with the primer set GLOMERWT0/GLOMER1536 (Wubet et al., 2006), followed by the semi-nested second PCR reaction with the forward general fungal primer NS31 (Simon et al., 1992) including the A adaptor and a 10 bp multiplex identifier (1 of 60 different MIDs), and the B adaptor including the reverse modified AMF primer AM1a and AM1b (Morris et al., 2013). The first PCR was carried out at a 25 µl reaction volume with 0.5 µl of diluted DNA template (5–20 ng $µl^{-1}$), 12.5 µl GoTaq Green Mastermix 2× (Promega, Mannheim, Germany), 1 µl of each primer (25 µM) on an Eppendorf Mastercycler DNA Engine Thermal Cycler PCR (Eppendorf, Hamburg, Germany) with the following PCR conditions: 98 °C for 30 s, 5 cycles of 94 °C for 30 s, 60 °C (-1 °C/cycle, 4 cycles) for 30 s, 72 °C for 1 min, and 25 cycles of 94 °C for 30 s, 55 °C for 30 s, 72 °C for 1 min, and for extension 72 °C for 5 min. For the semi-nested PCR, two separate amplifications were performed using 1 µl of the diluted amplified product of PCRI (1:10), 25 µl GoTaq Green Mastermix 2x, and 1 µl of each primer (25 µM); these 50 µl-reactions were run under the following conditions: 98 °C for 30 s, followed by 30 cycles of 94 °C for 30 s, 63 °C for 30 s, 72 °C for 1 min, and 72 °C for 5 min.

Each sample in both PCR amplification steps was amplified in triplicate and accompanied by a negative control. The semi-nested PCR amplified products were pooled per sample, taking into account the amplicon concentration (checked by a 1.5% agarose gel). Pooled samples (30 µl each) were purified with the QIAquick Gel Extraction Kit (Qiagen GmbH, Hilden, Germany) following the manufacturer's recommended protocol. The purified products were quantified by fluorometry using Quant-iT™

PicoGreen ® dsDNA Assay Kit (Life Technologies GmbH, Darmstadt, Germany) as suggested by Roche Diagnostics GmbH (Mannheim, Germany) for amplicon library preparation. Equimolar concentrations of 60 MID tagged amplicons were loaded into individual lanes on a GS-FLX LUMITRAC 600 plate (Titanium Series) separated with a four-lane gasket and sequenced at the Department of Soil Ecology, UFZ – Helmholtz-Centre for Environmental Research (Halle/Saale, Germany).

6.6.3. Bioinformatic analysis of sequence data

Sequence read quality filtering and splitting of the dataset into individual samples was performed using mainly MOTHUR (Schloss et al., 2009). Sequences were trimmed using the "keepfirst" command in order to discard sequences with less than 300 bp and chopping at least 50 bp from potential noisy sequence ends. Simultaneously, all sequences with average quality scores of below 20 as well as MID- and primer sequences were removed. Sequences were then downsampled to the smallest read number per sample (1,562 sequences per sample) and potential chimeric sequences were identified and removed by UCHIME (Edgar et al., 2011) as implemented in MOTHUR. These quality-filtered sequences were clustered into OTUs based on the algorithm implemented in CD-HIT-EST (Huang et al., 2010) with a sequence similarity threshold of 97%. The representative sequence for each resulting OTU was compared to a GAST (Global Alignment for Sequence Taxonomy)-based taxonomic assignment of an NCBI based fungal reference data set (Huse et al., 2008) at the 97% similarity level. All non-Glomeromycota OTUs were removed from the dataset (≈ 11% of sequences). Representative sequences (most abundant sequence per OTU) of the Glomeromycota OTUs were further taxonomically assigned by using the MaarjAM virtual taxa reference database (web-based database for studies of the diversity of arbuscular mycorrhizal fungi, version 0.8.1 beta; Öpik et al., 2010).

The raw SSU DNA sequences were deposited in the National Center for Biotechnology Information (NCBI) Sequence Read Archive (SRA) under study accession number SRP137677. In addition to all measured values, the analyzed and processed data used in this study can be found in the BExIS database (https://www.bexis.uni-jena.de/).

6.6.4. Environmental properties

The interdisciplinary approach of the *SCALEMIC Experiment* permits data from previous works on various environmental properties of the site to be used in the present study. We collected information on plant diversity (richness, Shannon index) on three sampling dates (May, June, and October) and plant biomass (aboveground biomass of grasses, herbs and legumes; root and litter biomass; Regan et al. (2014), Regan et al. (2015), Klaus et al. (2016)). We also measured soil texture, bulk density, water content, mineral nitrogen (N_{min} = NH_4^+ + NO_3^-), total carbon and nitrogen, extractable organic carbon and extractable nitrogen (EOC, EN), bioavailable phosphate (PO_4^{3-}), pH, bacterial and fungal biomass (phospholipid fatty acid (PLFA) content; Regan et al. (2014)); as well as bacterial and archaeal abundances (qPCR on 16S rRNA; Regan et al. (2017)). These variables were used in statistical analyses to determine their explanatory power with respect to AMF OTU richness and community composition (see detailed list of environmental properties in Table S6-4).

6.6.5. Statistical analyses

Statistical analyses were performed using the software R (version 3.4.0; R Development Core Team, 2017) unless stated otherwise. First, to test whether rare AMF taxa (OTUs represented by ≤ 3 sequence reads per sample) affected estimates of beta-diversity, we performed Procrustes correlation analysis based on Bray Curtis dissimilarity using the protest function (Peres-Neto and Jackson, 2001) of the "vegan" R-package (Oksanen et al., 2013). This approach provides information about congruence between two non-metric multidimensional scaling (NMDS) ordinations; in our case AMF data matrices comprising all OTUs and only abundant OTUs (OTUs represented by > 3 sequence reads per sample) with 999 permutations. Results indicated nearly identical ordinations in the presence or absence of rare AM fungal OTUs on AMF beta-diversity (Procrustes correlation coefficient = 0.9915, $p = 0.001$). Hence, all subsequent analyses were performed using the relative abundance AMF community matrix excluding singletons, doubletons and tripletons.

To assess the spatial distribution of the richness of all AMF OTUs, and of the OTUs belonging to the genera *Glomus* and *Claroideoglomus*, semivariogram analyses were performed using the R package "gstat" (Pebesma, 2004). Data were checked for normality of distribution and were log or square root transformed if necessary according to McBratney and Webster (1986). As environmental data did not show general distribution trends across the study site in preliminary analyses, isotropy was assumed for semivariogram analysis. Subsequently, empirical semivariograms for the three AMF groups at each sampling date were computed separately. In cases where empirical semivariograms indicated spatial autocorrelation, semivariogram models were fitted using the “fit.variogram” function. Bin sizes were restricted to minimum 35 points per bin; spherical, exponential and linear models were fitted using the default method of the “fit.variogram” function. The model with the lowest sum of squared error (SSErr) was selected. To estimate the amount of variance that was spatially correlated, the percent spatial structure was calculated by subtracting the nugget effect from the sill, and dividing the remaining, or partial sill, variance by the sill variance. Kriged maps for semivariogram models were generated with ArcGIS (ESRI, 2010, Environmental Research Institute, Redlands, CA, USA).

The effects of sampling date and environmental variables on the OTU richness of all AMF and of the genera *Glomus* and *Claroideoglomus* were assessed using LME models accounting for the spatial sampling design. First, different model structures were tested with SAS 9.4 (SAS Institute Inc., Cary, USA) using subplot number as random block effect, and models were evaluated and chosen based on Akaike’s information criterion (AIC) (see Table S6-5). The addition of spatial autocorrelation structures as well as addition of a random effect for pairs of sampling locations did not substantially improve model fit, and this was also the case for an addition of temporal autocorrelation structure. As the model was to be used repeatedly for selection of important covariates, we chose a model that included a subplot effect and residual error as random effects. The resulting model structure was as follows:

$$y_{ijk} = \mu + b_j + \beta_1 x_{ijk(1)} + \cdots + \beta_n x_{ijk(n)} + e_{ijk}$$

where y_{ijk} is the value of the response variable for the i-th sampling date on the j-th subplot at the k-th sampling location, b_j is the random effect for the j-th subplot, $\beta_{1\text{–}n}$ are the slopes of the regression on the predictor variables (= fixed effects) $x_{ijk(1\text{–}n)}$, and e_{ijk} is the independently normally distributed error term with constant variance. This model structure was subsequently used for all LMEMs, which were computed in R using the package “nlme” (Pinheiro et al., 2017). We separately assessed the effects of sampling date and environmental variables in univariate models for each independent variable for total AMF OTUs, *Glomus,* and *Claroideoglomus*. To detect those environmental variables which were most strongly related to the observed temporal effects, additional LMEMs were computed on the combination of individual environmental variables together with sampling date. The best predictors among plants as well as abiotic and biotic soil properties were then included in the final LMEMs. These contained all significant drivers, and were set up separately for total AMF OTUs, *Glomus*, and *Claroideoglomus*. Models with best predictor variables were selected based on lowest AIC (based on full maximum likelihood) using the "stepAIC" function with forward and backward selection, and checked for homoscedasticity and normal distribution of residuals. Spearman correlations of environmental variables in the final models revealed no considerable multicollinearity. Explained unique variance of dependent variables by independent variables and random effects was assessed following the approach of Nakagawa and Schielzeth (2013) using the function "sem.model.fits" of the "piecewiseSEM" package (Lefcheck, 2016). Separate models were calculated for models that contained plant diversity data because these were only available at three sampling dates.

To assess AMF beta-diversity, Sørensen distances (β_{SOR}), as well as their turnover (β_{SIM}) and nestedness (β_{SNE}) components, were calculated using a function generalizing the "beta.sample" algorithm from the R package "betapart" (Baselga and Orme, 2012); see supplement material for further details). In accordance with the nested study design, the means of the distances between all combinations of within-subplot repetitions were calculated. Significance of groupings of community composition by sampling date and subplot were assessed by analysis of similarities (ANOSIM), as implemented in the R package "vegan" (Oksanen et al., 2018). To compare community structures at different sampling dates within and between subplots, the complete Sørensen distances between all samples were calculated and the median values of all pairwise distances matching each comparison were extracted and visualized using the R package "beanplot" (Kampstra, 2008). Significance of comparisons was established using the non-parametric Mann-Whitney test.

To detect which environmental variables were sources of variation in β_{SOR}, permutational multivariate analysis of variance based on the Sørensen distance matrix was performed using the function "adonis" from the R package "vegan" (Oksanen et al., 2018). First, all z-transformed environmental variables were applied in separate univariate models, with stratification by sampling date. In a second model, all significant variables were combined in descending order of their significance in the first run, again with stratification by sampling date. Spearman correlations of the significant variables revealed no considerable multicollinearity.

Spearman correlations between the temporal developments of β_{SOR} between consecutive sampling dates (delta) at each subplot were calculated and visualized by hierarchical clustering of the inverse correlation by Ward's criterion using the R packages "dendextend" (Galili, 2015) and "vegan" (Oksanen et al., 2018). Correlation between patterns in temporal development of mean turnover to environmental parameters at each subplot was assessed using the "vegan" (Oksanen et al., 2018) implementation of Mantel's test.

In order to relate spatial and temporal patterns in β_{SOR}, the approach of Mellin et al. (2014) was adapted to the present dataset. Briefly, for spatial β_{SOR}, the average of the β_{SOR} values for each sampling date of AMF communities between each subplot and its neighbours was calculated. For temporal β_{SOR}, the mean delta at each sampling plot was calculated. Linear models between both β_{SOR} terms were fitted for 1000 different rarefactions and compared to null-models based on 1000 draws of species identities (based on their relative probability of occurrence among samples), while holding constant the total number of species in each sample. To detect further variables contributing to the spatio-temporal patterns in β_{SOR}, OTU richness at each subplot and environmental variables and their changes over time were included in the models.

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Authors declare no conflict of interests.

6.8. Author Contributions

KG, RSB and SK contributed equally to this work. EK, SM and HPP designed the *SCALEMIC Experiment*. KG, RSB, SK, KMR, EK, FB and TW developed the concept of the current study and KG, RSB and SK drafted the manuscript. KMR conducted DNA extractions and SK conducted AMF DNA amplification and preparation of sequencing libraries. SK and TW performed bioinformatic processing of sequences. RSB, SK, KMR, MF, DP, DB and SM provided data. RSB performed geostatistics and together with HPP fitted linear mixed effect models. KG and AHB performed multivariate statistics. KMR edited and corrected the manuscript's English. All authors read and revised the manuscript.

6.9. Originality-Significance Statement

Our study investigated temporal and spatial variability in arbuscular mycorrhizal fungi (AMF) α- and β-diversity at the plot scale (10 m x 10 m), linking these to shifts in the composition of their symbiotic plant partners within a vegetation period. This is amongst the first studies to characterize such short-term variations in both diversity measures at this small scale.

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7. Plant functional trait shifts explain concurrent changes in the structure and function of grassland soil microbial communities

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7.1. Abstract

1) Land-use intensification drives changes to microbial communities and the soil functions they regulate, but the mechanisms underlying these changes are poorly understood as land use can affect soil communities both directly (e.g. via changes to soil fertility) and indirectly (e.g. via changes to plant inputs).

2) The speed of microbial responses is also poorly understood. For instance, whether it is long-term legacies or short-term changes in land-use intensity that drive changes to microbial communities.

3) To address these topics, we measured multiple microbial functions, bacterial and fungal biomass and abiotic soil properties at two time intervals three years apart. This was performed in 150 grassland sites differing greatly in management intensity across three German regions.

4) Observed changes in microbial soil properties were related to both long-term means and short-term changes in: abiotic soil properties, land-use intensity, community abundance weighted means of plant functional traits and plant

biomass properties in regression and structural equation models. Plant traits, particularly leaf phosphorus, and soil pH were the best predictors of change in soil microbial function, as well as fungal and bacterial biomass, while land-use intensity showed weaker effects.

5) Indirect legacy effects, in which microbial change was explained by the effects of long-term land-use intensity on plant traits, were important, thus indicating a time lag between plant community and microbial change. Whenever effects of short-term changes in land-use intensity were present, they acted directly on soil microorganisms.
6) *Synthesis:* The results provide new evidence that soil communities and their functioning respond to short-term changes in land-use intensity, but that both rapid and longer time scale responses to changes in plant functional traits are at least of equal importance. This suggests that management which shapes plant communities may be an effective means of managing soil communities and the functions and services they provide.

7.2. Introduction

Land-use intensity is a major driver of plant and soil microbial communities throughout the world's grasslands (Smith and Rushton, 1994; Bossio et al., 1998; Keil et al., 2011; de Vries et al., 2012; Meyer et al., 2013). Intensification significantly impacts ecosystem processes, with major implications for the delivery of a wide range of grassland ecosystem services, including fodder production, soil carbon storage and clean water supply (Allan et al., 2015; Bach et al., 2016; Soliveres et al., 2016). To date, many conclusions about the impacts of land-use intensification have been drawn from comparative observational studies in which the properties of high intensity sites are compared to those undergoing low intensity management (Meyer et al., 2013; Allan et al., 2015; Manning et al., 2015). As a result, little is known regarding the mechanisms through which such changes operate, and the relative sensitivity of different ecosystem properties to short-term changes in land use relative to long-term legacies of past land use. Furthermore, we know little of how rapidly soil microbes, which are key drivers of nutrient cycling and other soil functions, respond to changes in land-use intensity and associated changes in vegetation.

Increases to grassland land-use intensity usually operate via increased livestock densities, higher rates of fertilisation and greater mowing frequency (Blüthgen et al., 2012). These actions affect communities of plants and soil microorganisms and the processes they regulate through a wide range of interrelated mechanisms, which we review in brief in the following section. Initially, the physical and chemical soil environment is altered. Soil compaction by livestock and machinery can occur, not only influencing soil moisture and temperature regimes, but also reducing microbial biomass (Boeddinghaus et al., 2015). Furthermore, nutrient availability to both microbes and plants is increased by fertilisation, with effects on microbial communities including increases in the abundance of bacteria relative to fungi (de Vries et al., 2012), and a shift of microbial life strategies towards copiotrophic microbial taxa (Leff et al., 2015). These changes in nutrient status can also cause widespread changes to soil microbial properties and functions, including altered microbial biomass, and soil enzyme activities (Kandeler and Eder, 1993; Bardgett and Leemans, 1995; Donnison et al., 2000). Nitrogen (N) fertilisation in the form of reduced N can also lead to soil acidification by nitrification (Bardgett et al., 1999). In turn, soil pH can affect microbial communities and soil carbon cycling (Fierer and Jackson, 2006; Rousk et al., 2009; Fornara et al., 2011). Some combination of these effects is therefore likely to be responsible for observed changes in the microbial community, e.g. fungal and bacterial abundance, and its function, such as soil enzyme activities, under grassland management intensification. However, the impact of these direct effects of intensification is accompanied by additional effects that operate via the plant community, which we term here indirect effects. High land-use intensity typically reduces plant species diversity and selects for plants with a ‘fast’ life history strategy (Pfestorf et al., 2013) typified by leaves with high N and phosphorus (P) content, thin and/or low density, rapid turnover times and low dry matter content, reflecting low concentrations of structural compounds (Reich, 2014). These traits can affect soil function by altering the chemistry and quality of litter inputs to the soil (Wardle et al., 2004; Orwin et al., 2010; Reich, 2014). Accordingly, community level measures of “fast-slow” traits (e.g. the community abundance weighted mean, CWM) can represent an integrative measure of vegetation responses to the long-term environment (Garnier et al., 2004), and the overall quality and quantiy of litter inputs to the soil from the dominant species of the plant community (Grime, 1998). Such measures have been found to explain variation in soil microbial community composition and carbon storage in several studies (Wardle et al., 1998; Garnier et al., 2004; de Vries et al., 2012; Manning et al., 2015). The symbiosis between mycorrhiza and plants is also affected by soil nutrient concentrations (Treseder, 2004). The intensity of this symbiosis can be utilized as a plant functional trait, and related to ecosystem function (Akhmetzhanova et al., 2012). In contrast, aboveground biomass measures reflect more a fluctuating “snapshot” measure of vegetation response. Production typically increases in response to N addition, while belowground biomass is largely unaffected (Lee et al., 2010). At the same time plant cutting, e.g. through mowing and grazing, alters root exudation, and therefore soil microbial properties (Bardgett et al., 1998).

Under ‘real-world’ field conditions, the changes described above occur concurrently and are difficult to disentangle experimentally. As a result, the interrelationships between these changes have typically been examined in microcosm experiments focussing on a subset of these changes (Bardgett et al., 1999; Manning et al., 2006) and field studies are scarce. Therefore, little is known regarding the relative importance of the mechanisms described above in driving changes to soil function in “real-world” ecosystems. However, identifying the relative roles of the pathways described here is important as it not only provides insight into the fundamental drivers of soil systems, but also allows relevant management practices to be identified (e.g. liming for pH, sowing of plant functional types).

An additional knowledge gap concerns the temporal dynamics of the changes described above. To date, most studies of temporal changes have investigated either single grassland sites over the course of a single year (e.g. Regan et al. 2017), or studied temporal development gradients by sampling different sites in chronosequences (e.g. Kulmatiski and Beard, 2008). Such work provides limited information on the speed and magnitude of responses of communities to land-use change over intermediate (up to 10 years) timescales, especially as time lags in the response of soil microbes to land-use intensification may be common (Foster et al., 2003). In the case of grassland soil function for example, plant communities, and their functional properties, may take several years to fully respond to changes in land-use intensity (Poptcheva et al., 2009). These changes may, in turn, take time to be manifested in the activities of soil microorganisms that feed upon plant derived soil organic matter. Furthermore, recent work has argued that land-use legacies are not just important in determining current ecosystem function, but also in shaping responses of ecosystems to future changes (Perring et al., 2016). For example, the soil nutrient content reflects past land-use intensity and influences the effect of new nutrient inputs by determining the level of nutrient limitation of soil biota and plants (Richter et al., 2000; Perring et al., 2016).

To address the knowledge gaps described above we investigated whether the functioning and composition of microbial communities rapidly tracks short-term changes (within three years) in land-use intensity or if such changes are driven by the longer-term history of the site (legacy effect). Next, we asked whether changes in soil properties and functions were best explained by direct or indirect effects of land-use intensity changes or by changes in intermediate properties, namely changes to soil pH, plant functional traits and the quantity and nutritional quality of plant biomass (Table S7-1 gives an overview over the hypothesized pathways). We addressed these questions within the context of the large-scale and long-term Biodiversity Exploratories project (Fischer et al., 2010) by utilizing data from 150 grassland sites in three regions of Germany.

7.3. Materials and Methods

7.3.1. Study regions

Data were collected from 150 grassland sites spread evenly (50 each) across three regions of Germany within the framework of the Biodiversity Exploratories project (www.biodiversity-exploratories.de): Schwäbische Alb (South-West), Hainich-Dün (Central) and Schorfheide-Chorin (North-East) (see Figure S7-1). All three contain protected areas, with sites spanning a wide range of management intensities (Fischer et al., 2010). The regions differ in their climate and soil types: the South-West region is a biosphere reserve on calcareous bedrock with karst phenomena. Soils are typically shallow with bedrock typically 10–15 cm below the soil surface and clay rich soils. The Central region also has a parent material of calcareous bedrock and clayey-loamy soil texture, while the North-East region is a young glacial landscape with predominantly sandy and organic soils. Further details on the regional characteristics are given in Table S7-2.

7.3.2. Land-use intensity

Land-use intensity was measured as grazing intensity (number of livestock grazing units per year), frequency of mowing events per year and amount of N-fertilizer applied annually. These vary between years depending on the farmers management decisions and were assessed annually since 2006 for all 150 sites via questionnaires given to the farmers. This data was used to calculate a land-use intensity index (LUI) in which these three components are standardised according their full range within each region, given equal weighting and summed (for details see appendix 1 and Blüthgen et al., 2012). The resulting LUI is a dimensionless number ranging between 0, representing no land management, and 4.41, very intensive land-use. Preliminary analyses showed that the LUIs of the years prior to sampling (2010 and 2013) were more strongly related to soil microbial activity and biomass in 2011 and 2014, respectively, than the LUI of the actual sampling years, most likely because most farming actions in the study year happened during or after the spring soil sampling period. Therefore, the LUIs of 2010 and 2013 were chosen and the change between these years was used in analyses.

7.3.3. Soil sampling

Soil samples were collected simultaneously in all three regions within two weeks in May 2011 and May 2014. All 150 grassland plots were sampled along two orthogonal transects of 20 m (Figure S7-2). Sampling points were shifted by 50 cm in 2014 compared to 2011 to avoid an overlap of sampling positions. On each plot, 14 samples from 0–10 cm depth were taken using core augers (diameter ≈ 52 mm). Samples were mixed, cooled and transported to a field lab, then sieved (< 2 mm) and frozen at -20 °C, all within eight hours of sampling.

7.3.4. Soil microbial analyses

Microbial biomass carbon (C_{mic}) and nitrogen (N_{mic}) were measured using the chloroform-fumigation-extraction method (CFE) of Vance et al. (1987) modified according to Keil et al. (2011). Microbial phosphorus (P_{mic}) was measured by combining methods of Kouno et al. (1995) and McLaughlin et al. (1986). Details of all laboratory analyses are described in appendix 1.

Microbial functions were measured as the enzyme activities of beta-glucosidase (EC 3.2.1.21, hereafter glucosidase), beta-xylosidase (EC 3.2.1.37, hereafter xylosidase), N-acetyl-beta-glucosaminidase (EC 3.2.1.52, hereafter chitinase), phosphatase (EC 3.1.3.2) and urease (EC 3.5.1.5) as well as denitrification enzyme activity (DEA). The first four enzymes were determined by fluorescence measures after Marx et al. (2001), as described in (Berner et al., 2011). Urease activity was measured photometrically after Kandeler and Gerber (1988). Denitrification enzyme activity was measured according to Smith and Tiedje (1979) and Keil et al. (2015).

Microbial community composition, in terms of bacterial and fungal biomass, was measured from soil phospholipid fatty acid (PLFA) composition. Extraction was conducted according to Frostegard et al. (1991) and alkaline methanolysis was performed after Dowling et al. (1986) to gain fatty acid methyl esters (FAME). Each FAME was classified as bacterial or fungal according to Ruess and Chamberlain (2010). PLFA data was then used to calculate the fungal to bacteria ratio (F:B). Fungal biomass was also determined as ergosterol content of bio-membranes according to a modified approach of Djajakirana et al. (1996).

7.3.5. Soil abiotic analyses

Soil pH was measured in 0.01 M $CaCl_2$ (1:2.5 ratio of soil:$CaCl_2$-solution). Each site was equipped with a weather station monitoring soil temperature (mean of measures in 5 and 10 cm depth) and moisture (10 cm depth). Volumetric soil moisture was recalculated as percent of the water holding capacity of each plot and is referred to as soil water content (SWC) hereafter. *A priori* data analyses revealed that microbial variables were best predicted by weather data, when it was calculated as arithmetic mean over a period of 30 days prior to the sampling date. These values were used in subsequent analyses.

7.3.6. Plant data

Every year since 2008, from middle of May to middle of June, the percentage cover of all vascular plant species was estimated in a 4 m × 4 m quadrat at all sites. This data was combined with data on plant traits from the TRY database (Kattge et al., 2011) (for full reference list of the TRY database data see appendix 1) to calculate CWM of the following plant traits: specific leaf area (SLA, $mm^2\ g^{-1}$ DM), leaf P content (leaf P) and leaf N content (leaf N) both in $mg\ g^{-1}$ DM. In addition, the CWM for mycorrhizal intensity (MycInt, % colonized root length) was calculated from the database of Akhmetzhanova et al. (2012). Community abundance weighted means were used to represent plant trait effects according to the mass ratio hypothesis, which postulates that ecosystem properties are driven by the traits of the dominant species in a community (Grime, 1998; Garnier et al., 2004). While intraspecific variation in traits can be significant, CWMs are likely to capture much between-community level trait variations over large environmental gradients with significant species turnover.

Plant biomass was sampled in May 2011 and 2014 adjacent to the vegetation record by cutting the aboveground (living) plant biomass ($g\ m^{-2}$) in five 0.25 m^2 squares 2–3 cm above ground. The pooled composite sample of each site was dried (48 h at 80 °C), milled and the nutritional quality of plant biomass was measured thereafter: percent neutral detergent fibre (NDF), acid detergent fibre (ADF) and acid detergent lignin (ADL, lignin), as well as percent P and N content of the biomass were analysed using near-infrared spectroscopy (NIRS) as described in Klaus et al. (2016) and Kleinebecker et al. (2011). From these measures, cellulose (= ADF – ADL) and hemicellulose (= NDF – ADF) content were calculated according to Kirchgeßner (2014).

7.3.7. Historic and change data

Legacy effects, *sensu* James (2015), are defined as the effects of long-term environmental conditions on the current status of a system and changes in this system in the following years. In our study legacy effects were considered those of the land-use intensity and plant functional traits that occurred up to five years before 2011, thus distinguishing them from current, short-term changes between the two sampling years: 2011 and 2014. To differentiate legacy effects of land-use intensity and plant functional traits from the effects of short-term changes in these properties, we calculated separate measures for these time periods and termed them “historic” (h) and “changes” (Δ) for the ecosystem variables. Historic LUI was calculated as the mean LUI of 2006–2010, historic CWM traits as the mean from 2008–2011 (see Table S7-3 for details). The changes for each variable (*y*) on each site (*i*) in between the measured years 2011 and 2014 were calculated as

$$y_{i\Delta} = (y_{i2011} - y_{i2014}) \times -1$$

with 2011 serving as base year. Pairwise *t* tests were used to identify significant differences between the investigated years. To make data for multiple variables comparable, the differences between the years were expressed as percent change with 2011 (respectively 2010 for LUI) as initial value. Historic values were calculated as the arithmetic mean over several years. An overview on all variables used in this study is given in Table S7-4.

7.3.8. Statistical analyses

Statistical analyses were performed in R versions 3.3.2 and 3.4.2 (R Core Team, 2016, 2017). Preliminary analyses showed strong differences between the three regions for most variables and strong confounding of several factors with region (e.g. soil texture, soil type and climate). Therefore, the three regions were analysed separately in subsequent statistical procedures.

7.3.8.1. Statistical modelling of changes in soil properties

We used a model selection approach to identify the environmental variables (historic and change measures) that best explained changes in microbial soil properties between 2011 and 2014. This was done with forward selection according to a hypothesized “hierarchy of controls” in which ultimate controls of soil properties were added before proximate drivers (Díaz et al., 2007). In accordance to prior knowledge presented in the introduction, explanatory variables were grouped and added in the following sequence: 1) fundamental abiotic soil properties, 2) land-use intensity variables, 3) ΔpH, as change in pH on this time scale was most likely driven by land-use change (e.g. from N-fertilisation and liming), 4) CWMs of plant functional traits, and 5) plant biomass properties, as these are partly controlled by the functional traits and respond more rapidly to changes in growing conditions. See Table S7-5 for details.

Utilizing this approach, we compared multiple linear mixed effect models for every microbial response variable in each region, using the lme function of the nlme package (Pinheiro et al., 2017). First, spatial correlation structures were tested for their significance (i.e. exponential, Gaussian, spherical, linear spatial correlation and rational quadratics). Secondly, as it comprises many unmeasured variables, soil type was tested as a random effect. If these terms did not increase model likelihood, a linear model was fitted (Crawley, 2015). This resulted in only linear models in the South-West, while some models in the Central and North-East regions included spatial autocorrelation structures (five times) or soil type (four times). Variable selection was based on Akaike’s information criterion (AIC), with new variables retained if they lowered AIC by > 2 and were significant in a likelihood ratio deletion test ($p < 0.05$). If several variables remained in the model, their first order interaction was tested. The fit of the final model was assessed based on normal distribution and heteroscedasticity of model residuals. As the range of most variables was relatively short, only linear terms were fitted. For the final selected models explained variance was calculated as the change in R^2 after deletion of each separate level of effects, and for all fixed effects (marginal R^2), according to the method of Nakagawa and Schielzeth (2013). R^2 values for each level and interaction were derived by subtracting the R^2 of the simplified model from that of the full model. Variance shared between predictors was calculated as the marginal R^2 minus the sum of the R^2 for each level of effects.

7.3.8.2. Structural equation models

Hierarchical regression modelling indicated that land-use intensity was not the most important driver of changes in microbial soil properties (see results). However, it is possible that effects of land-use intensity were present, but not detected, because land-use intensity was correlated with, and is the driver of, better predictors, e.g. changes to plant properties. This hypothesis was tested by using structural equation modelling (SEM). Due to differences between regions separate SEMs were fitted for each region. As the maximum replication was therefore 50 we limited the number of pathways to allow for reliable parameter estimation (see Table S7-6.1 for model parameters). Based on the hierarchical regression results the change and legacy effects of pH, CWM MycInt, CWM leaf P, plant biomass and plant lignin content were selected as mediator variables, as these were the best predictors in those models and, in case of CWM leaf P and plant biomass, representative of other significant plant variables (see Figure S7-3 a-c). See Figure 7-1 a, b) for details of SEM structures and Table S7-1 for details of the hypothesized pathways. Indirect pathways between LUI and microbial variables were calculated by multiplying the direct pathways between LUI, mediator and microbial variable, e.g., LUI_h and CWM leaf P_h with the pathway of CWM leaf P_h and ΔC_{mic}. Separate models were run for each microbial soil property and each of the mediator variables in the software package lavaan (Rosseel, 2012). As random effects were only retained in 9 of 42 regression models simple linear regression formula were used in the SEMs. Maximum likelihood estimation (ML) was chosen to fit models, and results were robust to the use of an alternative estimator (appendix 1). Model selection for the best mediator variable was based on two steps: 1) lowest AIC value, 2) if applicable, chi-square test results (lowest) and associated p-values ($p > 0.05$) (see Table S7-6.1 for model fits). Data were scaled between [0;1] to yield similar ranges and to allow comparison of standardized estimates between SEMs (Scherber et al., 2010). In the North-East region, all models differed significantly from the observed data co-variance matrices and no model could be selected for this region. Therefore our hypothesis of indirect land-use intensity effects could not be supported for the North-West region. This was most likely due to weak associations between variables (see Figure S7-3 c) in this region, where neither LUI nor plant traits have strong relationships with soil properties (Table 7-1, Allan et al., 2015). Additional statistical information is given in appendix 1, and an example of the R-code used for hierarchical regressions and SEMs in appendix 2.

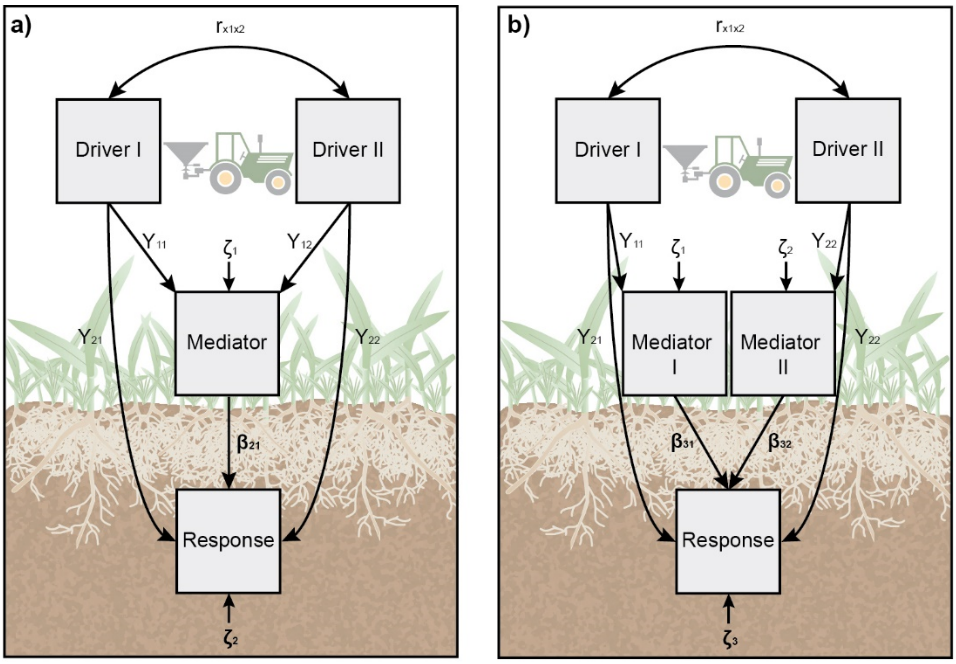


Figure 7-1: a) causal diagram of SEMs with one mediator variable (changes) for all regions, b) causal diagram of SEMs with both, historic and change values of mediator variable for all regions. LISREL notation is used. Driver I = LUIh, Driver II = ΔLUI, mediator variables (I and II in order of appearance) are i) CWM leaf Ph and ΔCWM leaf P, ii) CWM MycInth and ΔCWM MycInt, iii) pHbv and ΔpH, iv) Δplant biomass and v) Δlignin, response = endogenous soil microbial variable. Details on the hypothesized pathways are given in Table S7-1.

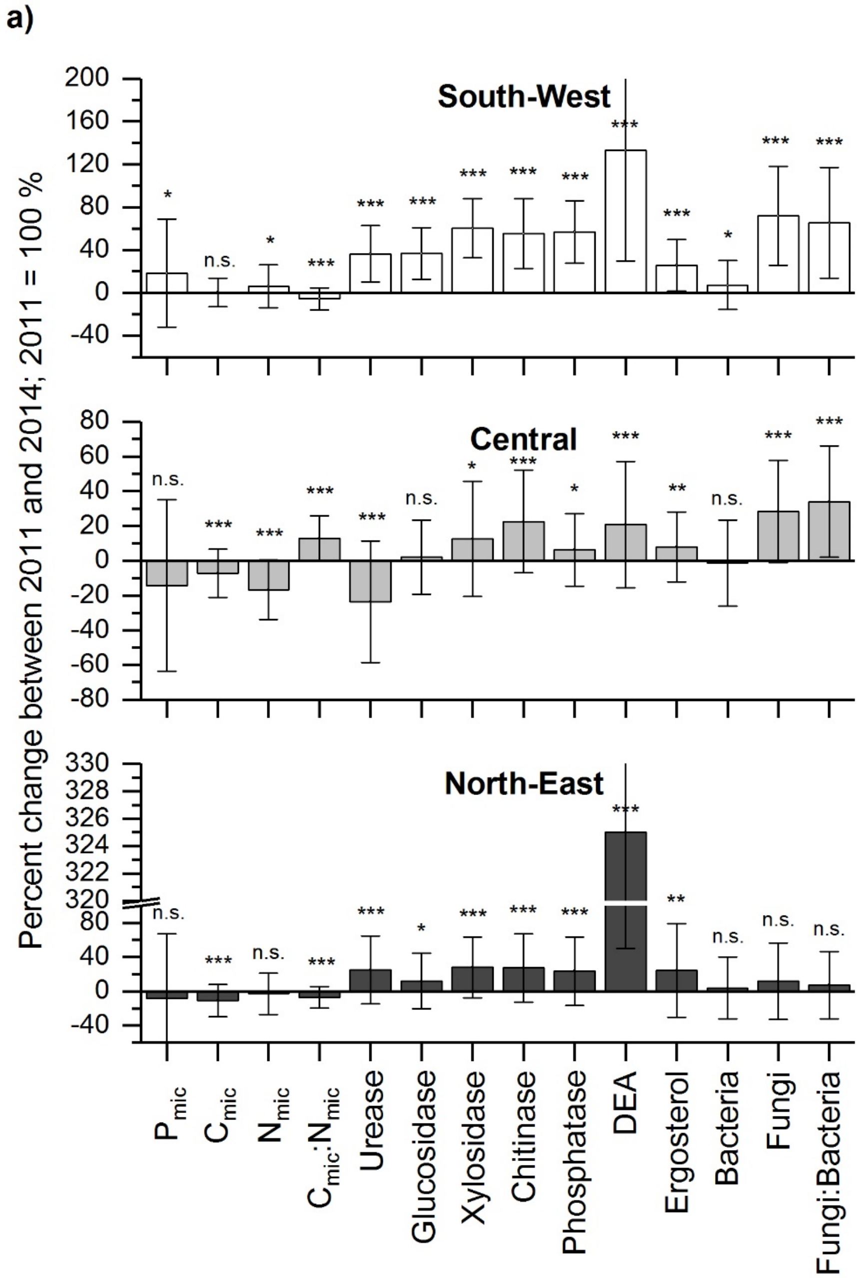
7.4. Results

7.4.1. Changes over time

Changes in soil microbial and environmental properties between 2011 and 2014 varied greatly between sites and regions (Figure 7-2 a-b). Changes in some variables were directional. Soil enzyme activities involved in C, N and P cycling, and particularly denitrification enzyme activity, were generally higher in 2014 in all three regions (Figure 7-2 a). Fungal biomass increased in all three regions (PLFA means between +11% and +72%), while microbial biomass C and N changed little in the South-West and North-East, and generally declined in the Central region. Plant biomass was much higher in 2014 compared to 2011 in all regions (Figure 7-2 b), most likely due to the hot and dry spring of 2011 (reflected by the lower SWC and higher temperature prior to sampling in the Central and North-East regions). This was accompanied by general increases in the nutritional quality of plant biomass in terms of P, cellulose, hemicellulose and lignin content, while plant biomass N either did not change (North-East) or declined (Central and South-West regions, mean values between -10% and -13%). Compared to plant biomass, the CWM of plant functional traits and LUI showed relatively smaller changes at most sites. pH changed little in the South-West and Central regions (standard deviations ≈ ±1.5%), but moderately in the North-East (standard deviations ±5.7%).

7.4.2. Recent history

The background value of pH and the historic means of pH, LUI and plant traits in each region are displayed in Figure 7-3. CWM plant traits of the fast-slow-gradient were 'fastest' in the North-East, while LUI was equally distributed across all three regions. The Central region has on average the highest pH background values (6.9), although the North-East shows the widest range of pH values.


a)
Percent change between 2011 and 2014; 2011 = 100 %
South-West
200
160
120
80
40
0
-40
* n.s. * *** *** *** *** *** *** *** *** * *** ***
Central
80
60
40
20
0
-20
-40
-60
-80
n.s. *** *** *** *** n.s. * *** * *** ** n.s. *** ***
North-East
330
328
326
324
322
320
80
40
0
-40
n.s. *** n.s. *** *** * *** *** *** *** ** n.s. n.s. n.s.
P_{mic}
C_{mic}
N_{mic}
C_{mic}:N_{mic}
Urease
Glucosidase
Xylosidase
Chitinase
Phosphatase
DEA
Ergosterol
Bacteria
Fungi
Fungi:Bacteria

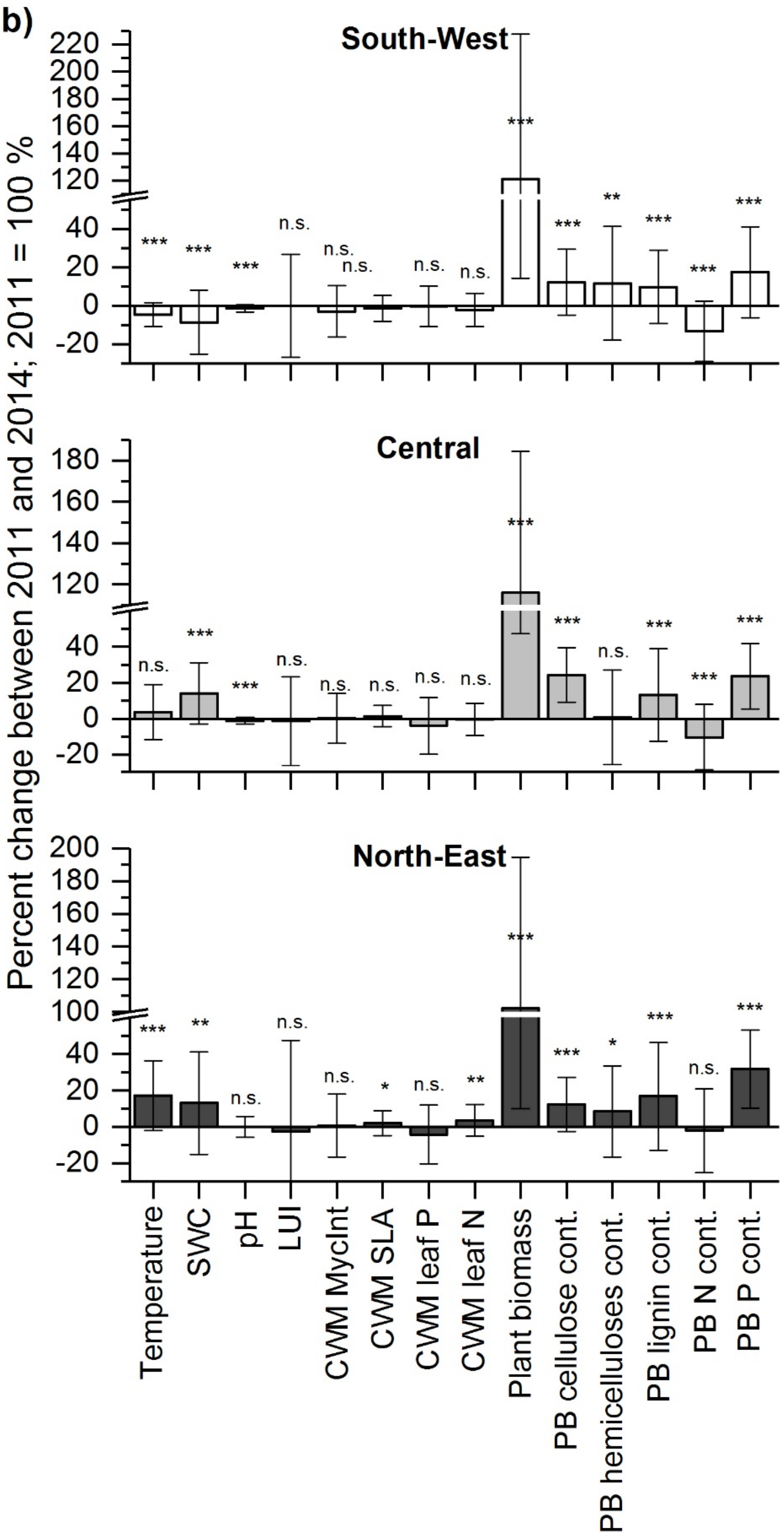


Figure 7-2: Mean regional changes in variables between 2011 and 2014 displayed as percent change of 2014 based on 2011 a) microbial soil properties and b) environmental, land management and plant variables. Whiskers indicate standard deviation. Significant differences between the investigated years in each region based on pairwise t tests are displayed as: $p < 0.001$ = ***, $0.001 < p < 0.01$ = **, $0.01 < p < 0.05$ = *, $p > 0.05$ = not significant (n.s.).

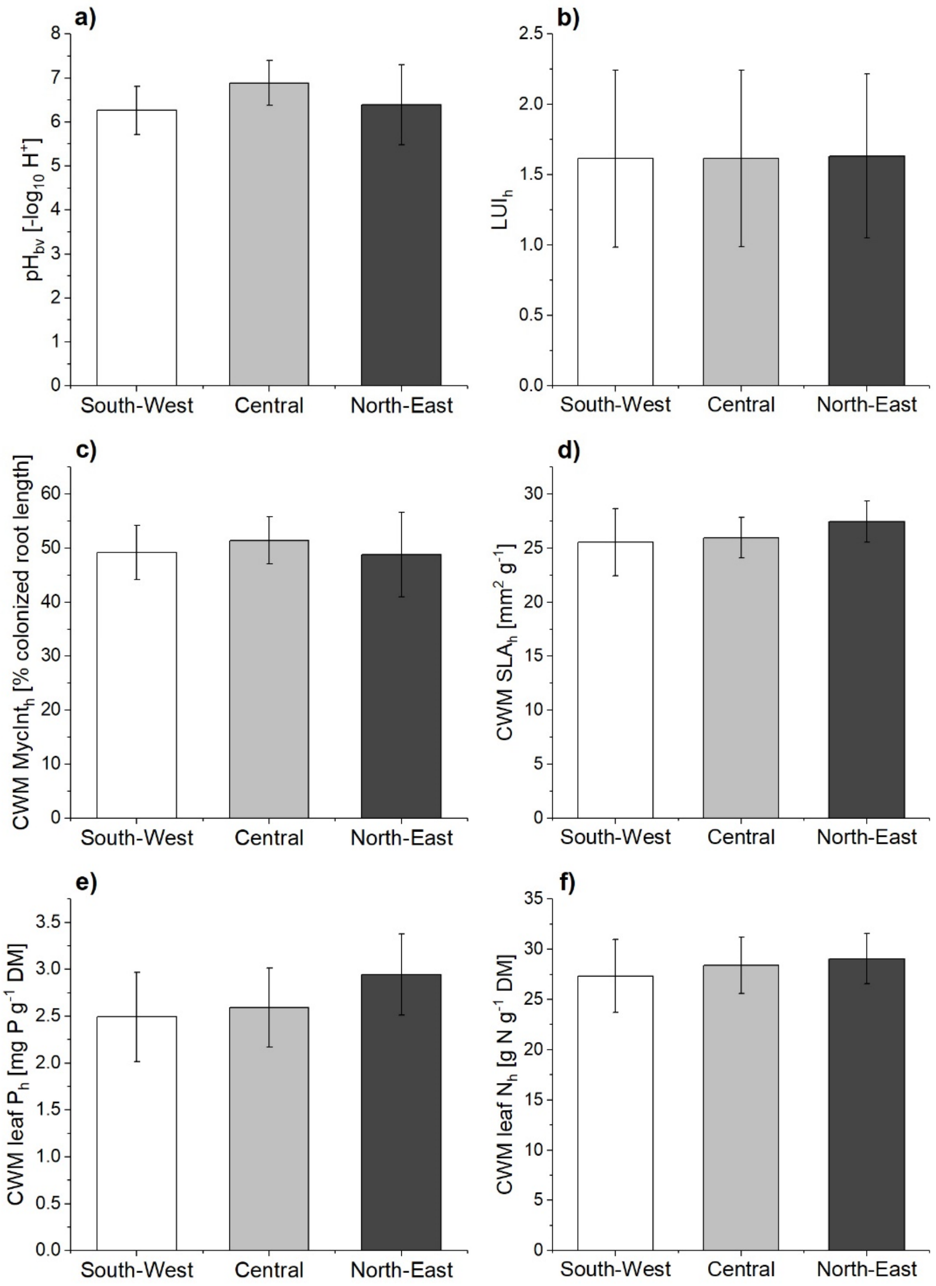


Figure 7-3: Mean values of explanatory variables for a) background values of pH and historic mean values of b) LUI, c) CWM MycInt, d) CWM SLA, e) CWM leaf P and f) CWM leaf N (mean per region). Whiskers indicate standard deviation.

7.4.3. Drivers of microbial change

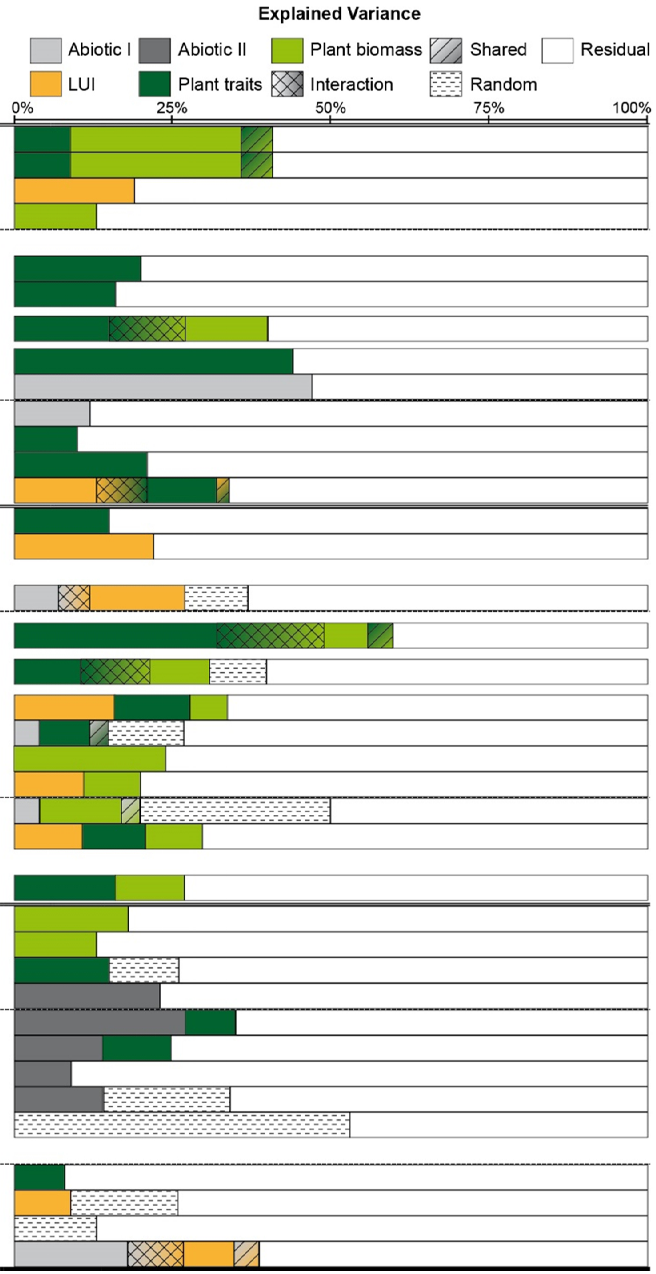
In all three regions model selection showed that changes in plant community properties, particularly plant functional traits, were better able to explain changes in microbial soil properties than changes in land-use intensity and environmental drivers, especially in the South-West (Table 7-1). However, in the Central region LUI effects were also retained in 36% of the models, and in the North-East the influence of changing pH was important (retained in 36% of the models), especially in explaining changes in enzymatic activities and the ΔC_{mic}:N_{mic} ratio.

Changes in most microbial properties were driven by just one or two explanatory variables (43% and 33% percent of all models, respectively); interactions between variables were much rarer (present in 21% of all models). Furthermore, recent changes were more often linked to the changes in microbial soil properties than were legacy effects (retained in 54% and 27% of models, respectively). Of the abiotic environmental properties, it was soil pH which most often explained soil microbial changes (retained in 32% of models). In contrast, temperature had little influence (retained in 7% of models) and SWC none at all. Changes in pH did not alter soil microbial properties in the South-West and Central regions, but negatively impacted ΔC_{mic}:N_{mic}-ratio and positively affected several enzyme activities in the North-East, where it also explained, on average, 16% of the unique variance.

Increases in LUI were accompanied by a reduction in fungi, in that short-term changes in LUI were negatively related to Δergosterol content in the South-West, and to Δfungal abundance in the Central region (Table 7-1). The contrary was found in the more organic soils of the North-East. Legacy effects of LUI were rarely related to microbial soil properties in the South-West (only to ΔP_{mic}) and not at all in the North-East, but were retained in 29% of the models in the Central region.

Table 7-1: Results of hierarchical regressions in South-West, Central and North-East Germany. Models are displayed in form of: $y_i = b_0 + b_1x_{1i} + b_2x_{2i} + \ldots + b_kx_{ki} + \varepsilon_i$. Bars indicate the percentage of unique variance explained by each level based on R^2; Δ = change, $_h$ = historic, n = number of observations. Explained variance is the marginal R^2 attributable to each level of effect. In case of “no model fit”, model assumptions of homoscedasticity of variance and normal distribution were not met and therefore no reliable model could be selected.

Region	Category	Model	n
South-West	Biomass	ΔC_{mic} = -29.29 + 112.5 * ΔCWM leaf P + 17.89 * Δplant biomass cellulose content	44
		ΔN_{mic} = 0.45 + 25.29 * ΔCWM leaf P + 4.1 * Δplant biomass cellulose content	44
		ΔP_{mic} = -12.45 + 12.16 * LUI_h	34
		ΔC_{mic}:N_{mic} ratio = -0.27 - 0.09 * Δplant biomass cellulose content	44
	Function	Δglucosidase = no model fit	
		Δxylosidase = -110.65 + 10.45 * CWM SLA_h	44
		Δchitinase = 243.39 + 30.95 * ΔCWM SLA	41
		Δurease = 342.39 - 5.35 * CWM $MycInt_h$ + 504.22 * Δplant biomass N content - 9.16 * CWM $MycInt_h$: Δplant biomass N content	44
		ΔDEA = -0.31 + 0.67 * ΔCWM leaf P + 0.65 * CWM leaf P_h	44
		Δphosphatase = 4403 - 558.37 * pH_{bv}	44
	Community	Δbacteria = 3.02 - 15.52 * ΔTemp	44
		Δfungi = 16.12 - 0.4 * CWM SLA_h	44
		Δfungi:bacteria ratio = 0.14 - 0.04 * CWM leaf P_h	44
		Δergosterol = 8.85 - 18.99 * ΔLUI - 2.24 * CWM leaf P_h + 6.28 * ΔLUI:CWM leaf P_h	44
Central	Biomass	ΔC_{mic} = 238.62 - 10.83 * CWM SLA_h + 8.13 * ΔCWM leaf N	48
		ΔN_{mic} = 4.86 - 13.26 * LUI_h	48
		ΔP_{mic} = -6.56	43
		ΔC_{mic}:N_{mic} ratio = -2.23 + 0.32 pH_{bv} + 3.76 * LUI_h - 0.48 * pH_{bv}:LUI_h	48
	Function	Δglucosidase = -2827 + 100.78 * CWM SLA_h - 388.54 * ΔCWM leaf P + 25.65 * Δplant biomass - 0.94 * CWM SLA_h:Δplant biomass	48
		Δxylosidase = 16.71 + 99.42 * ΔCWM leaf P + 0.03 * Δplant biomass - 1.05 * ΔCWM leaf P:Δplant biomass	46
		Δchitinase = 207.82 - 85.2 * LUI_h - 109.92 * ΔCWM leaf P + 25.3 * Δplant biomass lignin content	48
		Δurease = 75.45 + 10.16 * ΔTemp - 46.88 * CWM leaf P_h	43
		ΔDEA = -0.19 + 0.003 * Δplant biomass	48
		Δphosphatase = 144.22 - 129.23 * LUI_h + 0.79 * Δplant biomass	48
	Community	Δbacteria = -71.64 + 8.66 * pH_{bv} + 0.08 * Δplant biomass	48
		Δfungi = 0.84 - 1.82 * ΔLUI + 0.27 * ΔCWM leaf N + 0.01 * Δplant biomass	48
		Δfungi:bacteria ratio = no model fit	
		Δergosterol = 16.01 - 0.54 * CWM leaf N_h + 0.89 * Δplant biomass lignin content	45
North-East	Biomass	ΔC_{mic} = -125.43 + 0.33 * Δplant biomass	49
		ΔN_{mic} = -13.27 + 0.06 * Δplant biomass	49
		ΔP_{mic} = -5.12 - 15.65 * ΔCWM leaf P	45
		ΔC_{mic}:N_{mic} ratio = -0.42 - 1.04 * ΔpH	49
	Function	Δglucosidase = 194.69 + 729.2 * ΔpH - 17.46 * ΔCWM MycInt	49
		Δxylosidase = 78.3 + 98.46 * ΔpH - 3.88 * ΔCWM MycInt	49
		Δchitinase = 128.63 + 147.47 * ΔpH	49
		Δurease = 51.61 + 102.7 * ΔpH	49
		ΔDEA = 1.15	49
		Δphosphatase = no model fit	
	Community	Δbacteria = -39.19 + 0.85 * CWM $MycInt_h$	49
		Δfungi = 0.46 + 0.44 * ΔLUI	49
		Δfungi:bacteria ratio = 0.01	49
		Δergosterol = 15.39 - 2.09 * pH_{bv} + 14.58 * ΔLUI - 1.96 * pH_{bv}:ΔLUI	49



Plant functional traits were the most frequently selected explanatory variables (retained in 55% of all models, and in 71% in the South-West). They also explained most of the unique variance across all hierarchical regression levels, both in the South-West and Central Region (up to 44% and 49%, respectively), thus indicating that they were important drivers of changes to soil properties. Of these, CWM leaf P was the most important, and it was significantly related to soil microbial properties in all three regions. Its change and historic values were both negatively and positively related to microbial variables including: ΔC_{mic}, ΔN_{mic}, ΔP_{mic}, enzyme activities of ΔDEA, Δurease, Δglucosidase, Δchitinase and Δxylosidase, Δfungi:bacteria-ratio and Δergosterol content. The other plant traits had less consistently strong effects and were never important in all three regions.

Overall, plant functional traits were more important and explained more unique variance than plant biomass properties in all three regions. However, where plant biomass or its nutritional properties, i.e. cellulose and lignin content, were retained in models, their increases were consistently related to increases in soil microbial variables.

7.4.4. Direct and indirect land management effects

Structural equation modelling consistently selected CWM leaf P as the most likely mediator variable for every soil microbial property. The selected models showed that indirect legacy effects of historic LUI operated via historic CWM leaf P in the South-West for function and community measures, but that direct effects of ΔLUI also played a role. In contrast direct effects of historic LUI drove changes in microbial biomass in both regions and in functions in the Central region; indirect effects of ΔLUI were not found at all (Figure 7-4, see Tables S7-6.1-3 for parameter values). In the South-West and Central regions historic LUI strongly positively affected historic CWM leaf P ($r \approx 0.72$ South-West, $r \approx 0.64$ Central). The SEMs also showed that changes in CWM leaf P were independent of LUI change, but important drivers of change in many soil properties, a result consistent with the hierarchical models.

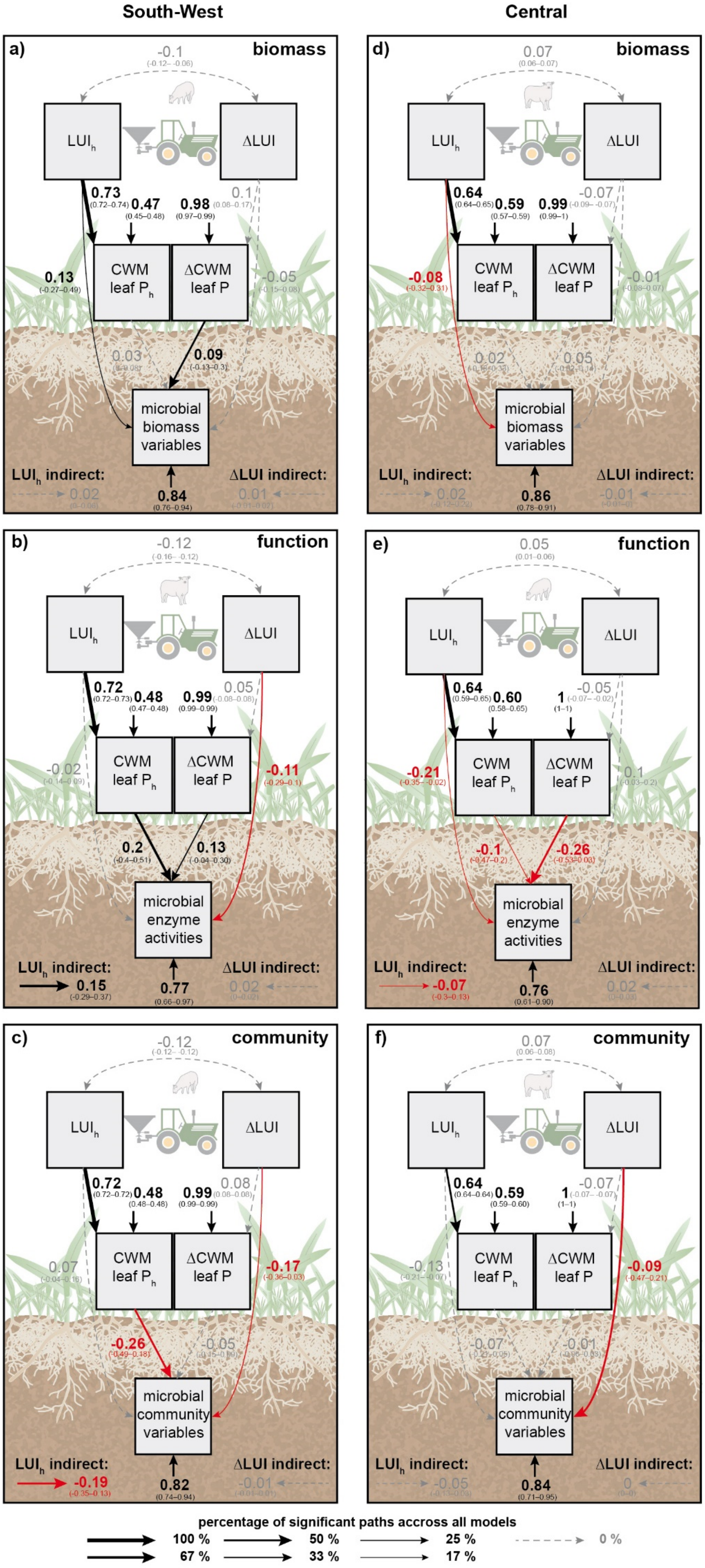

South-West
Central
a)
biomass
-0.1
(-0.12– -0.06)
LUI_h
ΔLUI
0.73
(0.72–0.74)
0.47
(0.45–0.48)
0.98
(0.97–0.99)
0.1
(0.08–0.17)
0.13
(-0.27–0.49)
CWM leaf P_h
ΔCWM leaf P
-0.05
(-0.15–0.08)
0.03
(0–0.08)
0.09
(-0.13–0.3)
microbial biomass variables
LUI_h indirect:
0.02
(0–0.06)
0.84
(0.76–0.94)
ΔLUI indirect:
0.01
(-0.01–0.02)
b)
function
-0.12
(-0.16– -0.12)
0.72
(0.72–0.73)
0.48
(0.47–0.48)
0.99
(0.99–0.99)
0.05
(-0.08–0.08)
-0.02
(-0.14–0.09)
-0.11
(-0.29–0.1)
0.2
(-0.4–0.51)
0.13
(-0.04–0.30)
microbial enzyme activities
LUI_h indirect:
0.15
(-0.29–0.37)
0.77
(0.66–0.97)
ΔLUI indirect:
0.02
(0–0.02)
c)
community
-0.12
(-0.12– -0.12)
0.72
(0.72–0.72)
0.48
(0.48–0.48)
0.99
(0.99–0.99)
0.08
(0.08–0.08)
0.07
(-0.04–0.16)
-0.17
(-0.36–0.03)
-0.26
(-0.49–0.18)
-0.05
(-0.15–0.09)
microbial community variables
LUI_h indirect:
-0.19
(-0.35–0.13)
0.82
(0.74–0.94)
ΔLUI indirect:
-0.01
(-0.01–0.01)
d)
biomass
0.07
(0.06–0.07)
0.64
(0.64–0.65)
0.59
(0.57–0.59)
0.99
(0.99–1)
-0.07
(-0.09– -0.07)
-0.08
(-0.32–0.31)
-0.01
(-0.08–0.07)
0.02
(-0.18–0.33)
0.05
(-0.02–0.14)
microbial biomass variables
LUI_h indirect:
0.02
(-0.12–0.22)
0.86
(0.78–0.91)
ΔLUI indirect:
-0.01
(-0.01–0)
e)
function
0.05
(0.01–0.06)
0.64
(0.59–0.65)
0.60
(0.58–0.65)
1
(1–1)
-0.05
(-0.07– -0.02)
-0.21
(-0.35– -0.02)
0.1
(-0.03–0.2)
-0.1
(-0.47–0.2)
-0.26
(-0.53–0.03)
microbial enzyme activities
LUI_h indirect:
-0.07
(-0.3–0.13)
0.76
(0.61–0.90)
ΔLUI indirect:
0.02
(0–0.03)
f)
community
0.07
(0.06–0.08)
0.64
(0.64–0.64)
0.59
(0.59–0.60)
1
(1–1)
-0.07
(-0.07– -0.07)
-0.13
(-0.21– -0.07)
-0.09
(-0.47–0.21)
-0.07
(-0.21–0.05)
-0.01
(-0.06–0.03)
microbial community variables
LUI_h indirect:
-0.05
(-0.13–0.03)
0.84
(0.71–0.95)
ΔLUI indirect:
0
(0–0)
percentage of significant paths accross all models
100 %
50 %
25 %
0 %
67 %
33 %
17 %

Figure 7-4: Summarized results of the SEMs of the South-West and Central regions. Figures a-f show the error weighted means of standardized estimates over all paths (with minimum and maximum estimates) for microbial variables: biomass (C_{mic}, N_{mic}, P_{mic}, C_{mic}:N_{mic} ratio), function (enzyme activities of glucosidase, xylosidase, chitinase, urease, DEA, phosphatase) and community composition (bacterial and fungal PLFA, fungi:bacteria ratio, ergosterol content). Path thickness relates to percentage of significant paths within each variable group. Dotted lines indicate paths that were never significant. The original estimates for each analyzed variable and overall path strengths are given in Table S6.2.

7.5. Discussion

Our study revealed that changes in plant properties were stronger and more consistent drivers of short-term changes in soil microbial properties than either changes in, or the legacy of, land-use intensity. Of the evaluated plant variables, the CWM of plant traits, particularly CWM leaf P, explained more variance in soil microbial properties than plant biomass or its nutritional quality. However, pH change was related to changes to soil microbes and associated enzyme activities in the sandy and organic material rich soils of the North-East.

The finding that the influence of plant properties on soil microorganisms was stronger and more frequent than that of land-use intensity contrasts with studies that showed strong linkages between bacterial abundance, enzyme activities and fertilisation rates (Bardgett and McAlister, 1999; Ritz et al., 2004). Plant N content, either measured as a functional trait or in biomass, showed only weak, if any, effects on changes in microbial soil properties, which is surprising, as plant N has been found to relate to grassland soil properties in the past (e.g. Manning et al., 2015, Semchenko et al., 2018). Instead, it was the CWM of leaf P, as either a change or legacy effect, that showed strong relationships with soil microbes. These relationships were also stronger than those with CWM SLA which has been shown to be strongly related to wide range of ecosystem properties (Garnier et al., 2004; de Vries et al., 2012; Allan et al., 2015; Manning et al., 2015). Among the plant traits, leaf P content correlates and is closely interlinked with SLA and leaf N, which together can characterise the fast-slow spectrum of plant growth behaviour described by Reich (2014) and Díaz et al. (2016). Therefore, although CWM leaf P was the best explanatory variable in our analyses, its effects cannot be completely disentangled from those of SLA and leaf N. Previously, de Vries et al. (2012) showed a positive association between bacterial dominance and plant communities possessing “fast” traits. Our own results confirm and extend this finding by demonstrating that such linkages operate over short time scales, with changes in F:B ratio tracking changes in plant community P content and other related fast-slow traits. In our study, declines in the relative abundance of fungi with increases in fast plant traits were observed repeatedly. While the effects of CWM leaf P are likely to be associated with general shifts in the quality and quantity of litter inputs, the stronger effect of CWM leaf P in our study compared to the other fast-slow traits may be linked to a relatively greater P than N limitation in our study regions. Phosphorus availability is limited under high pH (compare Figure 7-3 a) and the amount of recalcitrant P in the calcareous South-West and Central regions has been shown to be much larger than in the North-East region (Alt et al., 2011). This may lead to P limitation in these calcareous regions, thus explaining the strong positive associations between P rich plant material that enters the soil and microbial activity, as the organic P is mineralized by phosphatase enzymes of both microbial and plant origin. Microcosm studies have shown that short term changes in soil microorganisms and soil processes are strongly linked to plant traits (Bardgett et al., 1999; Orwin et al., 2010). Our field study not only supports these findings, but also shows that the long-term history of plant traits on a site can strongly influence soil microorganisms.

We observed a large increase in plant biomass between the sampling dates, which can be accounted for by the much drier spring of 2011 than that of 2014. This difference in weather conditions did not directly affect the soil microorganisms though, as effects of mean soil temperature over 30 days prior to sampling were minimal and soil moisture effects were undetectable. As plant biomass and its nutritional quality in terms of cellulose, hemicellulose or lignin content, were generally positively related to soil microbial properties, we conclude that plant growth positively influences soil microbial biomass and the speed of nutrient cycling. The observed relationship could be driven by inputs of plant material, but also by correlated increases in rhizodeposits (Swinnen et al., 1995), which demonstrated a positive association with microbial biomass (Bardgett et al., 1998; Eisenhauer et al., 2017) and enzyme activity (Spohn et al., 2013). The main source of extracellular enzymes in soils are microorganisms (Das and Varma, 2011), although there is a small contribution of roots and soil animals (Acosta-Martínez and Tabatabai, 2011; Kandeler et al., 2011).

We found pronounced variation in the relative importance of different drivers of changes in microbial soil properties among the three study regions. As many properties differ between the regions, the cause of differences remains speculative, but differences in soil conditions, namely texture, soil type and water regime are prominent. For example in the North-East, changes in microbial soil properties were often linked to changes in soil pH. Contrary to expectations, this may not be driven by land management, e.g. liming or ammonium fertilization, as the explained variance would have been attributed to land use. Instead we suggest that the lower buffering capacity of the sandy soils made alteration in the redox-potential caused by shifts in the water regime more likely, compared to the other regions. Enzymatic activities were strongly affected by changing pH levels, which is in accordance with the importance of pH for soil enzyme activities reported by Acosta-Martínez and Tabatabai (2011). While microbial activity was affected by pH, the F:B ratio, i.e. the community composition of soils, did not respond to pH changes, likely because pH varied by a maximum of 1.6 units within a site. This small range probably explains why this finding differs from studies which found strong pH effects on microbial community composition; these reported pH values ranging from 3 to 9 (Fierer and Jackson, 2006; Griffiths et al., 2011). Plant trait effects were much weaker in the North East region, most likely because LUI has little effect on trait values there, which are fast throughout the region (Figure 7-3, Allan et al., 2015). The magnitude of variation over key ranges of driver variables may generally explain the variability in the importance of abiotic factors and biotic drivers such as plant diversity and traits in large-scale observational studies (e.g. Diaz et al., 2007, Manning et al., 2015, Ratcliffe et al., 2017). Wider studies across an even fuller range of conditions, e.g. across the full range of pH and N and P limitation, are required to gain a mechanistic understanding of these context dependencies.

Results from all three regions demonstrated that short-term changes in environmental, land-management and especially plant variables have important and rapid effects on soil microbial properties. Structural equation modelling added further insight to this finding by providing evidence that these changes operate directly, via changes in land management and nutrient inputs. Meanwhile, legacy effects of land-use intensity also acted, but more indirectly via plant functional traits. However, short-term trait effects were the most common driver of microbial change in most cases. Our results showed that legacy effects of land-use can be strong drivers of current changes to soil microbes and their activity. However, there was little evidence that land-use legacies affected the impact of current land-use changes (Perring et al., 2016), as significant interactions between land-use change and land-use history were not observed. To our knowledge, we are the first study to demonstrate a legacy effect of land-use intensity on changes to the function and community composition of soil microorganisms. We suggest that plant mediated legacy effects are due to the long-term and cumulative effects of land-use intensity on plant communities, which take several years to adjust to management practices. Furthermore, we hypothesise that the importance of these legacy effects in driving soil microbial changes, relative to short-term variation in land management, is due to a time lag between changes in soil microbial communities, which decompose not only fresh but also old organic material. Therefore, part of the microbial community is feeding on 'historic' substrates, i.e. more recalcitrant, older soil organic carbon (Müller et al., 2016), and this component 'catches up' with the land-use change and corresponding vegetation change as vegetation inputs related to more recent land-use changes enter these more slowly cycling pools.

7.6. Conclusion

By studying the changes in microbial soil properties in successive years on 150 sites in three regions together with environmental, land management and plant properties at the sites, we were able to show that vegetation change was an important driver of changes in soil microbial communities and activities. Although these results demonstrate a context dependency in the strength and nature of trait mediated effects, they add to a growing body of evidence that plant traits play a key role in the regulation of belowground communities, with 'fast' traits promoting active and bacterial dominated communities (Díaz et al., 2007; Orwin et al., 2010; Grigulis et al., 2013; Semchenko et al., 2018) while also showing new evidence that the plant trait effects can operate both rapidly and over longer time scales in field conditions. Importantly, we were also able to show that legacy effects of land-use intensity can be strong and that they are mediated by functional plant traits, in particular leaf P, which was consistently the best predictor, among many, of belowground changes between years. Our results suggest that restoration efforts which shape and redirect plant communities may be an effective means of managing soil communities and the functions and services they provide, but that such efforts may take a long time to prove their effectiveness.

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7.8. Author Contributions

RSB and PM wrote the manuscript. RSB, SM, DB, SB, MF, NH, JK, VHK, TK, YO, DP, DS, IS, MS, ES, EK and PM provided data. RSB analysed data. PM, EK and SM initiated the study. PM and RSB designed the analyses. All authors read and revised the manuscript.

7.9. Data accessibility

All data used for this study are archived within the BExIS database of the Biodiversity Exploratories project: dataset ID 24867 (https://doi.org/10.25829/bexis.24867-1.1.23) (Boeddinghaus et al., 2019), Ecological Archives E093-059 (Akhmetzhanova et al., 2012) and the TRY database (Kattge et al., 2011). The references of data request 250 from the TRY database is given in appendix 1.

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8. General discussion

Based on the three studies presented in this thesis, the impact of land management on microbial biogeography and the relationships between plants and the spatial and temporal distributions of soil microorganisms were assessed. Thereby pronounced differences between the investigated regions were apparent in the first (Chapter 5) and third (Chapter 7) studies. The underlying causes were not determined within the studies, but can likely be assigned to differences between the regions with respect to climate, i.e., mean annual temperature, mean annual precipitation, length of vegetation period (mean of days > 5 °C a^{-1} in the period from 2009–2014: Schwäbische Alb 230 days, Hainich-Dün 238 days, Schorfheide Chorin 242 days), soil depth, hydrologic budgets of the soils, and soil types. The latter differed strongly between regions investigated in the first study (Leptosols in the Schwäbische Alb and predominantly Stagnosols in the Hainich-Dün) and was a significant random factor in some of the linear mixed effect models in the third study. A previous review of Parkin (1993) pointed out the strong influence of soil type and water distribution on soil microorganisms at the landscape level. Soil systematics groups soils with similar developmental stages and occurred processes into soil types (Blume and Fleige, 2018). Thereby the processes necessary to reach the current developmental stage occur mainly over long-time periods and therefore reflect long-term environmental conditions at a site, such as bedrock material, climate, topography, and plant cover. Therefore, possible legacy effects of these long-term processes on soil microorganisms could be reflected by the effect of soil type and would explain the strong influence depicted by Parkin (1993).

8.1. Influences of abiotic site characteristics on soil microbial properties

Apart from regional differences, several abiotic soil properties turned out to play crucial roles for the spatial and temporal distributions of soil microorganisms in the three studies. Repeatedly, an impact of pH was found in all three studies. Changes in pH affected soil microbial community structure, abundance, and function in their spatial (Chapter 5 and Chapter 6) and temporal (Chapter 6 and Chapter 7) distributions and can therefore be regarded as a major abiotic impact factor even at the investigated plot scale. At the continental and field scales this had been shown before, e.g., by Fierer and Jackson (2006) and Rousk et al. (2010), respectively.

Nutrient content in soils in terms of N significantly influenced the spatial distribution of microbial soil properties in the first (Chapter 5) and second (Chapter 6) studies. Thereby the grouped N variables (N_t, NH_4^+, NO_3^-, and EN) were positively correlated with soil enzyme activities in 15 out of 18 sites in Procrustes rotation tests. A positive relationship between N content and soil enzyme activities was also found by Kandeler and Eder (1993). In their study, enzyme activities increased with increasing N addition to soils. Different N forms also explained spatial variations in beta-diversity of AMF OTUs in the second study. The slight negative effect of ammonium on alpha-diversity of total AMF OTUs in this study is in line with the studies of Leff et al. (2015), Bardgett et al. (1999a), and Titus and Lepš (2000), who detected negative relationships between N enrichment and fungi in grassland soils.

Unlike expected from multiple studies on soil microbial abundance, activity, and function (e.g., Wallenstein and Burns, 2011, Bergstrom et al., 1998, Marhan et al., 2010, Pulford and Tabatabai, 1988), soil water content did not play a significant role in the spatial or temporal distributions of soil microbial properties in the three studies presented here. Its effect on the temporal distribution of AMF alpha-diversity of total and *Glomus* OTUs was eliminated by other environmental variables. This was surprising especially considering the markedly dry periods in 2011. With regard to enzyme activities, it must be taken into account, that measurements were not performed *in situ*. Rather the laboratory analyses were conducted at optimum temperature (30–37 °C) in soil slurries, which provide optimal diffusion rates of substrate to extracellular enzymes, which may not have been active due to diffusion limitations under water shortage outside in the grasslands (Wallenstein and Weintraub, 2008). Similarly, the measures undertaken to analyze microbial biomass (CFE and PLFA) and AMF diversity (18S rDNA pyrosequencing) do not differentiate between active and dormant cells.

Physical soil properties such as bulk density (first study) and soil texture (second study) proved to be important factors for spatial distributions of microbial activity, abundance, and diversity. The structural habitat of soils is regarded as a crucial basis for all soil microbial properties (Baveye et al., 2018). Its characteristics such as texture, bulk density, and pore size distribution markedly affect the habitable environment of soil microorganisms. Amongst others they determine nutrient storage, e.g., K in clay minerals, water infiltration rates, and oxygen availability in soils (Amelung et al., 2018). Severely compacted soils, e.g., induced by heavy loads of slurry barrels driven across a grassland site, are characterized by low water infiltration rates and inhibited percolation and thereby low aeration, leading to anoxic soil conditions (Cramer, 2006). This in turn leads, amongst others, to an increase in denitrification, as denitrifying microorganisms increasingly use nitrate as a terminal electron acceptor instead of oxygen under oxygen limited conditions (Robertson and Groffman, 2015). Pore space and pore size distribution also affect predator-prey relationships between bacteria and protozoa, as described by Rutherford and Juma (1992). They pointed out that bacteria are largely protected from predation in fine pores < 2 µm as protozoa have restricted access to pores < 2.4 µm. As pore size distribution is largely influenced by soil texture, with greater amounts of fine pores in finely textured soils (clay > silt > sand), a higher number of bacteria in the presence of protozoa was detected in silty clay compared to a sandy loam (Rutherford and Juma, 1992). In addition, the experiment of Sleutel et al. (2012) found that fungi benefited more from coarser soil pore structures than bacteria. This is in line with the findings of the second study, where already a slight increase in silt content, which is connected to an enlargement of habitable pore space in the clay dominated soil of the site, increased alpha-diversity of total AMF OTUs and also explained variation in beta-diversity of AMF OTUs across the site. The described effects of the physical-structure of a soil turn it into an important environmental variable for microbial studies.

8.2. Effects of land-management on soil microorganisms

The effects of land-management differed between the studies – while land-use intensity had no effect on the biogeography of microbial biomass and enzyme activities in the first study (Chapter 5), mowing in July may have been responsible for the decrease in AMF OTU richness in August in the second study (Chapter 6). Whether the more heterogenous spatial distribution of AMF in August and November was induced by the mowing event, could not be proven in this study. Nevertheless, the second study demonstrated that the spatial patterns of AMF alpha and beta-diversity changed within a season in this low land-use intensity grassland. This seasonal shift in spatial patterns is likely transferable to total microbial biomass and enzyme activities, which was found, e.g., by Regan et al. (2014) and Regan et al. (2017), respectively. That no land-use intensity related spatial patterns were detectable in the first study is therefore not necessarily indicative of no land-use intensity effect at all. It is possible that general trends in microbial spatial distribution patterns, i.e., their ranges of spatial autocorrelation, due to land-use management exist, but can only be shown by repeated samplings across a season, as each grassland site could have its own seasonal fluctuation, which could additionally differ between the investigated microbial properties. The difference in the results of the first study compared to the results of Keil et al. (2011) and Berner et al. (2011), who found significantly higher ranges for soil microbial properties such as microbial biomass C and N in low compared to high land-use intensity grasslands in same nine sites of the Schwäbische Alb that were investigated in the first study, is likely due to the different statistical approaches used to detect spatial patterns in the data. The studies of the *SCALEMIC Experiment* (Regan et al., 2014; Regan et al., 2015; Stempfhuber et al., 2016; Regan et al., 2017), including the second study of this thesis, as well as the first study presented here used semivariogram analyses to detect spatial autocorrelation, whereas Keil et al. (2011) and Berner et al. (2011) used linear mixed effect models with spatial covariance structure.

The third study (Chapter 7) revealed an impact of land-use intensity on changes in soil microbial properties, directly via changes in land-use intensity, but also via direct and indirect legacy effects of historic land-use intensity. Thereby, the negative direct impacts of changes in land-use intensity confirmed the results of the studies by Rousk et al. (2011), Strecker et al. (2015) and Orwin et al. (2010). These studies repeatedly found negative effects of high land-use intensity in terms of high nutrient levels on fungal abundances or microbial activity. Based on the findings of the aforementioned studies, the negative effects of direct land-use intensity, i.e., a decrease in microbial soil properties with an increase in land-use intensity index and vice versa, found in the third study are likely due to altered N dynamics in the soil. A reduction of root exudates due to increasing N fertilization, as described by Kuzyakov and Domanski (2000) and Kuzyakov et al. (2001), could be a reason for the observed negative land-use intensity effect, as root exudates are an important C source for soil microorganisms (Hütsch et al., 2002). The general link between plant functional traits and rhizodeposition described in Chapter 3.1 may not be tightly coupled enough, to reflect short-term changes in land-use intensity as measured in the third study. Herz et al. (2018), using a variety of plant traits, most of them root related, found that traits explained 2–4% of root exudation. Therefore, the measured plant functional traits and nutrient concentrations in aboveground biomass used in the third study may have been insufficient to detect indirect effects of short-term changes in land-use intensity via root exudation. Measuring root exudation in the field is complicated

(Herz et al., 2018), but would certainly improve our understanding of the effects of short-term changes in land-use intensity on soil microbial processes.

Over longer time periods, the measured plant functional properties were sufficient to detect indirect legacy effects of land-use intensity though. As described at length in the introduction (Chapter 3.1), land-use intensity has various effects on grassland plant communities, which adapt over the long-term in species composition and biomass productivity to the prevailing land management regimes. With regard to soil microorganisms, the legacy effects of land-use intensity on changes in soil microbial properties indicate a time lag in the microbial reactions. This is likely due to the fact that soil microbes not only use the fresh resource pools provided, but also utilize relatively stable organic matter pools as resources; a behaviour which is related to the priming effect (Kuzyakov et al., 2000). In the long-term, the close coupling between land-use intensity, plant characteristics and soil microorganisms in the studied grassland ecosystems is reflected in the mediatory property of plant functional traits towards soil microorganisms.

In general, the impact of land-use management and its intensity as assessed in all three studies was lower than expected and stands behind effects of abiotic soil properties, such as pH, or plant properties. The measures used for land-use intensity in the first and third studies, i.e,. land-use intensity classes and index, have a shortage in reflecting the real impact land-use intensity has on nutrient fluxes of grasslands. The land-use intensity classes are more a measure of land management type than of intensity, as pure pastures can have very high grazing densities and are thereby intensively used in terms of defoliation and input of easily available nutrients in form of urine and feces. The land-use intensity index developed by Blüthgen et al. (2012) is a comparably much more accurate measure of grassland land-use intensity. But in terms of nutrient fluxes it is little accurate, as it does not take into account the nutrient outputs of the sites and only assesses nutrient inputs in form of N. Unfortunately, more accurate measures were not possible within the Biodiversity Exploratories at the time of the studies, as data on the yield of the mowed sites was very vague (yield often given only as above or below 65 dt ha^{-1}) and plant biomass measures are made only once a year. Given a much closer approximation of the yield of the mown sites in the future, it would be possible to calculate nutrient budgets, including P, which would very likely be much more meaningful with regard to microbial processes in soils.

8.3. Plant-microbe interactions in grassland soils

The long-discussed effect of plant diversity on soil microbial properties that has been shown in experimental studies (Bardgett et al., 1999b; Zak et al., 2003; Eisenhauer et al., 2010) could not be confirmed by the three studies incorporated in this thesis. Effects of plant diversity were not observed with regard to microbial biogeography in the first study (Chapter 5), nor were they related to AMF beta-diversity in the second study (Chapter 6). A small portion of the variance in alpha-diversity of total AMF OTUs and *Glomus* was explained by plant species richness, which had a negative impact. Neither diversity indices such as the Shannon/Wiener index, nor percent coverage by plant functional groups such as legumes, grasses, or forbs showed strong effects on microbial abundances or distributions. They did not show any effect on the changes in soil microbial properties in the third study (Chapter 7) either. A number of studies showed contrasting results with increasing microbial biomass as plant diversity increases. In these studies, plant diversity effects were detected on a gradient between monocultures and three (Steinauer et al., 2016), six (Eisenhauer et al., 2017), and up to 60 plant species mixtures (Eisenhauer et al., 2010); thereby the latter detected no significant difference between effects of eight, 16 or 60 plant species mixtures. In another study, the effect of plant species richness on plant biomass production was eliminated in communities with eight or more species (Buchmann et al., 2018). The site of the *SCALEMIC Experiment* was characterized by a very dense rooting zone in a species rich (12–20 species per 400 cm^2) (Regan et al., 2014) grassland. Plant roots of diverse species grow tightly intermingled in such a site. Therefore the direct effect of a single plant species or individual is difficult to impossible to assess using bulk soil samples taken with core augers. Also, Regan et al. (2014) did not find a relationship between plant species composition and soil microbial properties. Even by analysing rhizosphere soil samples, no species specific effects of six different species on enzyme activities of beta-glucosidase, beta-xylosidase, N-acetyl-beta-glucosaminidase or phosphatase in the species rich grassland soils of the Schwäbische Alb could be detected (Master thesis by M. Boob, data unpublished). Overall, the 150 investigated sites of the Biodiversity Exploratories were comparably rich in plant species with 12 (Schwäbische Alb and Hainich-Dün) to 65 (Hainich-Dün) species per site and a median of 21 to 30 (Schorfheide Chorin and Hainich-Dün) across sites, which is possibly the reason for the insignificance of plant diversity measures. Instead, where tested, plant functional properties played a crucial role for soil microbial properties. The observed changes in soil microbial properties in the third study were largely explained by changes in and historic values of plant functional traits, especially leaf P content, and by plant biomass and its nutritional quality. This is in line with findings of de Vries et al. (2012), who found links between plant functional traits of the fast-slow gradient of life history strategy and soil microbial community composition. Total root and legume shoot biomass also explained a portion of the spatial distribution of AMF alpha-diversity in the second study. The positive link between plant productivity and soil microbial properties was also shown by Bardgett et al. (1999b) in terms of root and shoot biomass and soil microbial abundance. The observed increase in microbial activity and abundance was likely due to increased rhizosphere depositions, which increase together with plant biomass production (Aulakh et al., 2001) and defoliation (Bokhari and Singh, 1974; Paterson and Sim, 1999). The close linkage between increasing quantities of root exudates and increasing soil microbial biomass, especially fungal biomass, was, e.g., shown by Eisenhauer et al. (2017).

The observed greater importance of plant functional and biomass properties, compared to diversity measures, for soil microbial properties such as abundance, function, and community composition in the investigated “real-world” ecosystem of agricultural grasslands holds great potential to understand ecosystem processes and services. The fact that plant functional traits, here leaf P content, can display the mediator function of plants for indirect legacy effects of land-use intensity that occur over longer time periods to soil microbial properties is proof of this potential. Future studies focusing on above- and below-ground relationships should, therefore, incorporate functional traits where possible.

8.4. Drivers of microbial distribution

The longstanding debate as to whether niche or neutral theory related processes determine microbial distribution tends towards niche related processes: various studies have found influences of environmental properties, e.g., by pH and organic C content, on microbial diversity, abundance, or function (Fierer and Jackson, 2006; Dequiedt et al., 2011). In the studies presented in this thesis, plant functional properties, pH, soil texture, soil N content, and land-use intensity significantly influenced microbial diversity, community composition, abundance, and function. But neither in the second (Chapter 6) nor in the third (Chapter 7) studies more than 50% of the microbial variation could be explained by environmental properties. The first study (Chapter 5) did not in particular evaluate the variance explained by environmental effects apart from land-use intensity classes, which explained only 15%–19% of the total microbial variance (Figure 5-6). These findings suggests that either niche related processes, while definitely playing a determinant role for soil microbial properties, together with neutral processes drive microbial distribution, with neutral processes playing the major role, or that relevant niche related processes could not be detected due to important but unmeasured environmental processes, or due to the means of the study designs. The three studies were set up to determine important environmental drivers at the macroscale, while processes which directly influence the investigated organisms occur at the microscale (Purcell, 1977). Baveye et al. (2018) nicely reviewed this obstacle to soil microbial investigations throughout the last decades. They pointed out that more distinct research at the microscopic level is necessary in order to understand microbe-environmental interactions also at the macroscopic level. In fact, the discovery of true distance-decay relationships in microorganisms is limited by the strongly differing dispersal rates by which soil microorganisms are transported (Frey, 2015). While microbes can, on the one hand, be transported over hundreds of kilometres individually and attached to soil particles by wind, their individual range of movement is, on the other hand, especially in case of prokaryotes, highly limited to a few micro- to millimetres. Therefore, on the investigated plot scale a mix of dispersal ranges is possible, with individual patches due to favourable nutrient, oxygen, or soil moisture conditions and available symbionts. At the plot scale in grassland soils a high diversity of plant species exists with very dense rooting systems, making it difficult, if not impossible, to disentangling single plant species effects. At the same time, the plot scale is too small to encompass large differences in environmental properties and too large to investigate conditions at the microscale. This mixture of conditions is likely also a reason, why such a large amount of the observed variation in the three studies presented in this thesis could not be assigned to niche related processes. This problem of resolution for niche and neutral processes to be detected has been described for plants by Chase (2014). He pointed out, that at a small resolution level, stochastic processes prevail, while on larger scales the distinct differences between habitats favour the detection of niche related distributions of plants. At the larger scale, the comparison between two regions, the Schwäbische Alb and Hainich-Dün, in the first study showed strong differences between these two habitats, and the results obtained for the three regions in the third study also indicated differences in the reactions of soil microbial properties between regions which are likely due to the factors described at the beginning of this discussion.

9. General conclusion

The three studies presented in this thesis investigated microorganisms in grassland soils through the dimensions of space and time. Though they used different approaches and focused on different microbial properties, they detected some general patterns of microbial behaviour, which are summarized in Figure 9-1:

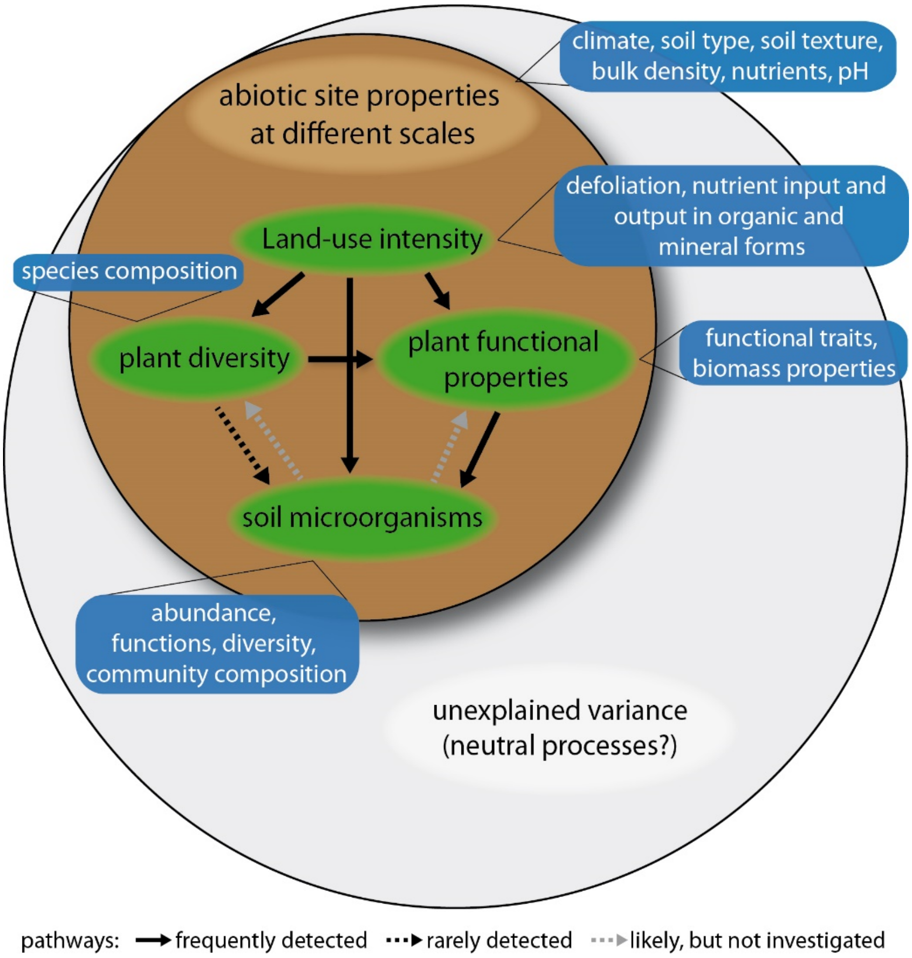

Figure 9-1: Summary of the thesis results. This figure displays the environmental factors explaining variance in soil microbial abundance, function, and community composition that were detected in this thesis. Land-use intensity, plant diversity, and plant functional properties affect soil microorganisms. They all act upon the background of abiotic soil properties which impact both the aforementioned factors and soil microorganisms. A large part of the variation in soil microorganisms could not be explained and might be assigned to neutral processes.

Abiotic site properties play a fundamental role in shaping microbial soil properties in various ways. They include, e.g., soil pH, resource and nutrient availability (C, N, P, etc.), texture, hydrologic balance, bulk density, climate (and by that length of the vegetation period), soil depth, and slope as well as soil type. They influence microbial properties directly and indirectly as they also affect the plant community and its properties and, to some extent, also determine the land management of grasslands. Thereby, their specificity is unique to each site at the investigated scale and acts as a foundation upon which other processes occur. This was especially apparent in the first study (Chapter 5), where abiotic site properties were closely related to soil microbes and their processes. Apart from abiotic soil properties, impacts of plants and land management on soil microorganisms were detected, though to varying degrees and often less strongly or differently than expected. Unlike originally anticipated, direct relationships between plant diversity and soil microbial properties could not be detected in the first or third (Chapter 7) studies and did not explain much of the AMF alpha-diversity in the second study (Chapter 6). The third study, however, showed a direct link between plant functional traits and plant biomass properties with soil microorganisms. Also, AMF alpha-diversity, in the second study, was related to root biomass. Therefore, it seems that the functional aspects of plant communities hold greater potential to explain above-belowground linkages in grassland ecosystems than plain diversity measures. The intensity of land management and its changes had a smaller effect on soil microbes in the first and third study than expected. Both studies disproved land-use intensity to be the strongest driver of soil microbial properties in grasslands and showed that it played a minor role for microbial spatial distribution patterns as well as for their temporal changes. The results of the third study even suggested a certain resilience of soil microbes towards changes in land-use intensity. Interestingly though, the third study showed that an indirect effect of land-use intensity on soil microbes via plant functional traits can occur, encouraging multidisciplinary studies to investigate ecosystem processes in the future. None of the studies could explain more than 50% of the microbial variation by the investigated environmental properties. Though it is likely that important environmental influences have not been detected, this could also be a hint towards a certain amount of randomness in spatial and temporal microbial distributions. This would imply that a strict temporal and spatial biogeography according to niche theory is as inaccurate as a strict stochastic distribution according to neutral theory. Instead, a certain amount of microbial spatial and temporal distribution patterns can be explained by the environment, but yet stochasticity may also play an important role. Whether the investigated relationships between plant functional properties and soil microorganisms act only in one direction, or to which degree microbes also affect plant species diversity and functioning, as proposed by Van Der Heijden et al. (2008), was not assessed in the present studies. This should be considered in future research.

10. Perspectives

Being able to predict effects of human activities, e.g., via land management, on nutrient cycles and on the services ecosystems provide, is crucial to prevent losses in soil and ecosystem functions in the future (Cardinale et al., 2012; Soliveres et al., 2016). To gain this ability, we need to understand the processes and capabilities of soil microbial communities to a much greater extent than we do at the moment. The question is, therefore, less “who is there?” than “what are the abilities of the microorganisms at a site and how are they interrelated with their environment?”. The three studies presented in this thesis showed that diversity measures are less well able to answer these questions than are functional properties, i.e., traits. It therefore seems a promising approach to investigate trait relationships between different organisms, such as plants and soil microorganism, to a greater extend in the future. Influenced by the studies of traits in macroorganisms, especially of plants, soil microbiologists are trying to define fitness and performance traits also in soil microorganisms (Green et al., 2008; Wallenstein and Hall, 2012). Given the vast species richness of soil microorganisms and the great challenge of assigning processes to individual species in a soil sample (Lennon et al., 2012), the investigation of functional traits in soil microbiology is still in its infancy. For macroorganisms, traits are measured at the level of individuals or populations (see trait definition by Garnier et al. (2016) in Chapter 3.1). Theoretically it is also possible to analyze, e.g., the production of alkaline phosphatase by a single bacterium as its capability to mineralize organic P. The activity level, as with plant functional traits, is thereby influenced by environmental conditions. A more practical approach, however, is to analyze for a number of functions within the nutrient cycle, e.g., nitrification and denitrification, of cultivable microorganisms in petri dish studies. As only about 1% of soil microorganisms are cultivable (Paul et al., 2015), this approach is not transferable to the uncountable number of microbes living in a single soil sample, which is the actual study object in most cases. As a solution to this problem, analogous to botanical studies, in which functional traits of whole plant communities are calculated as community abundance weighted means of the individual species and their proportions within the community, soil microbiologists could consider analyzing microbial functions within a soil sample, such as the measures of potential enzymatic activity or microbial gene expression, as functional traits of the given total microbial community at a certain location. As the interest would be focused on services and functions of the whole ecosystem under study, this could be a valid approach. In fact, a large number of possibilities to investigate functions in soil microbial communities already exist, ranging from the classical enzyme activity assays (Kandeler and Gerber, 1988) and fluorescence microplate assays (Marx et al., 2001) over *in situ* zymography (Spohn et al., 2013), to molecular techniques that detect functional genes such as *nirS*, *nirK*, and *nosZ* to characterize denitrifiers (Regan et al., 2017), or *mmoX* of methanotrophs (Farhan Ul Haque et al., 2018), and the growing field of studying metatranscriptomics (Crits-Christoph et al., 2018), that could be used to assess soil microbial functional traits in the context of ecosystem studies.

In addition to functional relationships between organisms, the physical habitat of soil microorganisms deserves more attention within ecosystem studies. As a number of studies have found significant impacts of soil type, texture, and porosity on soil microorganisms (e.g., Parkin, 1993; Tscherko, 1999, Oehl et al., 2017; Juyal et al., 2019) as well as on predator-prey relationships (Rutherford and Juma, 1992), and as was pointed out by Baveye et al. (2018), the physical structure of a soil is a factor that should be accounted for as a fundamental background for organismal functions in ecosystem studies.

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Supplementary material of Chapter 5

Table S5-1: Detailed land management activities of the investigated sites from 2006–2008 (see following pages). Data compiled by: Gockel, S., Schumacher, U., Lauterbach, R., Weisser, W.. Results of farmers questionaires from the Biodiversity Exploratories; data set number: 11740; source: http://www.biodiversity-exploratories.de/intranet/. The data has been published in condensed form in: Blüthgen et al. 2012. A quantitative index of land-use intensity in grasslands: Integrating mowing, grazing and fertilization. Basic and Applied Ecology 13, 207-220. Displayed is a short version of the complete questionaire data. LUI = land-use intensity; CAS = Calcium ammonium nitrate; GV = Großvieheinheit (500 kg animal weight); ha = hectare (10000 m^2); d = day; dt = 1 dt = 100 kg; N = nitrogen; n.a. = not applicable.

Exploratory	Year	Site	LUI class	Animals	GV/ha	GV/ha/d	Days of grazing	Additional feeding	Type of feeding	Cuts	Yield [dt/ha]	Number of Cuts	Manure [m³/ha]	Slurry [m³/ha]	Nitrogen [kg/ha]	Phosphor [kg/ha]	Type of fertilizer
Hainich National Park																	
	2006	HEG01	Meadow	n.a.	0	0	0	no	n.a.	2	<65	2	0	0	115	0	application for 1. and 2. aufwuchs
	2006	HEG02	Meadow	n.a.	0	0	0	no	n.a.	3	~ 65	2	0	0	100	0	CAS 8.4.06 70 kg N/ha; 26.6.06 30 kg N/ha
	2006	HEG03	Meadow	n.a.	0	0	0	no	n.a.	3	~ 65	2	0	0	100	0	CAS 8.4.06 70 kg N/ha; 26.6.06 30 kg N/ha
	2006	HEG04	Mown pasture	Mother cows	6.46	0.48	27	no	n.a.	1	>~85	1	0	0	27	0	CAS, April
	2006	HEG05	Mown pasture	Cattle	5.85	0.13	8	no	potentially salt stone	2	<65	2	0	0	60	0	max. 2 application (either 40/20 or 30/30)
	2006	HEG06	Mown pasture	Cattle	1.33	0.13	35	no	n.a.	1	<65	1	0	20	0	0	n.a.
	2006	HEG07	Pasture	Mother cows	1.11	1.11	365	yes	1 hay bale per week	0	n.a.	1	15	0	0	0	n.a.
	2006	HEG08	Pasture	Mother cows	1.11	1.11	365	yes	1 hay bale per week	0	n.a.	1	15	0	0	0	n.a.
	2006	HEG09	Pasture	Cattle	1.43	0.18	45	no	n.a.	0	n.a.	0	0	0	0	0	n.a.
	2007	HEG01	Meadow	Sheep	6	0	8	no	n.a.	3	< 65	2	0	0	135	0	CAS
	2007	HEG02	Meadow	Sheep	2	0	23	no	n.a.	3	~ 65	2	0	0	140	0	CAS
	2007	HEG03	Meadow	Sheep	2	0	23	no	n.a.	3	~ 65	2	0	0	140	0	CAS
	2007	HEG04	Mown pasture	Mother cows	7.11	0.31	16	no	n.a.	1	n.a.	0	0	0	27	0	CAS
	2007	HEG05	Mown pasture	Cattle	5.85	0.26	16	no	n.a.	2	~ 65	2	0	0	80	0	n.a.
	2007	HEG06	Mown pasture	Cattle	1.33	0.03	7	no	n.a.	1	~ 65	1	0	25	0	0	n.a.
	2007	HEG07	Pasture	Mother cows	1.24	1.24	365	yes	32 x 250 kg hay per week (December-March)	0	n.a.	0	0	0	0	0	n.a.
	2007	HEG08	Pasture	Mother cows	1.24	1.24	365	yes	32 x 250 kg hay per week (December-March)	0	n.a.	0	0	0	0	0	n.a.
	2007	HEG09	Pasture	Cattle	1.43	0.20	50	yes	in November on adjacent pasture	0	n.a.	0	0	0	0	0	n.a.
	2008	HEG01	Mown pasture	Sheep	6	0	9	no	n.a.	2	< 65	3	0	392	60	44	N as CAS, 08.04.2008; P as triple superphosphate, 23.04.2008
	2008	HEG02	Meadow	n.a.	0	0	0	no	n.a.	3	< 65	2	0	0	60	44	N as urea, 15.04.2008; P as triple superphosphate, 23.04.2008
	2008	HEG03	Meadow	n.a.	0	0	0	no	n.a.	3	< 65	2	0	0	60	44	N as urea, 15.04.2008; P as triple superphosphate, 23.04.2008
	2008	HEG04	Mown pasture	Mother cows	6.32	0.36	21	no	n.a.	2	n.a.	0	0	0	27	0	CAS
	2008	HEG05	Mown pasture	Cattle	4.56	0.20	16	no	n.a.	2	< 65	2	0	0	80	0	n.a.
	2008	HEG06	Mown pasture	Cattle	1.33	0.03	7	yes	Hay	1	~ 65	1	0	25	0	0	n.a.
	2008	HEG07	Pasture	Mother cows	1.25	0.90	263	yes	32 x 250 kg hay per week (Januar-March)	0	n.a.	0	0	0	0	0	n.a.
	2008	HEG08	Pasture	Mother cows	1.25	0.90	263	yes	32 x 250 kg hay per week (December-March)	0	n.a.	0	0	0	0	0	n.a.
	2008	HEG09	Pasture	Cattle	1.43	0.20	50	yes	in November on adjacent pasture	0	n.a.	0	0	0	0	0	n.a.

Exploratory	Year	Site	LUI class	Animals	GV/ha	GV/ha/d	Days of grazing	Additional feeding	Type of feeding	Cuts	Yield [dt/ha]	Number of Cuts	Manure [m^3/ha]	Slurry [m^3/ha]	Nitrogen [kg/ha]	Phosphor [kg/ha]	Type of fertilizer
Swabian Alb																	
	2006	AEG01	Meadow	n.a.	0	0	0	no	n.a.	2	~ 65	1	0	0	50	0	CAS, 1 x in spring
	2006	AEG02	Meadow	n.a.	0	0	0	no	n.a.	3	~ 75	2	0	30	100	0	n.a.
	2006	AEG03	Meadow	n.a.	0	0	0	no	n.a.	2	< 65	1	0	20	0	0	October
	2006	AEG04	Mown pasture	Cows	3.69	0.30	30	no	n.a.	1	~ 65	1	0	0	50	0	CAS, 1 x in spring
	2006	AEG05	Mown pasture	Cows, horses	5.42	0.31	21	yes	Hay, silage, oat, concentrated feed; horses were fed in the stable	1	~ 65	1	0	0	50	0	CAS, 1 x in spring
	2006	AEG06	Mown pasture	Cows, horses	6.91	1.14	60	yes	Hay, silage, oat, concentrated feed; horses were fed in the stable	1	~ 65	1	0	0	50	0	CAS, 1 x in spring
	2006	AEG07	Pasture	Sheep	8.57	0.09	4	no	n.a.	0	n.a.	0	0	0	0	0	n.a.
	2006	AEG08	Pasture	Sheep	3.40	0.37	40	no	n.a.	0	n.a.	0	0	0	0	0	n.a.
	2006	AEG09	Pasture	Sheep	4.84	0.08	6	no	n.a.	0	n.a.	0	0	0	0	0	n.a.
	2007	AEG01	Meadow	n.a.	0.00	0.00	0	no	n.a.	2	~ 65	1	0	0	35	0	CAS, 1 x in spring
	2007	AEG02	Meadow	n.a.	0.00	0.00	0	no	n.a.	3	~ 75	3	0	15	100	0	3 x slurry, 3 x N (1 x 150kg, 2 x 100kg) before cutting
	2007	AEG03	Meadow	n.a.	0.00	0.00	0	no	n.a.	3	< 65	0	0	20	0	0	n.a.
	2007	AEG04	Mown pasture	Cows	3.55	0.29	30	no	n.a.	1	~ 65	1	0	0	35	0	CAS, 1 x in spring
	2007	AEG05	Mown pasture	Cows, horses	5.88	0.34	21	yes	Hay, silage, oat, concentrated feed; horses were fed in the stable	1	~ 65	1	0	0	50	0	CAS, 1 x in spring
	2007	AEG06	Mown pasture	Cows, horses	11.45	1.88	60	yes	Hay, silage, oat, concentrated feed; horses were fed in the stable	1	~ 65	1	0	0	50	0	CAS, 1 x in spring
	2007	AEG07	Pasture	Sheep	7.69	0.08	4	no	n.a.	0	n.a.	0	0	0	0	0	n.a.
	2007	AEG08	Pasture	Sheep	3.70	0.28	28	no	n.a.	1	< 65	0	0	0	0	0	n.a.
	2007	AEG09	Pasture	Sheep	4.84	0.11	8	no	n.a.	0	n.a.						
	2008	AEG01	Meadow	n.a.	0.00	0.00	0	no	n.a.	2	~ 65	1	0	0	35	0	CAS, 1 x in spring
	2008	AEG02	Meadow	n.a.	0	0	0	no	n.a.	3	~ 75	3	0	15	100	0	3 x slurry, 3 x N (1 x 150kg, 2 x 100kg) before cutting
	2008	AEG03	Meadow	n.a.	0	0	0	no	n.a.	3	< 65	0	0	20	0	0	n.a.
	2008	AEG04	Mown pasture	Cows	3.55	0.29	30	no	n.a.	1	~ 65	1	0	0	35	0	CAS, 1 x in spring
	2008	AEG05	Mown pasture	Cows, horses	5.88	0.34	21	yes	Hay, silage, oat, concentrated feed; horses were fed in the stable	1	~ 65	1	0	0	50	0	CAS, 1 x in spring
	2008	AEG06	Mown pasture	Cows, horses	11.45	1.88	60	yes	Hay, silage, oat, concentrated feed; horses were fed in the stable	1	~ 65	1	0	0	50	0	CAS, 1 x in spring
	2008	AEG07	Pasture	Sheep	6.59	0.07	4	no	n.a.	0	n.a.	0	0	0	0	0	n.a.
	2008	AEG08	Pasture	Sheep	3.70	0.28	28	no	n.a.	1	< 65	0	0	0	0	0	n.a.
	2008	AEG09	Pasture	Sheep	4.84	0.11	8	no	n.a.	0	n.a.	0	0	0	0	0	n.a.

Table S5-2a: Average values (n = 54, with coefficient of variation (CV) %) of physico-chemical and biological variables per site in the Hainich National Park. LUI classes are indicated above site names (see following page).

Hainich	**High LUI class**			**Intermediate LUI class**			**Low LUI class**		
Site	**HEG1**	**HEG2**	**HEG3**	**HEG4**	**HEG5**	**HEG6**	**HEG7**	**HEG8**	**HEG9**
Soil water content	47.71	37.28	37.38	43.05	39.42	28.04	44.67	39.89	36.91
(% H_2O dw^{-1})	-7.49	-9.34	-10.71	-10.87	-7.01	-8.67	-10.01	-14.11	-8.51
Bulk density	0.98	1.2	1.18	1.06	1.13	1.32	1.01	1.1	1.1
(g cm^{-3})	-8.22	-9.53	-8.62	-6.94	-5.18	-6.47	-11.37	-12.79	-9.39
pH (0.01 $CaCl_2$)	6.92	7.29	7.29	6.87	7.11	5.64	7.09	7.14	7.18
	-1.11	-0.87	-1.02	-1.77	-0.84	-2.88	-1.41	-0.99	-1.31
Organic carbon (C_{org})	40.73	30.34	33.15	39.3	45.72	16.02	55.57	53.07	42.81
(mg C g^{-1})	-11.18	-12.33	-17.39	-14.98	-10.33	-15.18	-18.97	-23.71	-12.29
Total nitrogen (N_t)	4.55	3.04	3.02	3.81	3.75	1.62	5.27	4.75	3.26
(mg N g^{-1})	-14.86	-16.96	-16.6	-12.56	-10.19	-13.2	-17.47	-22.96	-9.75
C_{org}/N_t	9.1	10.07	11.08	10.27	12.21	9.84	10.53	11.16	13.16
	-15.68	-6.56	-16.94	-3.33	-4.2	-4.3	-3.62	-4.38	-9.31
Ammonium (NH_4^+)	13.08	12.33	8.21	12.53	13.02	6.42	16.48	12.75	21.6
(µg N g^{-1})	-20.71	-43.94	-43.48	-27.45	-35.74	-35.66	-35.36	-25.67	-26.06
Nitrate (NO_3^-)	1.45	5.19	3.1	1.56	8.32	0.15	10.13	8.14	0.22
(µg N g^{-1})	-90.31	-81.03	-107.4	-90.61	-67.02	-515.59	-92.05	-73.47	-358.85
Mineral nitrogen (N_{min})	14.53	17.52	11.32	14.09	21.35	6.57	26.61	20.86	21.83
(µg N g^{-1})	-22.15	-42.38	-39.6	-30.98	-30.44	-35.11	-37.38	-36.81	-26.54
Extractable organic carbon (EOC)	144.75	92.81	87.98	146.02	116.83	123.03	201.27	181.32	201.18
(µg C g^{-1})	-19.7	-21.36	-29.74	-21.99	-20.69	-28.43	-28.52	-19.64	-17.58
Extractable nitrogen (EN)	38.19	30.55	24.43	39.66	42.96	26.85	55.64	48.46	54.34
(µg N g^{-1})	-15.06	-30.87	-23.48	-13.46	-17.05	-18.52	-21.17	-24.31	-17.42
Microbial biomass carbon (C_{mic})	1249.34	890.39	837.44	1444.46	1085.46	392.34	1595.41	1320.85	990.84
(µg C g^{-1})	-14.01	-19.16	-21.65	-14.94	-13.26	-24.15	-21.87	-23.49	-19.62
Microbial biomass nitrogen (N_{mic})	158.63	113.19	105.03	173.02	127.64	46.05	231.34	183.91	134.56
(µg N g^{-1})	-15.76	-24.93	-26.17	-18.32	-15.06	-28.18	-22.64	-23.33	-20.87
C_{mic}/N_{mic}	7.9	7.97	8.07	8.41	8.54	8.67	6.93	7.19	7.4
	-5.73	-7.91	-7.55	-6.99	-6.06	-12.49	-7.28	-6.22	-6.29
β-glucosidase	1230.7	763.24	694.59	1157.29	825.38	596.02	1552.65	1902.52	574.91
(nmol MUF g^{-1} h^{-1})	-25.11	-46.36	-39.74	-34.2	-37.15	-29.91	-31.09	-47.89	-36.45
Chitinase	247.54	226.98	225.44	281.74	252.59	168.93	299.13	352.47	225.11
(nmol MUF g^{-1} h^{-1})	-30.74	-60.11	-44.81	-30.51	-45.63	-51.84	-34.58	-53.19	-30.54
Xylosidase	146.99	94.95	80.4	156.25	98.18	82.17	168.47	193.8	65.25
(nmol MUF g^{-1} h^{-1})	-36.26	-52.61	-41.36	-32.04	-43.27	-30.52	-39.11	-55.11	-42.48
Phosphatase	514.31	221.01	216.03	631.9	387.81	813.42	416.07	524.53	377.87
(nmol MUF g^{-1} h^{-1})	-25.89	-40.2	-34.73	-30.7	-37.58	-23.31	-30.39	-53.94	-36.13
Urease	183.9	104.22	101.36	169.13	104.48	40.64	229.83	238.49	93.35
(µg N g^{-1} 2 h^{-1})	-19.8	-24.41	-21.35	-23.76	-28.35	-24.74	-22.12	-29.87	-25.17

Table S5-2b: Average values (n = 54, with CV %) of physico-chemical and biological variables per site for the Swabian Alb (values were adopted from Berner et al. (2011)). LUI classes are indicated above site names (see following page).

Swabian Alb	**High LUI class**			**Intermediate LUI class**			**Low LUI class**		
Site	**AEG1**	**AEG2**	**AEG3**	**AEG4**	**AEG5**	**AEG6**	**AEG7**	**AEG8**	**AEG9**
Soil water content	73.11	63.21	63.07	69.92	74.31	59.01	58.25	76.41	61.52
(% H_2O dw^{-1})	-1.04	-0.57	-0.7	-1.12	-0.57	-1.22	-0.93	-0.81	-1.28
Bulk density	0.68	0.8	0.82	0.76	0.68	0.8	0.83	0.64	0.74
(g cm^{-3})	-16.95	-10.5	-6.89	-9.02	-9.44	-7.8	-6.34	-12.69	-12.06
pH (0.01 $CaCl_2$)	6.56	6.8	6.38	5.22	6.23	6.01	7.09	6.94	6.49
	-2.39	-2.22	-3.38	-3.39	-2.71	-6.51	-1.11	-4.05	-6.6
Organic carbon (C_{org})	76.68	57.4	47.83	57.14	76.28	56.49	47.23	72.49	57.69
(mg C g^{-1})	-12.15	-7.61	-8.31	-13.53	-6.09	-13.9	-8.18	-8.15	-15.95
Total nitrogen (N_t)	8.81	7.56	5.7	7.35	8.52	6.12	4.73	7.76	5.13
(mg N g^{-1})	-8.54	-5.99	-7.72	-12.58	-5.71	-13.72	-14.91	-7.79	-14.96
C_{org}/N_t	8.76	7.59	8.41	7.78	8.96	9.24	10.16	9.4	11.12
	-0.49	-0.7	-0.97	-0.86	-0.45	-0.43	-1.81	-0.93	-0.62
Ammonium (NH_4^+)	38.58	57.48	70.43	23.37	36.37	55.89	70.77	122.99	43.61
(µg N g^{-1})	-60.56	-30.69	-29.79	-26.42	-29.71	-25.68	-21.11	-28.85	-43.45
Nitrate (NO_3^-)	48.31	31.93	15.48	4.13	24.63	14.15	1.34	7.19	0.03
(µg N g^{-1})	-26.08	-36.34	-37.91	-65.6	-36.27	-48.69	-74.63	-56.51	-641.62
Mineral nitrogen (N_{min})	86.38	89,41	85.68	27.52	61	70.52	72.11	128.6	43.66
(µg N g^{-1})	-19.68	-23.48	-25.46	-26.17	-16.48	-18.89	-20.61	-28.07	-43.85
Extractable organic carbon (EOC)	260.23	271.94	177.78	281.33	259.4	217.36	210.04	318.54	277.96
(µg C g^{-1})	-19.53	-14.64	-16.07	-18.45	-10.35	-11.57	-26.44	-19.82	-16.74
Extractable nitrogen (EN)	74.08	158.97	116.81	91.65	113.27	111.64	53.54	186.33	105.12
(µg N g^{-1})	-18.32	-14.76	-22.11	-11.75	-10.7	-13	-23.33	-22.53	-19.33
Microbial biomass carbon (C_{mic})	2694.59	2151.98	1717.25	1493.01	2123.24	1617.44	1442.73	1935.07	1260.4
(µg C g^{-1})	-14.22	-10.01	-13.75	-17.2	-14.69	-18.75	-13.78	-8.7	-14.64
Microbial biomass nitrogen (N_{mic})	430.83	389.14	298.43	244.33	401.17	290.01	222.14	403.09	222.05
(µg N g^{-1})	-17.52	-13.02	-21.24	-22.08	-18.75	-15.93	-12.64	-21.79	-25.65
C_{mic}/N_{mic}	6.31	5.58	5.98	6.26	5.4	5.68	6.54	4.9	5.81
	-9.84	-10.53	-22.43	-17.59	-16.76	-16.83	-7.29	-12.44	-11.9
β-glucosidase	3377.18	2800	1575.58	1742.39	2520.4	1848.43	671.46	1816.07	1118.23
(nmol MUF g^{-1} h^{-1})	-27.71	-14.83	-14.14	-24.89	-19.74	-19.15	-19.93	-23.74	-24.3
Chitinase	888.99	866.77	493.98	593.9	747.9	655.51	416.06	714.8	710.44
(nmol MUF g^{-1} h^{-1})	-24.61	-15.11	-14.99	-28.66	-17.41	-16.27	-22.45	-18.49	-23.29
Xylosidase	585.46	525.4	330.03	365.46	554.92	461.22	127.01	325.51	225.57
(nmol MUF g^{-1} h^{-1})	-28.34	-17.77	-14.47	-23.97	-19.19	-15.31	-15.92	-21.41	-20.34
Phosphatase	1891.73	1734.24	1964.04	4365.2	3531.01	3654.76	1130.53	2172.77	1990.83
(nmol MUF g^{-1} h^{-1})	-20.68	-10.4	-11.67	-18.46	-17.42	-14.98	-12.63	-19.53	-18.21
Urease	221.51	300.7	154.99	142.8	248.14	167.12	114.95	172.44	88.3
(µg N g^{-1} 2 h^{-1})	-17.95	-13.51	-16.31	-29.64	-14.1	-26.79	-12.3	-25.34	-33.28

Table S5-3a: Spearman's rank correlation coefficients for sites HEG 1–9 from the Hainich National Park (see following page), LUI = land-use intensity, SWC = soil water content, BD = bulk density, C = carbon, N_t = total nitrogen, N_{min} = mineral nitrogen, EOC = extractable organic carbon, EN = extractable nitrogen, C_{mic} = microbial C, N_{mic} = microbial N, b-Glu = β-glucosidase, N-Ac = chitinase, Xyl = xylosidase, Phos = phosphatase. External data sources: a = Fischer et al. (2010), b = Blüthgen et al. (2012), c = Herold et al. (2014), d = Birkhofer et al. (2012). Grey color indicates non-significant correlations.

	Spearman's rank correlation coefficient																												
		land-use intensity class^a	LUI06-08^b	Fertilization intensity 06-08^b	Mowing frequency 06-08^b	Grazing intensity 06-08^b	Soiltype^c	sand^c	silt^c	clay^c	WHC^d	SWC of WHC	BD	pH	C	N_t	C/N_t	NH_4^+	NO_3^-	N_{min}	EOC	EN	C_{mic}	N_{mic}	C_{mic}/N_{mic}	b-Glu	N-Ac	Xyl	Phos	Urease
***P* -value (bonferoni corrected)**	land-use intensity class^a		0.95	0.96	0.97	-0.80	-0.29	0.08	-0.32	0.37	-0.01	0.04	0.15	0.10	-0.53	-0.29	-0.45	-0.39	-0.09	-0.44	-0.69	-0.68	-0.32	-0.40	0.44	-0.22	-0.20	-0.15	-0.25	-0.25
	LUI06-08^b	0.000					-0.18	0.03	-0.46	0.51	-0.13	0.12	0.21	0.20	-0.48	-0.28	-0.39	-0.42	0.11	-0.37	-0.74	-0.67	-0.34	-0.41	0.41	-0.21	-0.20	-0.16	-0.34	-0.26
	Fertilization intensity 06-08^b	0.000					-0.28	0.06	-0.27	0.31	0.06	0.02	0.12	-0.04	-0.51	-0.25	-0.54	-0.40	-0.10	-0.45	-0.62	-0.65	-0.32	-0.39	0.40	-0.18	-0.22	-0.11	-0.15	-0.23
	Mowing frequency 06-08^b	0.000					-0.09	-0.34	0.22	-0.18	0.34	-0.16	-0.42	-0.23	0.71	0.64	0.26	0.38	0.34	0.48	0.63	0.70	0.68	0.69	-0.35	0.56	0.37	0.49	0.32	0.63
	Grazing intensity 06-08^b	0.000					-0.09	-0.34	0.22	-0.18	0.34	-0.16	-0.42	-0.23	0.71	0.64	0.26	0.38	0.34	0.48	0.63	0.70	0.68	0.69	-0.35	0.56	0.37	0.49	0.32	0.63
	Soiltype^c	0.000	0.019	0.000	0.000	1.000		0.14	0.37	-0.37	-0.65	0.25	0.57	-0.16	-0.39	-0.56	0.05	-0.34	-0.18	-0.27	-0.13	-0.23	-0.48	-0.47	0.16	-0.36	-0.22	-0.29	0.20	-0.54
	sand^c	1.000	1.000	1.000	1.000	0.000	0.926		0.21	-0.42	0.12	-0.27	0.26	0.02	-0.27	-0.37	0.06	0.14	-0.27	0.05	-0.09	-0.02	-0.37	-0.38	0.17	-0.41	-0.23	-0.36	-0.02	-0.48
	silt^c	0.000	0.000	0.000	0.000	0.000	0.000	0.001		-0.97	-0.19	0.26	0.06	-0.72	-0.11	-0.20	0.03	-0.02	-0.55	-0.22	0.24	0.10	-0.08	-0.14	0.28	-0.16	-0.08	-0.05	0.64	-0.28
	clay^c	0.000	0.000	0.000	0.000	0.017	0.000	0.000	0.000		0.07	-0.11	-0.08	0.66	0.10	0.23	-0.07	-0.07	0.57	0.14	-0.29	-0.17	0.13	0.17	-0.21	0.22	0.11	0.12	-0.60	0.33
	WHC^d	1.000	1.000	1.000	1.000	0.000	0.000	1.000	0.028	1.000		-0.77	-0.54	-0.11	0.36	0.57	-0.36	0.48	0.12	0.38	0.39	0.43	0.55	0.56	-0.32	0.47	0.21	0.44	0.06	0.59
	SWC of WHC	1.000	1.000	1.000	1.000	0.306	0.000	0.000	0.000	1.000	0.000		0.20	-0.01	0.08	-0.10	0.44	-0.14	-0.02	-0.11	-0.13	-0.09	-0.15	-0.19	0.23	-0.17	0.04	-0.14	0.08	-0.23
	BD	0.419	0.001	1.000	0.126	0.000	0.000	0.000	1.000	1.000	0.000	0.007		0.09	-0.48	-0.56	-0.01	-0.38	-0.15	-0.32	-0.38	-0.43	-0.57	-0.56	0.25	-0.40	-0.26	-0.38	-0.10	-0.55
	pH	1.000	0.002	1.000	0.000	0.000	0.235	1.000	0.000	0.000	1.000	1.000	1.000		0.08	-0.06	0.40	0.13	0.33	0.26	-0.18	-0.02	-0.13	-0.05	-0.24	-0.18	-0.03	-0.28	-0.76	-0.03
	C	0.000	0.000	0.000	0.000	0.000	0.000	0.000	1.000	1.000	0.000	1.000	0.000	1.000		0.87	0.43	0.61	0.49	0.72	0.58	0.79	0.77	0.79	-0.45	0.58	0.46	0.49	0.11	0.72
	N_t	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.004	0.000	0.000	1.000	0.000	1.000	0.000		0.00	0.50	0.49	0.59	0.49	0.65	0.85	0.86	-0.41	0.73	0.48	0.66	0.17	0.88
	C/N_t	0.000	0.000	0.000	0.000	0.000	1.000	1.000	1.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000		0.36	0.16	0.41	0.25	0.40	0.06	0.08	-0.14	-0.11	0.11	-0.19	-0.20	-0.07
	NH_4^+	0.000	0.000	0.000	0.000	0.000	0.000	0.989	1.000	1.000	0.000	1.000	0.000	1.000	0.000	0.000	0.000		0.14	0.81	0.56	0.78	0.55	0.58	-0.39	0.28	0.30	0.25	0.07	0.41
	NO_3^-	1.000	1.000	1.000	1.000	0.000	0.018	0.000	0.000	0.000	1.000	1.000	0.309	0.000	0.000	0.000	0.129	0.956		0.59	-0.08	0.28	0.41	0.40	-0.17	0.40	0.22	0.30	-0.25	0.48
	N_{min}	0.000	0.000	0.000	0.000	0.000	0.000	1.000	0.000	0.792	0.000	1.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		0.43	0.82	0.59	0.62	-0.40	0.36	0.32	0.28	-0.06	0.50
	EOC	0.000	0.000	0.000	0.000	0.000	1.000	1.000	0.000	0.000	0.000	1.000	0.000	0.041	0.000	0.000	0.000	0.000	1.000	0.000		0.76	0.49	0.56	-0.49	0.39	0.37	0.37	0.34	0.44
	EN	0.000	0.000	0.000	0.000	0.000	0.000	1.000	1.000	0.084	0.000	1.000	0.000	1.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		0.68	0.71	-0.45	0.43	0.40	0.37	0.21	0.55
	C_{mic}	0.000	0.000	0.000	0.000	0.000	0.000	0.000	1.000	1.000	0.000	1.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	0.000	0.000	0.000		0.97	-0.32	0.70	0.50	0.67	0.24	0.86
	N_{mic}	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.986	0.090	0.000	0.024	0.000	1.000	0.000	0.000	1.000	0.000	0.000	0.000	0.000	0.000	0.000		-0.53	0.70	0.50	0.66	0.20	0.88
	C_{mic}/N_{mic}	0.000	0.000	0.000	0.000	0.000	0.125	0.090	0.000	0.001	0.000	0.001	0.000	0.000	0.000	0.000	0.746	0.000	0.061	0.000	0.000	0.000	0.000	0.000		-0.33	-0.25	-0.24	0.06	-0.43
	b-Glu	0.000	0.002	0.043	0.000	0.000	0.000	0.000	0.150	0.001	0.000	0.161	0.000	0.017	0.000	0.000	1.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		0.67	0.88	0.44	0.77
	N-Ac	0.003	0.005	0.001	0.049	0.000	0.000	0.000	1.000	1.000	0.004	1.000	0.000	1.000	0.000	0.000	1.000	0.000	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000		0.69	0.38	0.48
	Xyl	0.448	0.206	1.000	0.025	0.000	0.000	0.000	1.000	1.000	0.000	1.000	0.000	0.000	0.000	0.000	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		0.54	0.71
	Phos	0.000	0.000	0.359	0.000	0.000	0.005	1.000	0.000	0.000	1.000	1.000	1.000	0.000	1.000	0.054	0.002	1.000	0.000	1.000	0.000	0.001	0.000	0.004	1.000	0.000	0.000	0.000		0.16
	Urease	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.216	

Table S5-3b: Spearman's rank correlation coefficients for sites AEG 1–9 from the Swabian Alb (see following page). LUI = land-use intensity, WHC = water holding capacity, SWC = soil water content, BD = bulk density, C = carbon, N_t = total nitrogen, N_{min} = mineral nitrogen, EOC = extractable organic carbon, EN = extractable nitrogen, C_{mic} = microbial C, N_{mic} = microbial N, b-Glu = β-glucosidase, N-Ac = chitinase, Xyl = xylosidase, Phos = phosphatase. External data sources: a = Fischer et al. (2010), b = Blüthgen et al. (2012), c = Herold et al. (2014), d = Birkhofer et al. (2012). Grey color indicates non-significant correlations.

Spearman's rank correlation coefficient

		land-use intensity class^a	LUI06-08^b	Fertilization intensity 06-08^b	Mowing frequency 06-08^b	Grazing intensity 06-08^b	sand^c	silt^c	clay^c	WHC^d	SWC of WHC	BD	pH	C	N_t	C/N_t	NH_4^+	NO_3^-	Nmin	EOC	EN	C_{mic}	N_{mic}	C_{mic}/ N_{mic}	b-Glu	N-Ac	Xyl	Phos	Urease
***P*-value**	land-use intensity class^a		0.69	0.84	0.97	-0.54	-0.05	0.05	0.05	-0.21	0.45	0.10	-0.22	0.04	0.37	-0.70	-0.22	0.78	0.17	-0.22	0.08	0.52	0.40	0.07	0.61	0.24	0.62	0.05	0.58
(bonferoni	LUI06-08^b	0.000					-0.18	-0.03	0.23	-0.12	0.13	0.17	-0.42	-0.01	0.19	-0.53	-0.10	0.58	0.07	-0.22	0.42	0.28	0.27	-0.17	0.49	0.19	0.61	0.43	0.51
corrected)	Fertilization intensity 06-08^b	0.000					0.02	0.12	-0.01	-0.29	0.35	0.22	-0.28	-0.07	0.21	-0.64	-0.12	0.67	0.10	-0.26	0.34	0.37	0.31	-0.08	0.51	0.17	0.59	0.19	0.59
	Mowing frequency 06-08^b	0.000					-0.09	-0.03	0.11	-0.20	0.43	0.09	-0.18	0.06	0.40	-0.76	-0.11	0.78	0.25	-0.15	0.27	0.54	0.46	-0.03	0.64	0.27	0.63	0.07	0.64
	Grazing intensity 06-08^b	0.000					-0.20	-0.03	0.25	0.49	-0.53	-0.20	-0.36	0.25	0.06	0.33	-0.05	-0.24	-0.24	0.14	0.18	-0.20	-0.08	-0.25	-0.08	-0.02	0.05	0.64	-0.11
	sand^c	1.000	0.018	1.000	1.000	0.002		0.53	-0.90	-0.60	0.45	0.25	0.09	-0.23	-0.11	-0.15	-0.32	-0.13	-0.38	0.05	-0.37	-0.14	-0.25	0.30	-0.09	-0.06	-0.08	-0.22	0.03
	silt^c	1.000	1.000	1.000	1.000	1.000	0.000		-0.77	0.05	-0.04	-0.08	-0.01	0.24	0.16	0.12	-0.42	0.17	-0.31	0.13	-0.13	0.13	0.08	0.08	0.23	0.36	0.27	-0.06	0.23
	clay^c	1.000	0.000	1.000	1.000	0.000	0.000	0.000		0.45	-0.29	-0.18	-0.27	0.10	0.09	-0.05	0.23	0.01	0.24	-0.02	0.34	0.01	0.11	-0.26	0.02	-0.06	0.02	0.39	-0.11
	WHC^d	0.001	1.000	0.000	0.005	0.000	0.000	1.000	0.000		-0.60	-0.63	-0.13	0.73	0.54	0.25	-0.04	0.15	0.12	0.38	0.28	0.31	0.43	-0.32	0.32	0.39	0.29	0.39	0.16
	SWC of WHC	0.000	1.000	0.000	0.000	0.000	0.000	1.000	0.000	0.000		0.13	0.05	-0.08	0.17	-0.47	-0.06	0.19	0.03	-0.02	-0.12	0.21	0.09	0.20	0.21	-0.05	0.17	-0.11	0.29
	BD	1.000	0.052	0.000	1.000	0.006	0.000	1.000	0.023	0.000	1.000		-0.05	-0.66	-0.56	-0.10	0.01	-0.12	-0.12	-0.39	-0.22	-0.34	-0.42	0.24	-0.32	-0.36	-0.25	-0.20	-0.25
	pH	0.000	0.000	0.000	0.035	0.000	1.000	1.000	0.000	1.000	1.000	1.000		0.03	-0.08	0.27	0.53	-0.05	0.49	0.07	0.09	0.15	0.22	-0.16	-0.10	-0.04	-0.24	-0.76	0.10
	C	1.000	1.000	1.000	1.000	0.000	0.000	0.000	1.000	0.000	1.000	0.000	1.000		0.87	0.06	-0.08	0.39	0.20	0.50	0.30	0.58	0.64	-0.29	0.61	0.56	0.56	0.31	0.54
	N_t	0.000	0.010	0.002	0.000	1.000	1.000	0.276	1.000	0.000	0.125	0.000	1.000	0.000		-0.41	-0.19	0.63	0.21	0.45	0.29	0.74	0.73	-0.21	0.80	0.57	0.73	0.35	0.73
	C/N_t	0.000	0.000	0.000	0.000	0.000	0.373	1.000	1.000	0.000	0.000	1.000	0.000	1.000	0.000		0.26	-0.50	0.01	-0.02	-0.16	-0.33	-0.25	0.00	-0.47	-0.12	-0.44	-0.18	-0.46
	NH_4^+	0.001	1.000	1.000	1.000	1.000	0.000	0.000	0.000	1.000	1.000	1.000	0.000	1.000	0.023	0.000		-0.13	0.81	0.03	0.41	0.07	0.10	-0.15	-0.20	-0.11	-0.29	-0.37	-0.05
	NO_3^-	0.000	0.000	0.000	0.000	0.000	1.000	0.085	1.000	0.327	0.015	1.000	1.000	0.000	0.000	0.000	1.000		0.39	-0.07	0.20	0.79	0.69	-0.05	0.81	0.41	0.79	0.08	0.79
	N_{min}	0.085	1.000	1.000	0.000	0.000	0.000	0.000	0.000	1.000	1.000	1.000	0.000	0.003	0.003	1.000	0.000	0.000		0.10	0.45	0.51	0.49	-0.13	0.25	0.18	0.13	-0.34	0.33
	EOC	0.001	0.001	0.000	0.346	1.000	1.000	1.000	1.000	0.000	1.000	0.000	1.000	0.000	0.000	1.000	1.000	1.000	1.000		0.36	0.19	0.22	-0.12	0.22	0.44	0.11	0.16	0.16
	EN	1.000	0.000	0.000	0.000	0.025	0.000	1.000	0.000	0.000	1.000	0.000	1.000	0.000	0.000	0.226	0.000	0.006	0.000	0.000		0.27	0.35	-0.39	0.34	0.36	0.28	0.20	0.41
	C_{mic}	0.000	0.000	0.000	0.000	0.003	0.690	1.000	1.000	0.000	0.002	0.000	0.489	0.000	0.000	0.000	1.000	0.000	0.000	0.015	0.000		0.86	-0.09	0.80	0.52	0.72	0.03	0.78
	N_{mic}	0.000	0.000	0.000	0.000	1.000	0.000	1.000	1.000	0.000	1.000	0.000	0.000	0.000	0.000	0.000	1.000	0.000	0.000	0.001	0.000	0.000		-0.53	0.75	0.50	0.68	0.06	0.79
	C_{mic}/N_{mic}	1.000	0.082	1.000	1.000	0.000	0.000	1.000	0.000	0.000	0.005	0.000	0.184	0.000	0.002	1.000	0.389	1.000	1.000	1.000	0.000	1.000	0.000		-0.18	-0.10	-0.15	-0.13	-0.29
	b-Glu	0.000	0.000	0.000	0.000	1.000	1.000	0.000	1.000	0.000	0.002	0.000	1.000	0.000	0.000	0.000	0.004	0.000	0.000	0.000	0.000	0.000	0.000	0.042		0.66	0.93	0.32	0.87
	N-Ac	0.000	0.017	0.074	0.000	1.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.000	1.000	1.000	0.000	0.026	0.000	0.000	0.000	0.000	1.000	0.000		0.63	0.25	0.48
	Xyl	0.000	0.000	0.000	0.000	1.000	1.000	0.000	1.000	0.000	0.096	0.000	0.000	0.000	0.000	0.000	0.000	0.000	1.000	1.000	0.000	0.000	0.000	0.443	0.000	0.000		0.46	0.81
	Phos	1.000	0.000	0.009	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.005	0.000	0.000	0.000	0.041	0.000	1.000	0.000	0.221	0.004	1.000	1.000	1.000	0.000	0.000	0.000		0.14
	Urease	0.000	0.000	0.000	0.000	1.000	1.000	0.000	1.000	0.216	0.000	0.000	1.000	0.000	0.000	0.000	1.000	0.000	0.000	0.225	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.631	

Table S5-4: Results of semivariogram analyses with model details for HEG 1–9 and AEG 1–9 (see following pages). SWC = soil water content, BD = bulk density, C_{org} = organic carbon, N_t = total nitrogen, N_{min} = mineral nitrogen, EOC = extractable organic carbon, EN = extractable nitrogen, C_{mic} = microbial C, N_{mic} = microbial N; — = no semivariogram model could be fitted.

Site	Variable	SWC	BD	pH	C_{org}	N_t	C/N_t ratio	NH_4^+	NO_3^-	N_{min}	EOC	EN	C_{mic}	N_{mic}	C_{mic}/N_{mic} ratio	β-Glucosidase	Chitinase	Xylosidase	Phosphatase	Urease
HEG1	**model**	**Sph**	**Exp**	**Exp**	**Exp**	**Exp**	—	—	—	—	—	—	**Sph**	**Exp**	**Exp**	—	—	**Exp**	—	**Exp**
	Nug	12.0	0.01	0.00	20.8	4.09	—	—	—	—	—	—	3.E+04	0.00	0.16	—	—	0.02	—	0.01
	psill	1.30	0.04	0.09	277	36.2	—	—	—	—	—	—	1.E+05	0.01	8.26	—	—	0.11	—	0.01
	sill	13.3	0.05	0.09	297	40.3	—	—	—	—	—	—	2.E+05	0.02	8.43	—	—	0.13	—	0.01
	range	0.29	80.9	116	1548	0.46	—	—	—	—	—	—	457	56.2	506	—	—	116	—	4.61
	Spatial structure	9.75	87.3	96.6	93.0	89.8	—	—	—	—	—	—	85.3	78.5	98.1	—	—	87.9	—	59.7
	sum of squares	1018	0.00	0.00	7232	5959	—	—	—	—	—	—	2.E+09	0.00	0.19	—	—	0.03	—	0.00
HEG2	**model**	—	—	**Exp**	—	—	**Exp**	—	**Lin**	—	—	—	—	—	—	—	—	—	—	—
	Nug	—	—	0.05	—	—	0.00	—	0.06	—	—	—	—	—	—	—	—	—	—	—
	psill	—	—	0.65	—	—	0.48	—	5.76	—	—	—	—	—	—	—	—	—	—	—
	sill	—	—	0.70	—	—	0.48	—	5.82	—	—	—	—	—	—	—	—	—	—	—
	range	—	—	0.71	—	—	0.35	—	501	—	—	—	—	—	—	—	—	—	—	—
	Spatial structure	—	—	92.6	—	—	100.0	—	99.0	—	—	—	—	—	—	—	—	—	—	—
	sum of squares	—	—	1.98	—	—	0.42	—	0.07	—	—	—	—	—	—	—	—	—	—	—
HEG3	**model**	**Lin**	**Sph**	**Lin**	—	**Lin**	—	—	—	**Lin**	**Sph**	**Exp**	—	—	**Exp**	—	—	—	—	**Lin**
	Nug	0.00	0.01	0.00	—	0.00	—	—	—	0.02	7.57	14.9	—	—	0.14	—	—	—	—	0.01
	psill	0.01	0.00	0.36	—	0.08	—	—	—	0.11	691	51.5	—	—	0.50	—	—	—	—	0.04
	sill	0.01	0.01	0.36	—	0.09	—	—	—	0.13	699	66.4	—	—	0.64	—	—	—	—	0.05
	range	39.9	2.18	206	—	119	—	—	—	69.0	1.08	3.65	—	—	2.60	—	—	—	—	99.3
	Spatial structure	85.4	30.6	99.5	—	95.5	—	—	—	84.5	98.9	77.6	—	—	78.2	—	—	—	—	84.8
	sum of squares	0.00	0.00	0.00	—	0.00	—	—	—	0.00	8.E+06	5666	—	—	0.72	—	—	—	—	0.00
HEG4	**model**	**Sph**	**Sph**	**Sph**	**Exp**	**Sph**	—	—	—	—	—	—	**Sph**	**Sph**	**Sph**	—	—	**Exp**	—	**Sph**
	Nug	5.82	0.00	0.54	0.00	0.03	—	—	—	—	—	—	9484	71.5	0.00	—	—	0.00	—	0.01
	psill	18.6	0.01	1.23	40.9	0.23	—	—	—	—	—	—	4.E+04	1024	0.00	—	—	0.02	—	0.00
	sill	24.4	0.01	1.77	40.9	0.26	—	—	—	—	—	—	5.E+04	1096	0.00	—	—	0.02	—	0.01
	range	1.41	0.84	3.62	0.56	1.29	—	—	—	—	—	—	1.47	1.60	1.40	—	—	0.36	—	1.88
	Spatial structure	76.1	96.9	69.4	100.0	88.4	—	—	—	—	—	—	81.2	93.5	100.0	—	—	100.0	—	37.6
	sum of squares	628	0.00	15.8	4373	0.22	—	—	—	—	—	—	1.E+10	2.E+06	0.00	—	—	0.00	—	0.00
HEG5	**model**	**Nug**	—	**Sph**	—	—	—	**Lin**	—	—	—	—	—	—	—	—	—	—	—	**Exp**
	Nug	7.57	—	0.00	—	—	—	13.4	—	—	—	—	—	—	—	—	—	—	—	0.00
	psill	0.00	—	0.00	—	—	—	938	—	—	—	—	—	—	—	—	—	—	—	0.01
	sill	7.57	—	0.00	—	—	—	952	—	—	—	—	—	—	—	—	—	—	—	0.01
	range	1.10	—	1.99	—	—	—	595	—	—	—	—	—	—	—	—	—	—	—	0.46
	Spatial structure	0.00	—	100.0	—	—	—	98.6	—	—	—	—	—	—	—	—	—	—	—	100.0
	sum of squares	175	—	0.00	—	—	—	329	—	—	—	—	—	—	—	—	—	—	—	0.00
HEG6	**model**	**Exp**	—	**Exp**	**Exp**	**Exp**	—	**Exp**	—	**Lin**	—	**Exp**	**Exp**	**Exp**	**Exp**	—	—	—	—	—
	Nug	0.72	—	0.00	0.00	0.02	—	0.09	—	4.05	—	0.00	0.00	0.00	0.67	—	—	—	—	—
	psill	5.62	—	0.00	6.65	0.03	—	0.17	—	1343	—	0.01	1.E+04	197	0.68	—	—	—	—	—
	sill	6.34	—	0.00	6.65	0.05	—	0.26	—	1347	—	0.01	1.E+04	197	1.35	—	—	—	—	—
	range	0.47	—	0.63	0.45	0.99	—	2.01	—	2759	—	0.43	0.41	0.45	0.86	—	—	—	—	—
	Spatial structure	88.6	—	100.0	100.0	56.4	—	66.6	—	99.7	—	100.0	100.0	100.0	50.5	—	—	—	—	—
	sum of squares	53.8	—	0.00	57.7	0.01	—	0.06	—	98.8	—	0.00	1.E+08	9.E+04	0.21	—	—	—	—	—

Site	Variable	SWC	BD	pH	C_{org}	N_t	C/N_t ratio	NH_4^+	NO_3^-	N_{min}	EOC	EN	C_{mic}	N_{mic}	C_{mic}/N_{mic} ratio	β-Glucosidase	Chitinase	Xylosidase	Phosphatase	Urease
HEG7	**model**	—	—	**Sph**	**Sph**	**Sph**	—	**Exp**	**Sph**	**Exp**	**Sph**	**Sph**	**Exp**	—	**Sph**	—	**Nug**	—	—	**Lin**
	Nug	—	—	0.01	64.1	0.45	—	20.1	0.00	0.00	0.00	0.00	7.E+04	—	0.00	—	0.03	—	—	0.01
	psill	—	—	0.03	58.0	0.51	—	21.9	0.14	0.03	0.01	0.00	1.E+05	—	0.00	—	0.00	—	—	0.06
	sill	—	—	0.03	122	0.96	—	41.9	0.14	0.03	0.01	0.01	2.E+05	—	0.00	—	0.03	—	—	0.07
	range	—	—	61.1	1.78	1.94	—	1.12	1.36	1.04	2.11	3.17	3.32	—	1.85	—	1.33	—	—	73.4
	Spatial structure	—	—	83.5	47.5	53.5	—	52.1	100.0	89.2	78.9	39.7	59.5	—	73.6	—	0.00	—	—	92.2
	sum of squares	—	—	0.00	2.E+04	1.39	—	5186	0.06	0.00	0.00	0.00	2.E+10	—	0.00	—	0.01	—	—	0.00
HEG8	**model**	—	—	**Sph**	**Sph**	**Exp**	—	**Sph**	**Sph**	**Sph**	**Lin**	**Sph**	**Sph**	**Sph**	—	**Sph**	**Sph**	**Sph**	—	**Sph**
	Nug	—	—	0.00	44.9	0.00	—	0.00	0.02	0.00	1035	0.01	3.E+04	570	—	0.01	0.01	0.00	—	0.00
	psill	—	—	0.00	135	1.43	—	0.01	0.08	0.03	6.E+05	0.01	9.E+04	1714	—	0.04	0.05	0.06	—	0.02
	sill	—	—	0.01	180	1.43	—	0.01	0.10	0.03	6.E+05	0.01	1.E+05	2283	—	0.05	0.06	0.06	—	0.02
	range	—	—	1.04	0.82	0.33	—	0.99	1.30	1.26	4665	1.72	1.18	1.24	—	1.13	1.20	0.93	—	1.55
	Spatial structure	—	—	81.2	75.0	100.0	—	83.7	80.9	91.3	99.8	54.2	78.0	75.0	—	77.8	89.4	100.0	—	88.0
	sum of squares	—	—	0.00	6.E+04	6.49	—	0.00	0.12	0.02	9.E+06	0.00	2.E+10	1.E+07	—	0.00	0.01	0.01	—	0.00
HEG9	**model**	**Sph**	**Sph**	**Sph**	**Exp**	**Exp**	**Lin**	**Sph**	—	**Sph**	**Sph**	**Exp**	**Exp**	**Exp**	**Sph**	**Lin**	**Lin**	**Lin**	**Sph**	**Exp**
	Nug	3.58	0.01	0.00	12.1	0.00	0.43	0.01	—	0.01	0.00	39.7	199	24.2	0.07	0.02	0.01	0.02	0.01	0.00
	psill	9.08	0.01	0.00	13.2	0.11	64.2	0.00	—	0.01	0.01	97.2	5.E+04	887	0.09	0.13	0.41	0.19	0.03	0.01
	sill	12.7	0.02	0.01	25.3	0.11	64.6	0.01	—	0.01	0.01	137	5.E+04	911	0.16	0.15	0.43	0.21	0.04	0.01
	range	3.52	2.78	2.85	1.36	0.25	380	4.36	—	3.69	1.16	3.54	0.86	0.96	1.50	167	241	96.7	9.52	0.33
	Spatial structure	71.7	64.3	41.3	52.3	100.0	99.3	30.1	—	35.9	100.0	71.0	99.6	97.3	57.1	87.6	97.2	90.2	74.9	100.0
	sum of squares	55.8	0.00	0.00	817	0.02	5.62	0.00	—	0.00	0.00	3189	1.E+10	2.E+06	0.03	0.00	0.00	0.00	0.00	0.00
AEG1	**model**	—	**Exp**	—	—	—	**Lin**	**Exp**	**Exp**	**Lin**	—	—	—	—	—	**Nug**	—	**Nug**	—	—
	Nug	—	0.00	—	—	—	0.07	1.87	41.1	0.00	—	—	—	—	—	7.E+05	—	2.E+04	—	—
	psill	—	0.00	—	—	—	4.48	3.37	161	0.11	—	—	—	—	—	0.00	—	0.00	—	—
	sill	—	0.01	—	—	—	4.55	5.23	202	0.12	—	—	—	—	—	7.E+05	—	2.E+04	—	—
	range	—	1.14	—	—	—	554	3.15	3.07	154	—	—	—	—	—	1.35	—	1.35	—	—
	Spatial structure	—	65.4	—	—	—	98.5	64.3	79.7	96.3	—	—	—	—	—	0.00	—	0.00	—	—
	sum of squares	—	0.00	—	—	—	0.00	4.80	1513	0.00	—	—	—	—	—	2.E+12	—	1.E+09	—	—
AEG2	**model**	—	—	**Sph**	**Nug**	—	—	—	**Lin**	—	**Exp**	**Exp**	—	—	**Sph**	**Sph**	—	**Sph**	—	—
	Nug	—	—	0.01	18.5	—	—	—	0.02	—	627	147	—	—	0.11	2.E+04	—	2140	—	—
	psill	—	—	0.02	0.00	—	—	—	0.69	—	1285	484	—	—	0.28	2.E+05	—	8405	—	—
	sill	—	—	0.03	18.5	—	—	—	0.71	—	1911	630	—	—	0.39	2.E+05	—	1.E+04	—	—
	range	—	—	3.85	1.23	—	—	—	243	—	2.37	1.05	—	—	4.50	0.82	—	0.85	—	—
	Spatial structure	—	—	69.4	0.00	—	—	—	97.6	—	67.2	76.8	—	—	70.8	91.2	—	79.7	—	—
	sum of squares	—	—	0.00	1.E+04	—	—	—	0.00	—	1.E+07	2.E+06	—	—	0.40	5.E+11	—	2.E+09	—	—
AEG3	**model**	—	—	**Lin**	**Nug**	—	—	**Exp**	**Sph**	**Exp**	**Sph**	**Exp**	—	**Sph**	**Sph**	**Exp**	—	**Exp**	**Exp**	**Nug**
	Nug	—	—	2.47	12.7	—	—	0.01	10.7	0.00	307	0.00	—	0.00	0.00	1.E+04	—	1376	3.E+04	450
	psill	—	—	835	0.00	—	—	0.03	23.6	0.02	932	0.01	—	4533	0.01	4.E+04	—	1482	5.E+04	0.00
	sill	—	—	837	12.7	—	—	0.03	34.4	0.02	1239	0.01	—	4533	0.01	5.E+04	—	2857	8.E+04	450
	range	—	—	658	1.17	—	—	5.31	1.17	3.62	5.85	0.46	—	1.36	1.01	1.15	—	1.58	3.21	1.17
	Spatial structure	—	—	99.7	0.00	—	—	84.6	68.8	83.3	75.2	100.0	—	100.0	100.0	77.5	—	51.9	62.5	0.00
	sum of squares	—	—	182	3003	—	—	0.00	1076	0.00	3.E+05	0.00	—	9.E+07	0.00	9.E+09	—	1.E+07	1.E+10	6.E+06

Site	Variable	SWC	BD	pH	C_{org}	N_t	C/N_t ratio	NH_4^+	NO_3^-	N_{min}	EOC	EN	C_{mic}	N_{mic}	C_{mic}/N_{mic} ratio	β-Glucosidase	Chitinase	Xylosidase	Phosphatase	Urease
AEG4	**model**	—	—	—	—	—	—	—	—	—	**Lin**	—	—	—	**Lin**	—	—	—	—	—
	Nug	—	—	—	—	—	—	—	—	—	0.00	—	—	—	0.00	—	—	—	—	—
	psill	—	—	—	—	—	—	—	—	—	0.06	—	—	—	0.23	—	—	—	—	—
	sill	—	—	—	—	—	—	—	—	—	0.06	—	—	—	0.23	—	—	—	—	—
	range	—	—	—	—	—	—	—	—	—	45.9	—	—	—	169	—	—	—	—	—
	Spatial structure	—	—	—	—	—	—	—	—	—	98.5	—	—	—	99.3	—	—	—	—	—
	sum of squares	—	—	—	—	—	—	—	—	—	0.00	—	—	—	0.00	—	—	—	—	—
AEG5	**model**	**Nug**	—	**Sph**	**Nug**	**Sph**	**Exp**	**Exp**	**Exp**	**Sph**	—	—	**Exp**	**Exp**	**Sph**	**Exp**	**Sph**	**Exp**	**Exp**	**Exp**
	Nug	9.39	—	0.02	20.0	0.12	0.00	1.12	0.00	55.1	—	—	5.E+11	916	0.00	3.E+04	5925	0.00	0.00	578
	psill	0.00	—	0.02	0.00	0.10	0.00	110	61.1	61.4	—	—	6.E+11	7.E+06	1.41	2.E+05	1.E+04	1.E+04	0.01	716
	sill	9.39	—	0.04	20.0	0.21	0.00	111	61.1	117	—	—	1.E+12	7.E+06	1.41	2.E+05	2.E+04	1.E+04	0.01	1294
	range	0.96	—	2.98	0.96	1.91	6.32	0.25	1.20	1.62	—	—	0.96	4535	6.68	0.42	0.58	0.57	0.40	1.15
	Spatial structure	0.00	—	53.2	0.00	44.4	68.1	99.0	100.0	52.7	—	—	51.3	100.0	100.0	86.9	67.0	100.0	100.0	55.3
	sum of squares	609	—	0.00	888	0.10	0.00	4.E+04	3.E+04	1.E+04	—	—	2.E+25	5.E+07	1.99	2.E+11	3.E+09	7.E+08	0.00	9.E+06
AEG6	**model**	**Lin**	—	**Lin**	**Sph**	**Lin**	—	**Sph**	**Exp**	**Lin**	—	—	—	**Exp**	—	—	—	—	—	—
	Nug	7.73	—	0.06	0.00	0.00	—	41.1	0.00	55.5	—	—	—	0.00	—	—	—	—	—	—
	psill	1179	—	11.7	0.00	0.01	—	219	0.03	395	—	—	—	2333	—	—	—	—	—	—
	sill	1187	—	11.8	0.00	0.01	—	260	0.03	450	—	—	—	2333	—	—	—	—	—	—
	range	641	—	689	1.44	37.6	—	3.69	0.69	14.3	—	—	—	0.21	—	—	—	—	—	—
	Spatial structure	99.3	—	99.5	75.0	91.3	—	84.2	97.5	87.7	—	—	—	100.0	—	—	—	—	—	—
	sum of squares	2736	—	0.08	0.00	0.00	—	4.E+05	0.01	2.E+05	—	—	—	7.E+07	—	—	—	—	—	—
AEG7	**model**	—	—	—	—	—	—	—	**Sph**	—	**Exp**	**Exp**	—	**Sph**	**Sph**	**Lin**	**Exp**	—	—	**Exp**
	Nug	—	—	—	—	—	—	—	0.04	—	0.00	72.2	—	0.00	0.05	0.01	0.00	—	—	98.1
	psill	—	—	—	—	—	—	—	0.18	—	3146	87.0	—	0.00	0.22	0.11	0.01	—	—	108
	sill	—	—	—	—	—	—	—	0.22	—	3146	159	—	0.00	0.27	0.11	0.01	—	—	207
	range	—	—	—	—	—	—	—	3.65	—	0.36	0.42	—	2.07	2.44	132	1.49	—	—	0.85
	Spatial structure	—	—	—	—	—	—	—	82.8	—	100.0	54.6	—	84.0	81.5	95.4	80.5	—	—	52.5
	sum of squares	—	—	—	—	—	—	—	0.08	—	1.E+08	4.E+04	—	0.00	0.26	0.00	0.00	—	—	1.E+05
AEG8	**model**	—	—	**Exp**	—	**Sph**	—	**Sph**	**Exp**	**Sph**	—	**Sph**	**Sph**	**Sph**	—	**Sph**	—	—	—	**Sph**
	Nug	—	—	3.52	—	0.07	—	0.00	0.01	0.00	—	383	1.E+04	338	—	0.01	—	—	—	555
	psill	—	—	7.24	—	0.24	—	0.00	0.08	0.01	—	973	5.E+04	4970	—	0.01	—	—	—	1094
	sill	—	—	10.8	—	0.31	—	0.01	0.10	0.01	—	1356	7.E+04	5309	—	0.01	—	—	—	1649
	range	—	—	0.58	—	2.84	—	3.04	3.41	3.06	—	3.03	1.19	1.21	—	2.07	—	—	—	0.79
	Spatial structure	—	—	67.3	—	76.3	—	63.7	85.5	69.6	—	71.8	80.8	93.6	—	44.9	—	—	—	66.3
	sum of squares	—	—	184	—	0.21	—	0.00	0.00	0.00	—	1.E+06	3.E+09	3.E+07	—	0.00	—	—	—	2.E+07
AEG9	**model**	**Lin**	—	—	**Lin**	**Lin**	—	—	—	—	—	**Exp**	—	—	—	**Sph**	**Exp**	—	**Exp**	**Lin**
	Nug	9.75	—	—	0.00	0.00	—	—	—	—	—	0.00	—	—	—	0.00	0.00	—	7.E+04	0.01
	psill	1993	—	—	0.02	0.01	—	—	—	—	—	0.07	—	—	—	0.01	3.E+04	—	7.E+04	0.24
	sill	2003	—	—	0.02	0.01	—	—	—	—	—	0.07	—	—	—	0.01	3.E+04	—	1.E+05	0.25
	range	596	—	—	46.4	38.6	—	—	—	—	—	115	—	—	—	2.38	0.40	—	1.85	166
	Spatial structure	99.5	—	—	95.1	93.8	—	—	—	—	—	97.5	—	—	—	63.2	100.0	—	46.7	96.2
	sum of squares	649	—	—	0.00	0.00	—	—	—	—	—	0.00	—	—	—	0.00	6.E+09	—	1.E+11	0.00

Supplementary material of Chapter 6

Supplementary Figures

Supplementary Tables

Supplemental methods

We assessed the AMF beta-diversity according to the following formula (Baselga & Orme, 2012):

$$\beta_{\mathrm{SOR}} = \beta_{\mathrm{SIM}} + \beta_{\mathrm{SNE}}$$

with β_{SOR} as beta-diversity, which is the sum of β_{SIM}, the turnover component i.e. taxa replacement, and $\beta_{\mathrm{SNE},}$ the nestedness component, i.e. taxa gain and loss.

Supplemental results

Changes in AMF community composition were more pronounced between than within subplots (Figure S6-10 and Figure S6-11). In particular, AMF composition within single subplots differed relatively little between April and May, and between May and June the within-subplot diversity was still smaller than between-subplot diversity. This effect weakened after the observed changes in June and was no longer significant for the later time points (August, October and November). The changes in AMF community composition increased from spring to summer months and decreased again slightly in autumn (Figure S6-10).

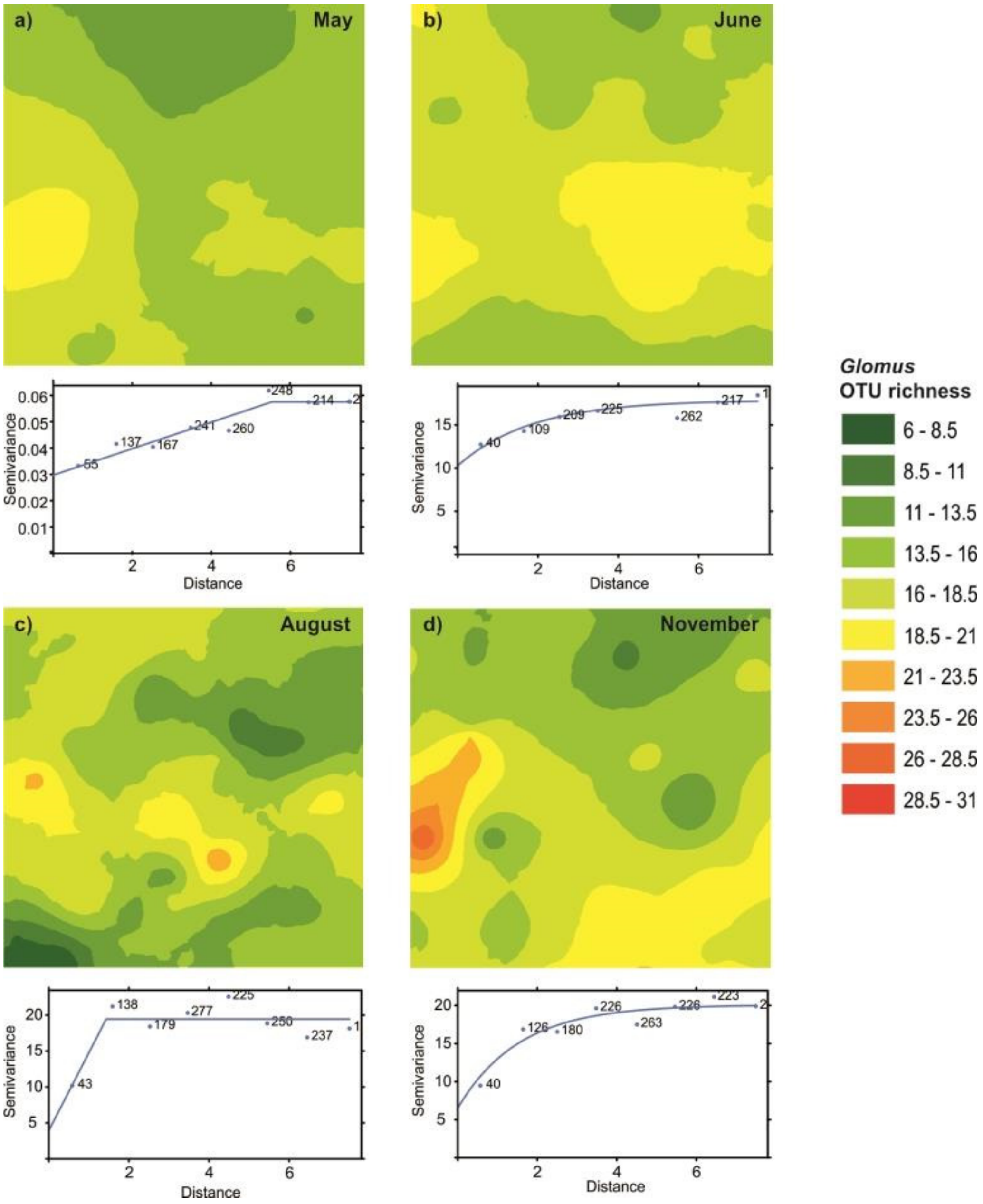

Figure S6-1: Spatial analysis of *Glomus* OTU richness grouped together per sampling date: a) May, b) June, c) August and d) November. Spatial patterns within the data were analyzed and calculated as semivariogram models and visualized as kriged maps using these models. Dimensions of all maps are 10 m x 10 m.

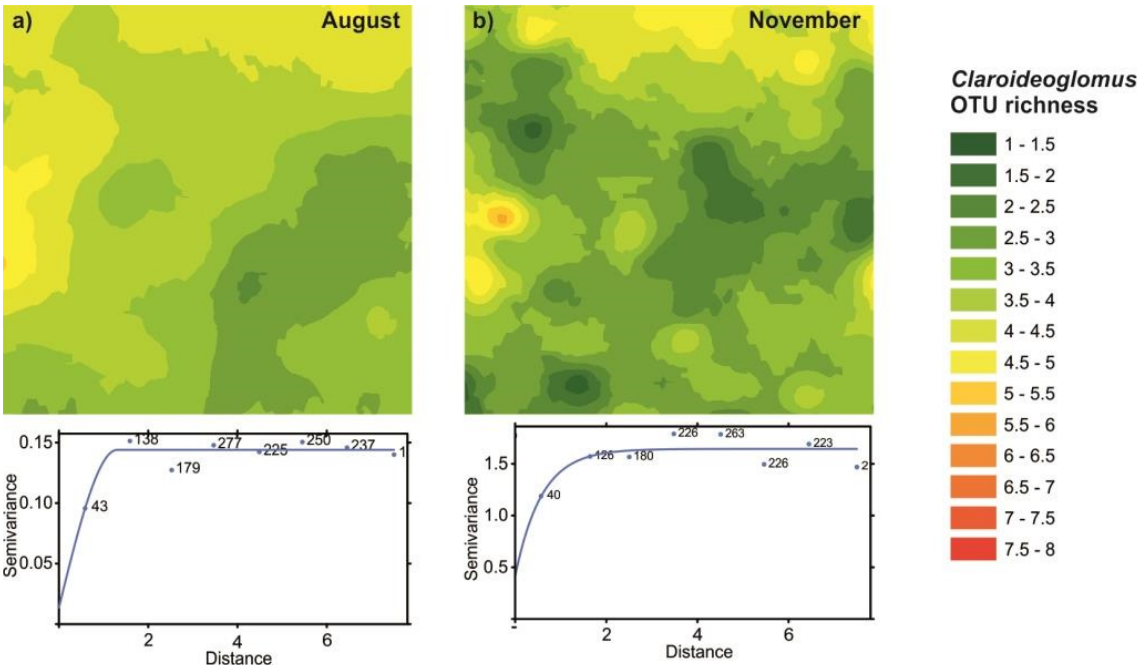

Figure S6-2: Spatial analysis of *Claroideoglomus* OTU richness grouped together per sampling date: a) August, b) November. Spatial patterns within the data were analyzed and calculated as semivariogram models and visualized as kriged maps using these models. Dimensions of all maps are 10 m x 10 m.

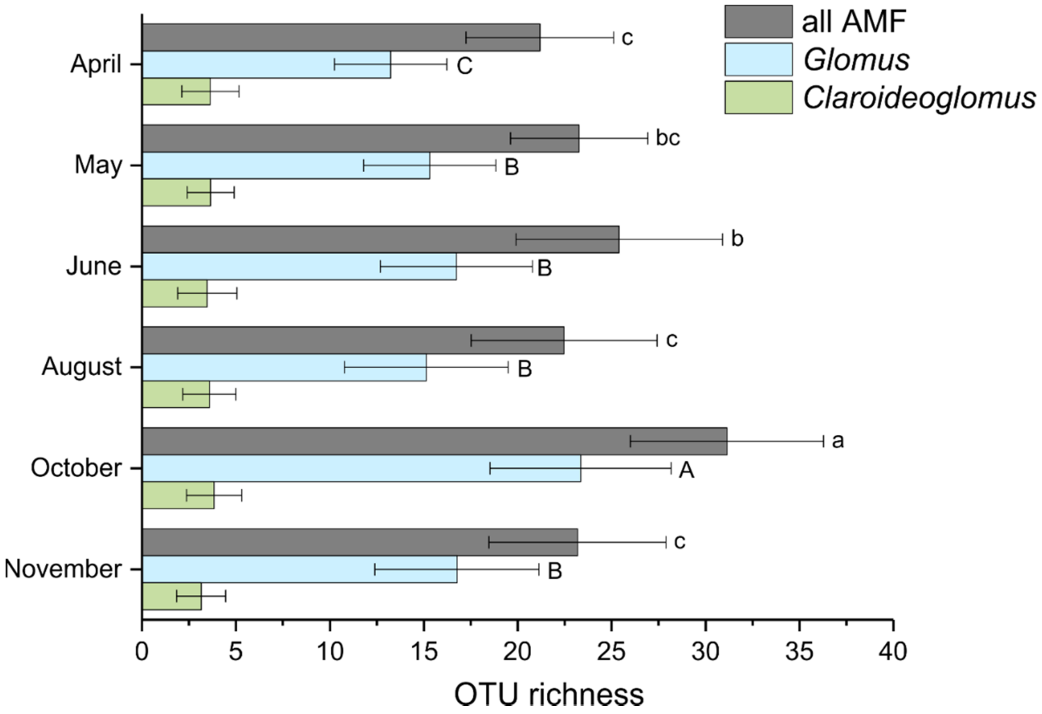

Figure S6-3: Seasonal distribution of total AMF OTUs and additionally for the OTUs assigned to the genera *Glomus* and *Claroideoglomus*, displayed as bar graphs; differences in significance ($p < 0.05$) are indicated by different letters above bars/boxplots. Given are mean values of subplots, whiskers indicate standard deviation.

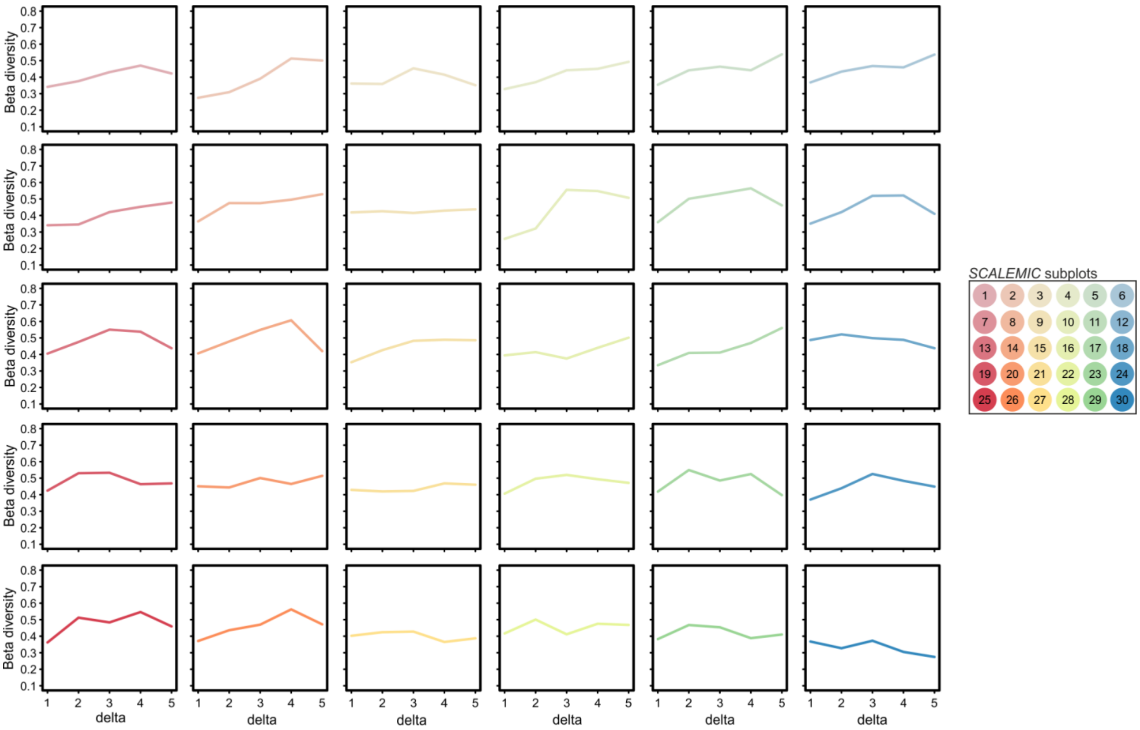

Figure S6-4: Patterns of variability within AMF beta-diversity for all subplots from one studied time point to the next (delta 1: April to May, delta 2: May to June, delta 3: June to August, delta 4: August to October and delta 5: October to November); lines represent the overall beta-diversity (β_{SOR}) observed in the partial data sets, computed using the R-package *betapart* (Baselga & Orme, 2012).

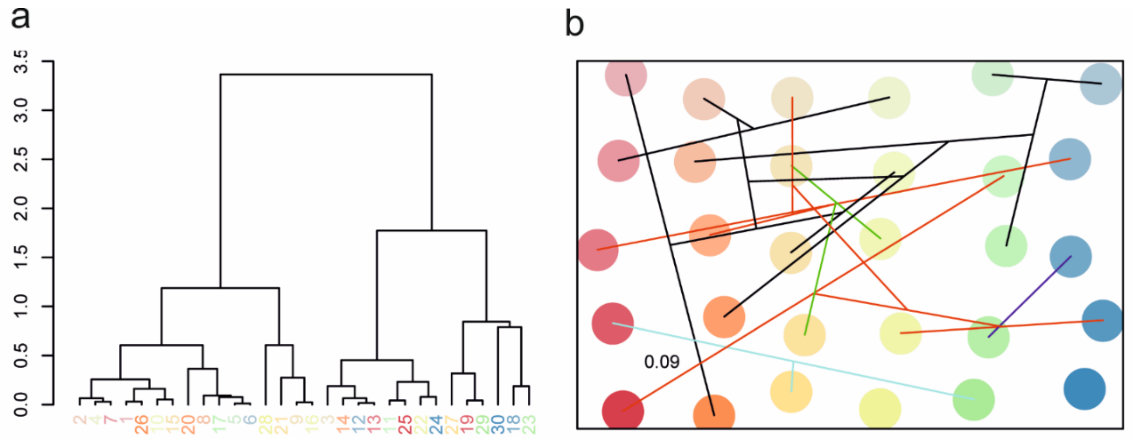

Figure S6-5: Correlation of the development of AMF beta-diversity (β_{SOR}) from one time point to the next (see Figure S6-3), represented as a) dendrogram; b) dendrogram overlaid on a jittered representation of the subplots. Crossing lines indicate that no correlation between spatial subplot position and development of AMF beta-diversity could be determined; displayed value: mean Mantel correlation coefficient of Euclidean distance of x- and y-values and the correlation between AMF beta-diversity developments of the subplots.

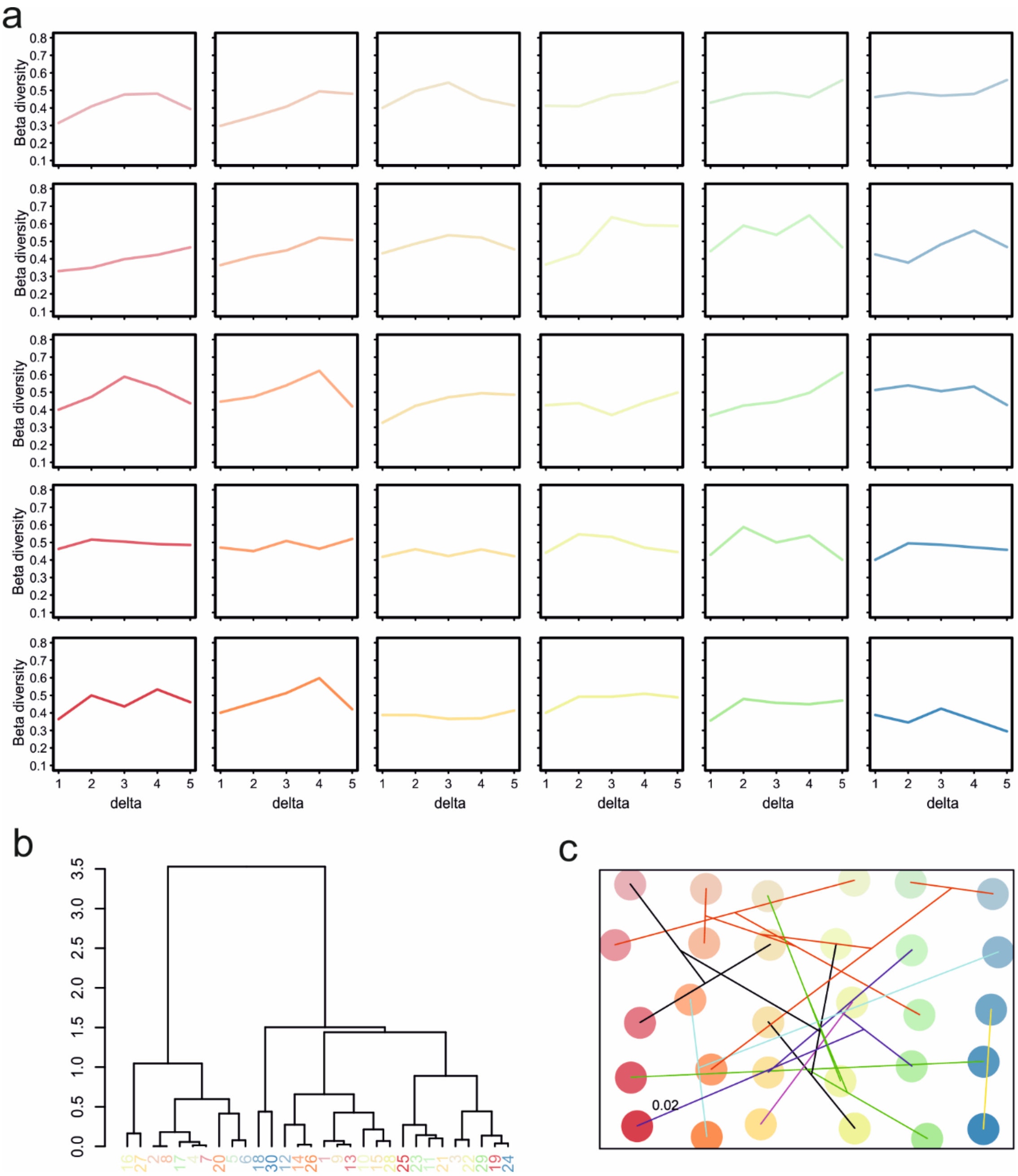

Figure S6-6: a) Patterns of variability within *Glomus* beta-diversity for all subplots from one studied time point to the next (delta 1: April to May, delta 2: May to June, delta 3: June to August, delta 4: August to October and delta 5: October to November); lines represent the overall beta-diversity (β_{SOR}) observed in the partial data sets, computed using the R-package betapart (Baselga & Orme, 2012); b) Dendrograms displaying the correlation between *Glomus* beta-diversity profiles; c) overlaid on jittered spatial representations of the subplots (displayed value: Mantel coefficient of correlation of Euclidean distance of x- and y-values and the *Glomus* beta-diversity development of the subplot).

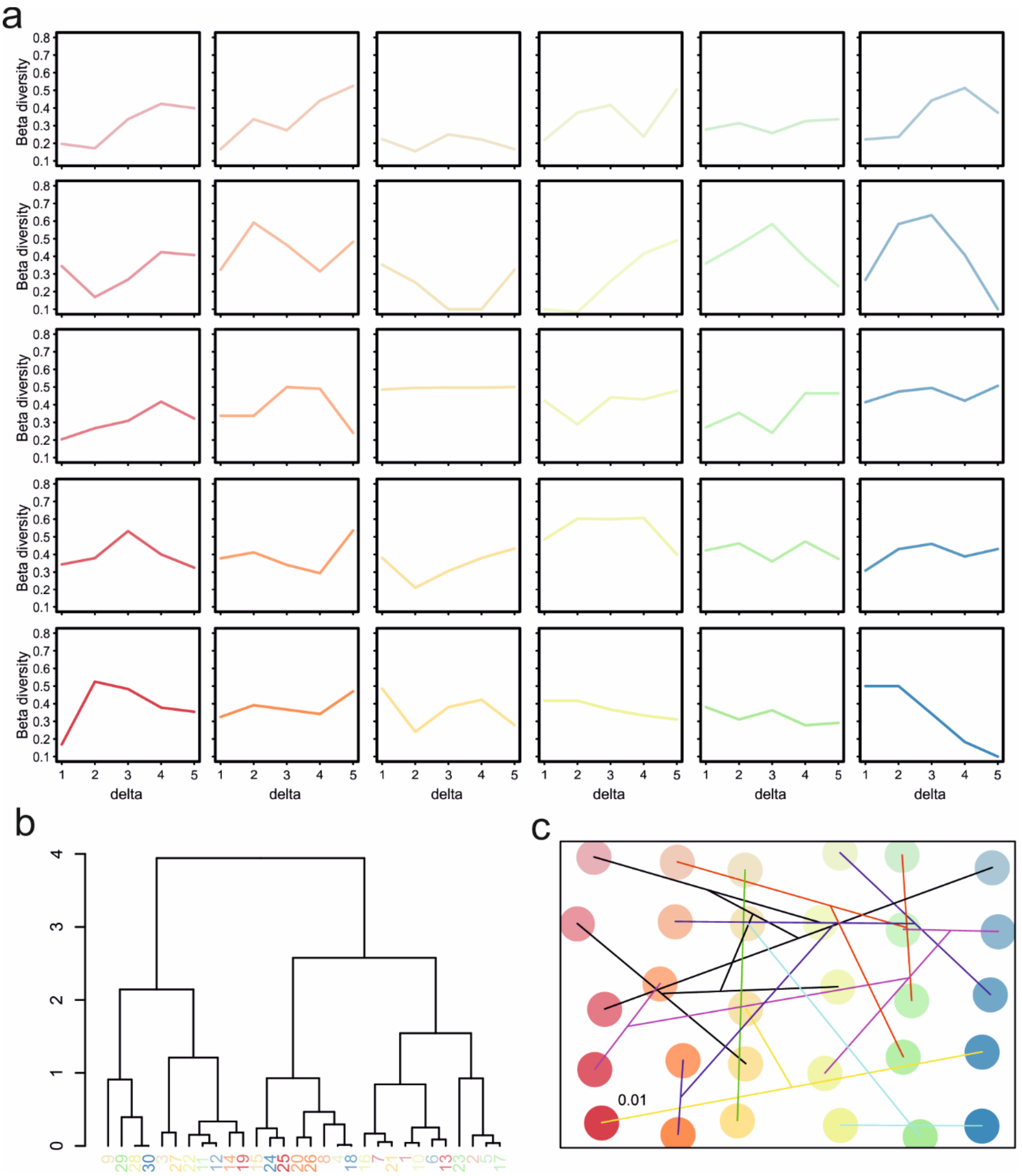

Figure S6-7: a) Patterns of variability within *Claroideoglomus* beta-diversity for all subplots from one studied time point to the next (delta 1: April to May, delta 2: May to June, delta 3: June to August, delta 4: August to October and delta 5: October to November); lines represent the overall beta-diversity (β_{SOR}) observed in the partial data sets, computed using the R-package betapart (Baselga & Orme, 2012); b) Dendrograms displaying the correlation between *Claroideoglomus* beta-diversity profiles; c) overlaid on jittered spatial representations of the subplots (displayed value: Mantel coefficient of correlation of Euclidean distance of x- and y-values and the *Claroideoglomus* beta-diversity development of the subplot).

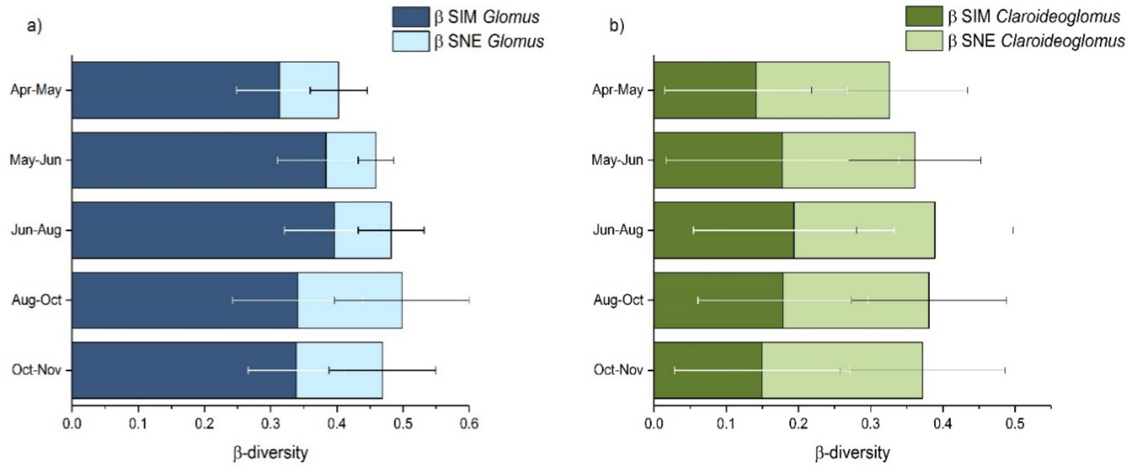

Figure S6-8: Patterns of variability within assemblages of a) *Glomus* and b) *Claroideoglomus* across the studied plot from one studied time point to the next. The stacked bars represent overall beta-diversity (β_{SOR}) observed in the partial data sets, computed using the R-package betapart (Baselga & Orme, 2012); darker sections of the bars represent the contribution of the turnover of the represented genus (β_{SIM}), whereas the lighter sections account for the nestedness of the represented genus (β_{SNE}); error bars represent variability between subplots.

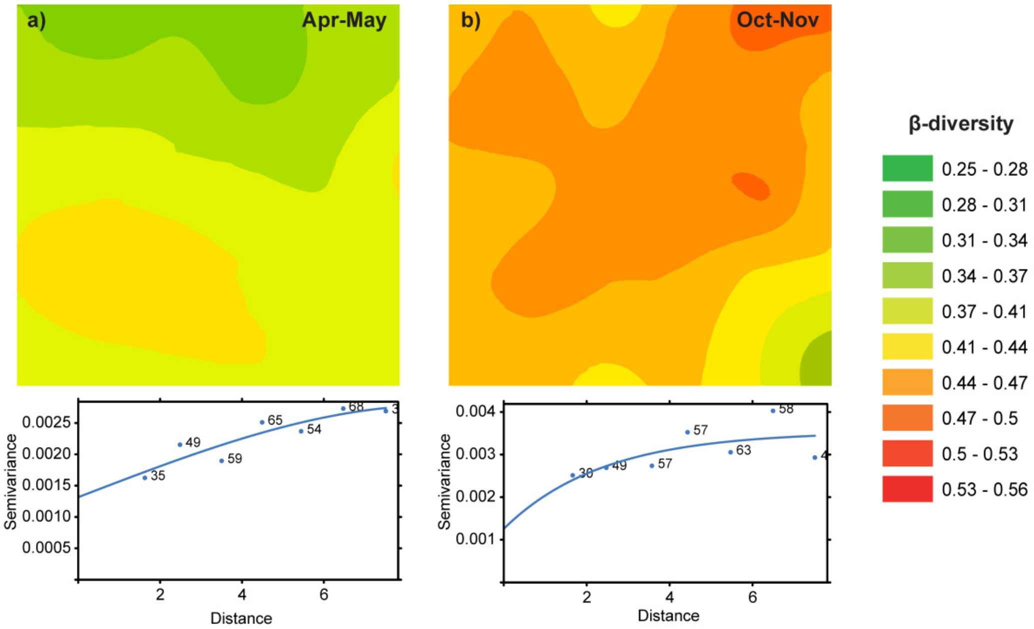

Figure S6- 9: Spatial analysis of AMF beta-diversity with all AMF OTUs grouped together from one time point to the next: a) April-May, b) October-November. Spatial patterns within the data were analyzed and calculated as semivariogram models (lower panel) and visualized as kriged maps (upper panel) using these models. Dimensions of all maps are 10 m x 10 m.

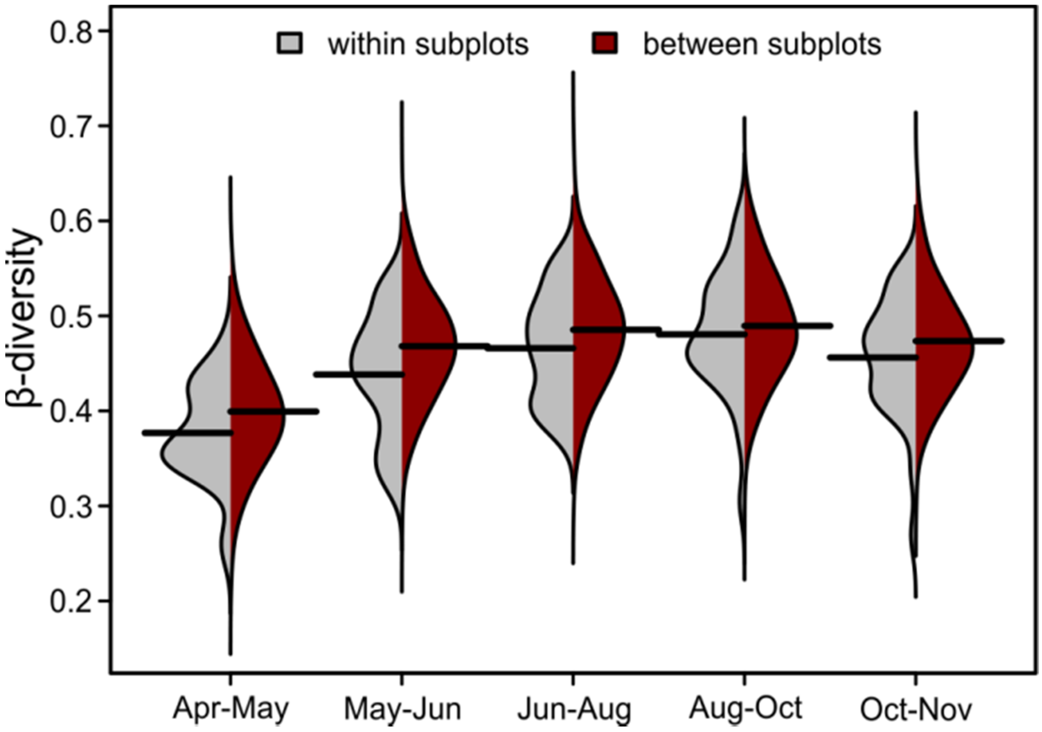

Figure S6-10: Histograms and comparisons of AMF beta-diversity (β_{SOR}) within and between subplots from one time point to the next; April-May ($p = 0.03644$), May-June ($p = 0.021$), June-August ($p = 0.08424$), August-October ($p = 0.5145$) and October-November ($p = 0.2616$); p-values below 0.05 indicate significant differences in AMF beta-diversity within and between subplots.

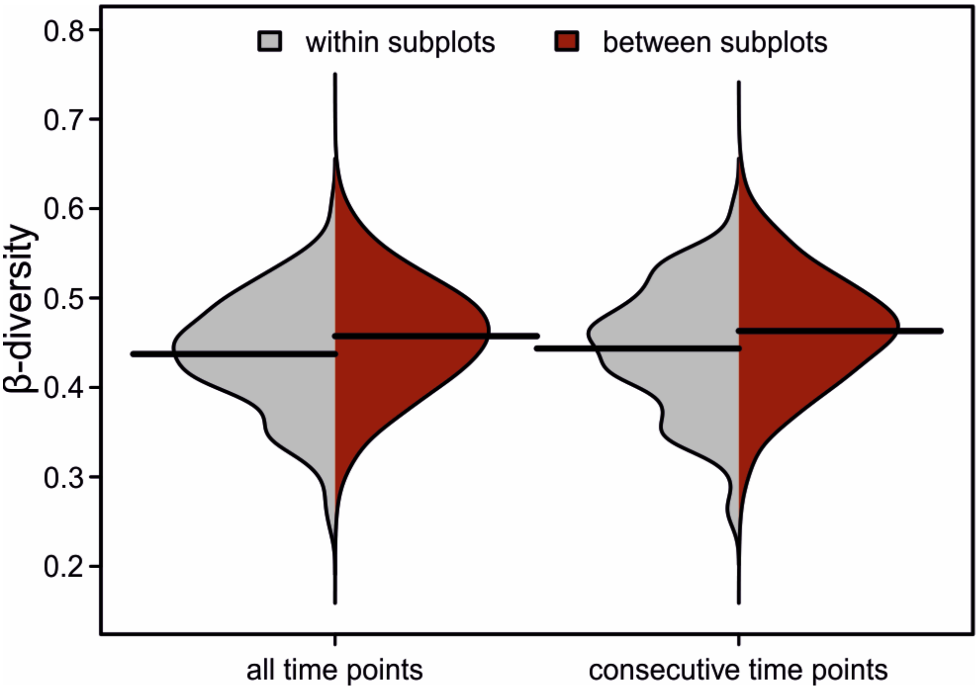

Figure S6-11: Histograms and comparisons of AMF beta-diversity (β_{SOR}) within and between subplots over all time points ($p < 0.001$) and from one time point to the next ($p = 0.0015$); *p*-values below 0.05 indicate significant differences in AMF beta-diversity within and between subplots.

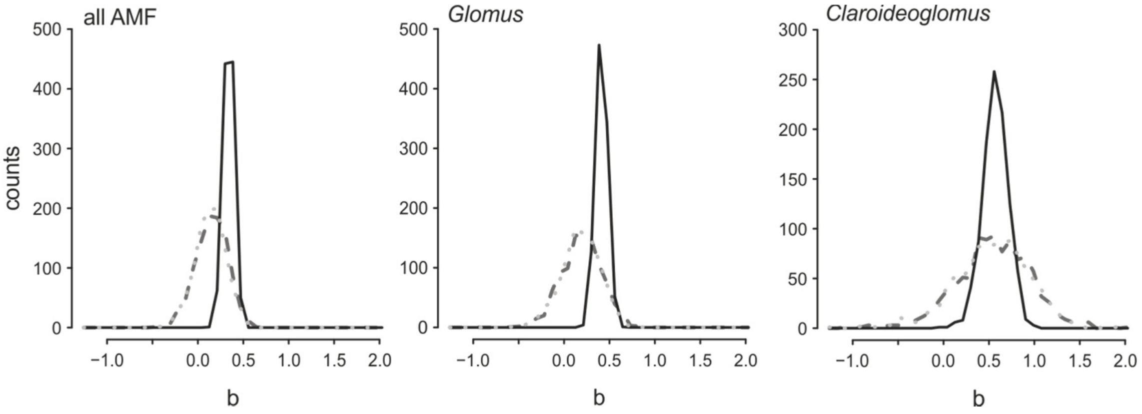

Figure S6-12: Histograms illustrate the distribution of regression coefficients (b) that account for the fitting of 1000 different rarefactions (black line), compared to null-models based on 1000 draws of species identities (based on their relative probability of occurrence among samples) of the whole dataset (grey dashed line) and timepoint-specific datasets (light grey dotted line).

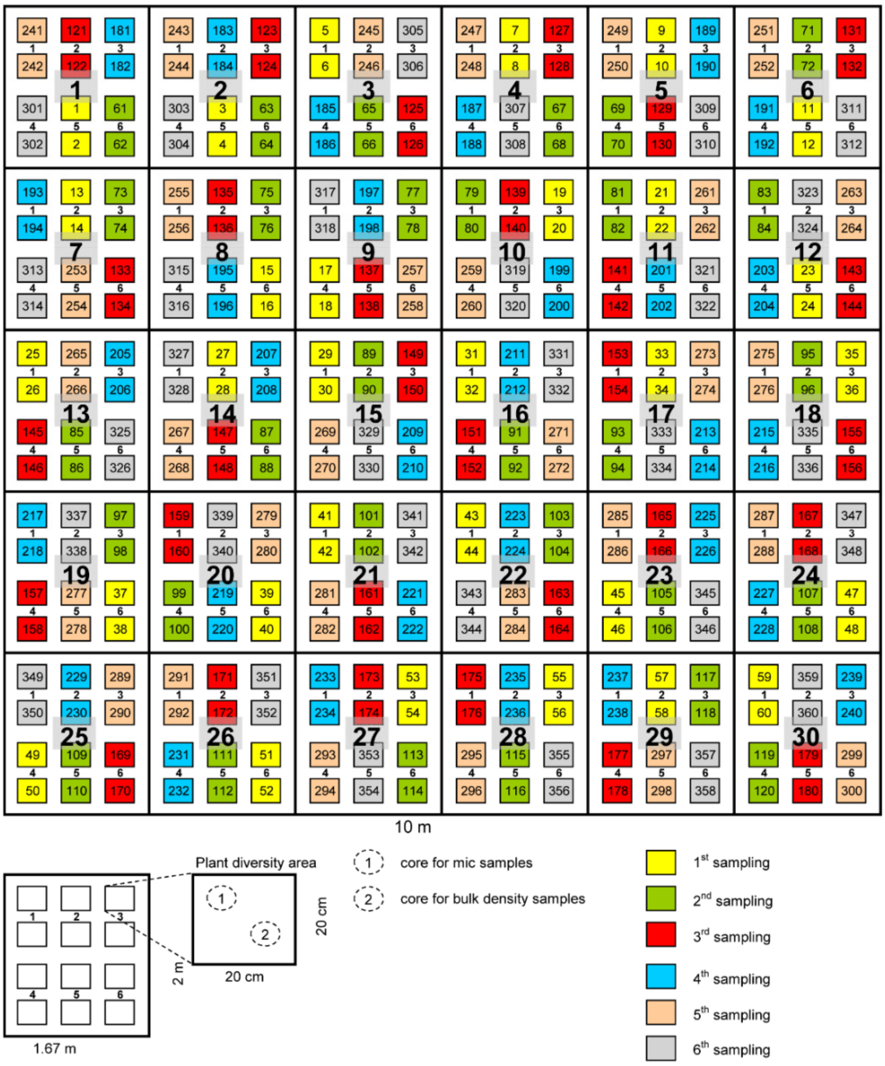

Figure S6-13: Sampling design of SCALEMIC Experiment (taken from Regan et al. (2014)).

Table S6-1: Percent distribution of overall AMF OTUs (genera) as supplement to the barplot (Figure 1) showing relative distribution of overall AMF OTUs (genera).

Genus	**April**	**May**	**June**	**August**	**October**	**November**
Glomus	69.0	73.9	71.3	73.3	76.8	77.0
Claroideoglomus	15.0	13.5	16.4	12.9	13.8	11.5
Diversispora	8.0	5.4	6.6	6.9	5.1	5.3
Archaeospora	3.0	2.7	2.5	2.6	2.2	2.7
Acaulospora	2.0	1.8	0.8	0.9	0.7	0.9
Ambispora	2.0	0.9	0.8	1.7	0.7	1.8
Paraglomus	1.0	1.8	1.6	1.7	0.7	0.9
OTUs in total	100	111	122	116	138	113

Table S6-2: Permutational multivariate analysis of variance based on the Sørensen distance matrix, stratified by sampling date for single environmental variables. Significance: n.s. = not significant, $0.01 < p < 0.05$ = *, $0.001 < p < 0.01$ =**.

explanatory variable	**significance**	**R^2 for significant variables**
soil water content	n.s.	
NH_4^+	n.s.	
N_{min}	n.s.	
EOC	n.s.	
NO_3^-	n.s.	
total plant cover	n.s.	
legume biomass	n.s.	
total plant biomass	n.s.	
silt content	**	0.020
forbs biomass	n.s.	
N_{mic}	**	0.021
pH	**	0.034
grass biomass	n.s.	
bacteria (PLFA)	*	0.011
C_{mic}	*	0.018
ratio gram+:gram- (PLFA)	n.s.	
gram- bacteria (PLFA)	**	0.011
gram+ bacteria (PLFA)	n.s.	
EON	*	0.027
root biomass	n.s.	
ratio Cmic:Nmic	**	0.025
ratio fungi:bacteria (PLFA)	n.s.	
litter biomass	n.s.	
bulk density	n.s.	
PO_4^{3-}	*	0.015
C_{total} content	*	0.008
N_{total} content	*	0.008
ratio C_{total}:N_{total}	n.s.	
fungi (PLFA)	n.s.	
bacteria 16S	n.s.	
x coordinate	**	0.024
y coordinate	**	0.019

Table S6-3: Permutational multivariate analysis of variance based on the Sørensen distance matrix, stratified by sampling date combining environmental variables. Significance: n.s. = not significant, $0.01 < p < 0.05$ = *, $0.001 < p < 0.01$ =**.

explanatory variable	**significance**	**R^2 for significant variables**
silt content	**	0.018
pH	**	0.019
N_{mic}	**	0.023
ratio C_{mic}:N_{mic}	n.s.	
PO_4^{3-}	n.s.	
EON	*	0.013
gram- bacteria (PLFA)	n.s.	
N_{total} content	n.s.	
C_{mic}	n.s.	
C_{total} content	*	0.008
bacteria (PLFA)	n.s.	
x coordinate	**	0.024
y coordinate	**	0.019

Table S6-4: Variables used to identify environmental influences on AMF abundances in alphabetical order. Given are the units and the sources of first publication. At each time point, variables were analyzed in both replicates of each of the 30 subplots (n = 60).

Environmental variable	Unit	Sampling times	Source
archaea 16S	copies g^{-1} DM	6	Regan et al. (2017)
bacteria (PLFA)	µg FAME g^{-1} DM	6	Regan et al. (2014, 2015)
bacteria 16S	copies g^{-1} DM	6	Regan et al. (2017)
bulk density	g cm^3	6	Regan et al. (2014, 2015)
clay content	%	1	Regan et al. (2014, 2015)
C_{mic}	µg C g^{-1} DM	6	Regan et al. (2014, 2015)
C_{total} content	%	6	Regan et al. (2014, 2015)
EOC	µg C g^{-1} DM	6	Regan et al. (2014, 2015)
EON	µg N g^{-1} DM	6	Regan et al. (2014, 2015)
forbes biomass	g 400 cm^{-2}	6	Regan et al. (2014, 2015)
fungi (PLFA)	µg FAME g^{-1} DM	6	Regan et al. (2014, 2015)
gram- bacteria (PLFA)	µg FAME g^{-1} DM	6	Regan et al. (2014, 2015)
gram+ bacteria (PLFA)	µg FAME g^{-1} DM	6	Regan et al. (2014, 2015)
grass biomass	g 400 cm^{-2}	6	Regan et al. (2014, 2015)
legume biomass	g 400 cm^{-2}	6	Regan et al. (2014, 2015)
litter biomass	g 400 cm^{-2}	6	Regan et al. (2014, 2015)
NH_4^+	µg N g^{-1} DM	6	Regan et al. (2014, 2015)
N_{mic}	µg N g^{-1} DM	6	Regan et al. (2014, 2015)
N_{min}	µg N g^{-1} DM	6	Regan et al. (2014, 2015)
NO_3^-	µg N g^{-1} DM	6	Regan et al. (2014, 2015)
N_{total} content	%	6	Regan et al. (2014, 2015)
pH		6	Regan et al. (2014, 2015)
plant species number	Count	6	Regan et al. (2014, 2015)
PO_4^{3-}	µg P g^{-1} DM	3	Regan et al. (2014, 2015)
ratio C_{mic}:N_{mic}		6	Regan et al. (2014, 2015)
ratio C_{total}:N_{total}		6	Regan et al. (2014, 2015)
ratio fungi:bacteria (PLFA)		6	Regan et al. (2014, 2015)
ratio gram+:gram- (PLFA)		6	Regan et al. (2014, 2015)
root biomass	g roots 400 cm^{-2}	6	Regan et al. (2014, 2015)
Shannon Index	–	3	Regan et al. (2014, 2015)
silt content	%	1	Regan et al. (2014, 2015)
soil water content	% DM	6	Regan et al. (2014, 2015)
total plant biomass	g 400 cm^{-2}	6	Regan et al. (2014, 2015)
total plant cover	%	4	Regan et al. (2014, 2015)

Table S6-5: Comparison of linear mixed effect models with different random structures using SAS 9.4 (SAS Institute Inc., Cary, USA). AIC = Akaike's information criterion, RCBD = randomized complete block design, POWA = anisotropic power, POW = power, EXP = exponential, ANOVA = analyses of variance, s.e.d. = standard error of difference.

Analysis	**AIC**	**Mean s.e.d.**
(1) One-way ANOVA (Regan et al. 2014, 2017)	2137.77	0.8568
(2) RCBD, random block	2090.94	0.7688
(3) RCBD, random block, random pair of sampling locations	2088.72	0.8354
(4) RCBD, random block, POWA spatial across field*	2089.31	0.8031
(5) RCBD, random block, POWA spatial within plot*	2088.46	0.8163
(6) RCBD, random block, POW=EXP spatial within plot	2085.46	0.8050
(7) RCBD, random block, POW=EXP spatial across field	2087.26	0.8020
(8) RCBD, random block, POWA spatial across field+ temporal*	2090.64	0.8472
(9) One-way ANOVA, POWA spatial across field + temporal	2096.29	0.8988
(10) One-way ANOVA, POWA spatial across field+ temporal + nugget	2074.57	1.7337

* Nugget did not yield improvement

References

Baselga, A., and Orme, C.D.L. (2012) betapart: an R package for the study of beta diversity. Methods in Ecology and Evolution 3: 808-812.

Regan, K.M., Nunan, N., Boeddinghaus, R.S., Baumgartner, V., Berner, D., Boch, S. et al. (2014) Seasonal controls on grassland microbial biogeography: Are they governed by plants, abiotic properties or both? Soil Biol Biochem 71: 21-30.

Regan, K.M., Nunan, N., Boeddinghaus, R.S., Baumgartner, V., Berner, D., Boch, S. et al. (2015) Corrigendum to "Seasonal controls on grassland microbial biogeography: are they governed by plants, abiotic properties or both?"[Soil Biology and Biochemistry 71 (April 2014)]. Soil Biology & Biochemistry 86: 2e214.

Regan, K., Stempfhuber, B., Schloter, M., Rasche, F., Prati, D., Philippot, L. et al. (2017) Spatial and temporal dynamics of nitrogen fixing, nitrifying and denitrifying microbes in an unfertilized grassland soil. Soil Biology and Biochemistry 109: 214-226.

Supplementary material of Chapter 7

Appendix 1:

Supplementary Figures

Supplementary Tables

1. Appendix 1: Details on materials and methods

1.1. Land-use intensity

Land-use intensity varied on the sites over the years depending on farm management, which was assessed via questionnaires every year (Vogt et al., submitted). The land-use intensity index (LUI) of Blüthgen et al. (2012) was used to assess mowing frequency as well as grazing and N-fertilization intensity standardized per region and is calculated by the formula:

$$LUI_i = \sqrt{\frac{F_i}{F_{mean,R}} + \frac{M_i}{M_{mean,R}} + \frac{G_i}{G_{mean,R}}}$$

Thereby *i* the site, *R* is the region, *F* is fertilization intensity in kg nitrogen ha^{-1} year^{-1}, *M* is number of cuts per year, and *G* is livestock density for grazing in livestock units days of grazing ha^{-1} a^{-1}, with 1 livestock unit = 500 kg animal life weight. Previous analyses have shown that the metric produces similar results when standardised by the means of all regions as the range of intensities with each is similar (Blüthgen et al., 2012, Allan et al., 2015).

1.2. Soil Microbial analyses

1.2.1. Microbial biomass measures

Microbial biomass carbon (C_{mic}) and nitrogen (N_{mic}) were measured using the chloroform-fumigation-extraction method (CFE) according to Vance, Brookes and Jenkinson (1987). Carbon and N were extracted from each, 24 h chloroform fumigated and non-fumigated, replicate (10 g) with 40 mL 0.5 M K_2SO_4 by shaking 30 minutes on a horizontal shaker at 150 rpm and subsequently centrifuging for 30 minutes at 4400 g. The supernatant was filtered, diluted by 1:4 and C and N concentrations in resulting extracts were measured on a TOC/TN analyzer (Multi N/C 2100S, Analytik Jena AG, Jena, Germany).

Microbial phosphorus (P_{mic}) was measured using a combination of methods by Kouno, Tuchiya and Ando (1995) and McLaughlin, Alston and Martin (1986). Conditioning of resin stripes was done using 0.5 M $NaHCO_3$ (pH = 8.5). Three aliquots of moist soil equalling 2 g of dry soil per sample were weighed into 50 mL polyethylene tubes and 30 mL distilled water (H_2O_{dest}) was added to each tube. One tube was non-fumigated (without aliquots (1) H_2O_{dest}), the second one was fumigated with 1 mL hexanol ((2) H_2O_{dest} and liquid hexanol) and at the third one 1 mL of 20 µg P mL^{-1} as dissolved KH_2PO_4 was added ((3) H_2O_{dest} and a P spike) to correct for P release during the fumigation. Soil samples were horizontally shaken for 16 hours with $NaHCO_3$ conducted resin membrane stripes. Afterwards, stripes were rinsed with H_2O_{dest} to remove adhering soil and transferred into fresh tubes. Afterwards, 30 mL 0.1 M sodium chloride/hydrochloric acid were added, and the resin stripes shaken for 2 hours to desorb P. To correct for sorption of P released during fumigation in the calculation of hexanol P, we used a sorption curve between non-fumigated and P spiked samples (Bünemann, 2008). We did not use a transformation factor for the calculated P_{hex} concentrations and used P_{mic} synonymously for P_{hex} in accordance with Oberson and Joner (2005) and Bünemann (2008).

1.2.2. Soil enzyme activities

Enzyme activities of beta-glucosidase (EC 3.2.1.21), beta-xylosidase (EC 3.2.1.37), N-acetyl-beta-glucosaminidase (EC 3.2.1.52), phosphatase (EC 3.1.3.2) and urease (EC 3.5.1.5) as well as denitrification enzyme activity (DEA) were measured in this study. The first four enzymes were determined using the method of Marx, Wood and Jarvis (2001) and fluorescent 4-methylumbelliferone substrates (4-MUF; Sigma-Aldrich, St. Louis, USA) together with a buffered solution of pH 6.1, as described in detail by Berner et al. (2011). Urease activity was measured photometrically according to Kandeler and Gerber (1988) as described in Schinner, Öhlinger, Kandeler and Margesin (1996).

Denitrification enzyme activity was measured after Keil et al. (2015) according to a method based on Smith and Tiedje (1979). Shortly, two replicates per soil sample with each 2 g fresh weight were weighed into three 118 mL flasks and 10 mL substrate solution (1.07 mM KNO_3 and 1 mM glucose) added. The bottles were closed air tight and oxygen was removed from the system by repeated evacuating and subsequently filling with N_2. 10 mL of N_2 were removed from the headspace and refilled with 10 mL of acetone-free acetylene. Bottles were incubated at 25 °C while shaking at 150 rpm and immediately, and after 30, 60 and 120 minutes 1 mL of the flask headspace was withdrawn with a gas-tight syringe and injected in pre-evacuated 5.9 mL exetainers (Labco scientific, UK) and 11 mL N_2 were added. Measurement of N_2O was done on a gas chromatograph (Agilent 7890 gas chromatograph equipped with an ECD detector, Agilent, Santa Clara, CA, USA). Potential N_2O release due to denitrification (ng N_2O g^{-1} dry soil h^{-1}) from soil was calculated from the linear regression of N_2O concentration against time.

1.2.3. Microbial community structure

Microbial community composition in terms of bacterial and fungal abundance was analysed using the phospholipid fatty acid composition of soils. Extraction was conducted following the protocol of Frostegard, Tunlid and Baath (1991). 2 g of soil were extracted with 9.2 mL of single-phase mixture (chloroform:methanol:citrate buffer (0.15 M, pH 4.0), 1:2:0.8, v:v:v) for 2 hours on a horizontal shaker (125 rpm) followed by centrifugation (2500 rpm, 10 minutes). The liquid phase was transferred into fresh centrifuge glasses and soil washed with 2.5 mL single-phase mixture, centrifuged (2500 rpm, 10 minutes) and the supernatant transferred as before. The supernatant solution was then mixed with 3.1 mL $CHCl_3$ and 3.1 mL citrate buffer on a horizontal shaker (275 rpm, 10 minutes) and centrifuged (2500 rpm, 10 minutes). 4 mL of the lower, lipid-containing phase was transferred into fresh test-tubes and the solvents evaporated on a heating plate at 37 °C under constant N_2 flow. The test-tubes with the dried lipid material were stored in a fridge over night at +4 °C.

For the lipid fractionation, material was solved in 3 x 100 µL $CHCl_3$ and transferred on silica columns (Bond Elut-SI, 500 mg, 3 mL Agilent Technologies Inc. ,Santa Clara, USA) in a Baker System. After flushing out the neutral lipids (5 mL $CHCl_3$) and glycolipids (20 mL acetone) the columns were flushed with 5 mL methanol; this last fraction of polar lipids was collected in centrifuge test-tubes. Under a constant N_2 stream the methanol was evaporated on a heating plate at 40 °C until the samples were dried.

As a third step the alkaline methanolysis was performed after Dowling, Widdel and White (1986) to gain fatty acid methyl esters (FAME). The resulting organic phase, consistent of FAMEs from phospholipids and solvents, was evaporated under a constant N_2 stream at 40 °C. For measurement at the gas chromatograph (AutoSystem XL. PerkinElmer Inc., Massachusetts, USA) samples were solved in 100 µL isooctane and stored in GC vials at 4 °C until measurement. Following Ruess and Chamberlain (2010) the PLFA FAMEs a15:0, i15:0, i16:0, and i17:0 together with cy17:0 and cy19:0 as well as 16:1ω7 were used to represent soil bacteria, while PLFA FAME 18:2ω6,9 served as a fungal indicator. The fungal to bacteria ratio (F:B) was calculated.

Fungal biomass was also determined as ergosterol content of bio-membranes according to the modified approach of Djajakirana, Joergensen and Meyer (1996). Ergosterol was extracted from 2 g of soil with 25 mL ethanol during 30 minutes shaking on a horizontal shaker at 150 rpm. Solid particles were sedimented by centrifugation for 30 minutes at 4422 × g. 10 mL of the supernatant were dried at 50 °C in a vacuum rotary evaporator (Martin Christ, RVC 2-25, Osterode am Harz, Germany). Dried extracts were dissolved in 1 mL methanol and samples transferred into 2 mL brown glass HPLC vials via cellulose-acetate filters (0.45 µm; Sartorius Stedim Biotech GmbH, Gottingen, Germany). Ergosterol in samples was quantified by HPLC analysis (Beckmann Coulter, System Gold 125, Fullerton, USA) using a 250 mm × 4.6 mm Spherisorb ODS II 5 µm column with a mobile phase of pure methanol, a flow rate of 1 mL minute^{-1} and a detection wavelength of 282 nm (Beckmann Coulter, System Gold 166 UV-detector, Fullerton, USA). Pure ergosterol (Sigma–Aldrich, St. Louis, USA) for calibration was dissolved in methanol and diluted to give final concentrations of 0.0, 0.1, 0.2, 0.5, 1.0, 2.0, 5 and 10 µg ergosterol mL^{-1}.

1.3. Abiotic soil analyses

Nitrate and ammonium were extracted from 10 g soil with 0.5 M K_2SO_4 solution (1:4, g soil:mL solution) following the isonorm protocol DIN ISO 14256-2 (2006) and measured with an AutoAnalyzer 3 (Bran & Luebbe, Norderstedt, Germany). Nitrate was measured at 550 nm wavelength and ammonium at 660 nm. To determine extractable organic carbon (EOC) and extractable nitrogen (EN) the extracts for analysing mineral nitrogen were diluted 1:4 and measured using a TOC/TN analyzer (Multi N/C 2100S, Analytik Jena AG, Jena, Germany). Total C (C_{org}) and total N (N_t) were measured by dry combustion using an elemental analyzer (VarioMax, Elementar Analysensysteme GmbH, Hanau, Germany). Inorganic C was determined after removal of organic C at a temperature of 450 °C for 16 h. The difference between total and inorganic C equals the organic C. Bulk density was calculated as g dry soil, excluding stones, per cubic centimeter.

1.4. Plant data

1.4.1. Plant traits

Single plant species trait values from the TRY database (Kattge et al., 2011) were obtained by averaging the data by author. This way, disproportionate contributions of one author to a single species was accounted for. Where trait data was not available for single species recorded at the field sites, the CWM was calculated using only known species. This only occurred for very few species which accounted overall for 0.05% of total plot coverage and therefore did not affect the overall results.

Reference list for request 250 from TRY database:

Dataset	Reference
Jasper Ridge Californian Woody Plants Database	Ackerly, D. D. and W. K. Cornwell. 2007. A trait-based approach to community assembly: partitioning of species trait values into within- and among-community components. Ecology Letters 10:135-145.
Plant Physiology Database	Atkin, O. K., M. H. M. Westbeek, M. L. Cambridge, H. Lambers, and T. L. Pons. 1997. Leaf respiration in light and darkness - A comparison of slow- and fast-growing Poa species. Plant Physiology 113:961-965.
Plant Physiology Database	Atkin, O. K., M. Schortemeyer, N. McFarlane, and J. R. Evans. 1999. The response of fast- and slow-growing Acacia species to elevated atmospheric CO2: an analysis of the underlying components of relative growth rate. Oecologia 120: 544-554.
The RAINFOR Plant Trait Database	Baker, T. R., O.L. Phillips, W.F. Laurance, N.C.A. Pitman, S. Almeida, L. Arroyo, A. DiFiore, T. Erwin, N. Higuchi, T.J. Killeen, S.G. Laurance, H. Nascimento, A. Monteagudo, D.A. Neill, J.N.M. Silva, Y. Malhi, G. Lopez Gonzalez, J. Peacock, C.A. Quesada, S. L. Lewis, and J. Lloyd. 2009. Do species traits determine patterns of wood production in Amazonian forests? Biogeosciences 6:297-307.
Wetland Dunes Database	Bakker, C., J. Rodenburg, and P. Bodegom. 2005. Effects of Ca- and Fe-rich seepage on P availability and plant performance in calcareous dune soils. Plant and Soil 275:111-122.
Wetland Dunes Database	Bakker, C., P. M. Van Bodegom, H. J. M. Nelissen, W. H. O. Ernst, and R. Aerts. 2006. Plant responses to rising water tables and nutrient management in calcareous dune slacks. Plant Ecology 185:19-28.
Plant Physiology Database	Campbell, C., L. Atkinson, J. Zaragoza-Castells, M. Lundmark, O. Atkin, and V. Hurry. 2007. Acclimation of photosynthesis and respiration is asynchronous in response to changes in temperature regardless of plant functional group. New Phytologist 176:375-389.

Dataset	Reference
Sheffield & Spain Woody Database	Castro-Diez, P., J. P. Puyravaud, and J. H. C. Cornelissen. 2000. Leaf structure and anatomy as related to leaf mass per area variation in seedlings of a wide range of woody plant species and types. Oecologia 124:476-486.
Sheffield & Spain Woody Database	Castro-Diez, P., J. P. Puyravaud, J. H. C. Cornelissen, and P. Villar-Salvador. 1998. Stem anatomy and relative growth rate in seedlings of a wide range of woody plant species and types. Oecologia 116:57-66.
Global Wood Density Database	Chave, J., D. Coomes, S. Jansen, S. L. Lewis, N. G. Swenson, and A. E. Zanne. 2009. Towards a world wide wood economics spectrum. Ecology Letters 12: 351-366.
Sheffield Database	Cornelissen, J. H. C. 1996. An experimental comparison of leaf decomposition rates in a wide range of temperate plant species and types. Journal of Ecology 84:573-582.
Sheffield Database	Cornelissen, J. H. C., B. Cerabolini, P. Castro-Diez, P. Villar-Salvador, G. Montserrat-Marti, J. P. Puyravaud, M. Maestro, M. J. A. Werger, and R. Aerts. 2003. Functional traits of woody plants: correspondence of species rankings between field adults and laboratory-grown seedlings? Journal of Vegetation Science 14:311-322.
Sheffield & Spain Woody Database	Cornelissen, J. H. C., B. Cerabolini, P. Castro-Diez, P. Villar-Salvador, G. Montserrat-Marti, J. P. Puyravaud, M. Maestro, M. J. A. Werger, and R. Aerts. 2003. Functional traits of woody plants: correspondence of species rankings between field adults and laboratory-grown seedlings? Journal of Vegetation Science 14:311-322.
Abisko & Sheffield Database	Cornelissen, J. H. C., H. M. Quested, D. Gwynn-Jones, R. S. P. Van Logtestijn, M. A. H. De Beus, A. Kondratchuk, T. V. Callaghan, and R. Aerts. 2004. Leaf digestibility and litter decomposability are related in a wide range of subarctic plant species and types. Functional Ecology 18:779-786.
Abisko & Sheffield Database	Cornelissen, J. H. C., M. J. A. Werger, P. CastroDiez, J. W. A. vanRheenen, and A. P. Rowland. 1997. Foliar nutrients in relation to growth, allocation and leaf traits in seedlings of a wide range of woody plant species and types. Oecologia 111:460-469.
Sheffield Database	Cornelissen, J. H. C., N. Perez-Harguindeguy, S. Diaz, J. P. Grime, B. Marzano, M. Cabido, F. Vendramini, and B. Cerabolini. 1999. Leaf structure and defence control litter decomposition rate across species and life forms in regional floras on two continents. New Phytologist 143:191-200.
Abisko & Sheffield Database	Cornelissen, J. H. C., P. C. Diez, and R. Hunt. 1996. Seedling growth, allocation and leaf attributes in a wide range of woody plant species and types. Journal of Ecology 84:755-765.
Sheffield Database	Cornelissen, J. H. C., P. C. Diez, and R. Hunt. 1996. Seedling growth, allocation and leaf attributes in a wide range of woody plant species and types. Journal of Ecology 84:755-765.

Dataset	Reference
Sheffield Database	Cornelissen, J. H. C., R. Aerts, B. Cerabolini, M. J. A. Werger, and M. G. A. van der Heijden. 2001. Carbon cycling traits of plant species are linked with mycorrhizal strategy. Oecologia 129:611-619.
Sheffield & Spain Woody Database	Cornelissen, J.H.C. 1999. A triangular relationship between leaf size and seed size among woody species: allometry, ontogeny, ecology and taxonomy. Oecologia 118: 248-255.
Jasper Ridge Californian Woody Plants Database	Cornwell, W. K. and D. D. Ackerly. 2009. Community assembly and shifts in plant trait distributions across an environmental gradient in coastal California. Ecological Monographs 79:109-126.
Jasper Ridge Californian Woody Plants Database	Cornwell, W. K., D. W. Schwilk, and D. D. Ackerly. 2006. A trait-based test for habitat filtering: Convex hull volume. Ecology 87:1465-1471.
ArtDeco Database	Cornwell, W. K., J. H. C. Cornelissen, K. Amatangelo, E. Dorrepaal, V. T. Eviner, O. Godoy, S. E. Hobbie, B. Hoorens, H. Kurokawa, N. Pérez-Harguindeguy, H. M. Quested, L. S. Santiago, D. A. Wardle, I. J. Wright, R. Aerts, S. D. Allison, P. van Bodegom, V. Brovkin, A. Chatain, T. V. Callaghan, S. Díaz, E. Garnier, D. E. Gurvich, E. Kazakou, J. A. Klein, J. Read, P. B. Reich, N. A. Soudzilovskaia, M. V. Vaieretti, and M. Westoby. 2008. Plant species traits are the predominant control on litter decomposition rates within biomes worldwide. Ecology Letters 11:1065-1071.
Global 15N Database	Craine, J. M., A. J. Elmore, M. P. M. Aidar, M. Bustamante, T. E. Dawson, E. A. Hobbie, A. Kahmen, M. C. Mack, K. K. McLauchlan, A. Michelsen, G. B. Nardoto, L. H. Pardo, J. Penuelas, P. B. Reich, E. A. G. Schuur, W. D. Stock, P. H. Templer, R. A. Virginia, J. M. Welker, and I. J. Wright. 2009. Global patterns of foliar nitrogen isotopes and their relationships with climate, mycorrhizal fungi, foliar nutrient concentrations, and nitrogen availability. New Phytologist 183: 980-992.
Roots Of the World (ROW) Database	Craine, J. M., W. G. Lee, W. J. Bond, R. J. Williams, and L. C. Johnson. 2005. Environmental constraints on a global relationship among leaf and root traits of grasses. Ecology 86:12-19.
Sheffield Database	Díaz, S., J. G. Hodgson, K. Thompson, M. Cabido, J. H. C. Cornelissen, A. Jalili, G. Montserrat-Martí, J. P. Grime, F. Zarrinkamar, Y. Asri, S. R. Band, S. Basconcelo, P. Castro-Díez, G. Funes, B. Hamzehee, M. Khoshnevi, N. Pérez-Harguindeguy, M. C. Pérez-Rontomé, F. A. Shirvany, F. Vendramini, S. Yazdani, R. Abbas-Azimi, A. Bogaard, S. Boustani, M. Charles, M. Dehghan, L. de Torres-Espuny, V. Falczuk, J. Guerrero-Campo, A. Hynd, G. Jones, E. Kowsary, F. Kazemi-Saeed, M. Maestro-Martínez, A. Romo-Díez, S. Shaw, B. Siavash, P. Villar-Salvador, and M. R. Zak. 2004. The plant traits that drive ecosystems: Evidence from three continents. Journal of Vegetation Science 15:295-304.
The DIRECT Plant Trait Database	Everwand G, Fry, EL, Eggers T, Manning P (2014) Seasonal variation in the relationship between plant traits and grassland carbon and water fluxes. Ecosystems 17, 1095-1108

Dataset	Reference
Fonseca/Wright New South Wales Database	Fonseca, C. R., J. M. Overton, B. Collins, and M. Westoby. 2000. Shifts in trait-combinations along rainfall and phosphorus gradients. Journal of Ecology 88: 964-977.
The VISTA Plant Trait Database	Fortunel, C., E. Garnier, R. Joffre, E. Kazakou, H. Quested, K. Grigulis, S. Lavorel, P. Ansquer, H. Castro, P. Cruz, J. Dolezal, O. Eriksson, H. Freitas, C. Golodets, C. Jouany, J. Kigel, M. Kleyer, V. Lehsten, J. Leps, T. Meier, R. Pakeman, M. Papadimitriou, V. P. Papanastasis, F. Quetier, M. Robson, M. Sternberg, J. P. Theau, A. Thebault, and M. Zarovali. 2009. Leaf traits capture the effects of land use changes and climate on litter decomposability of grasslands across Europe. Ecology 90:598-611.
Traits from Subarctic Plant Species Database	Freschet, G. T., J. H. C. Cornelissen, R. S. P. van Logtestijn, and R. Aerts. 2010. Evidence of the 'plant economics spectrum' in a subarctic flora. Journal of Ecology 98:362-373.
Traits from Subarctic Plant Species Database	Freschet, G. T., J. H. C. Cornelissen, R. S. P. van Logtestijn, and R. Aerts. 2010. Substantial nutrient resorption from leaves, stems and roots in a sub-arctic flora: what is the link with other resource economics traits? New Phytologist 186: 879-889.
The DIRECT Plant Trait Database	Fry, E.L., Power, S.A. Manning, P. (2014) Trait based classification and manipulation of functional groups in biodiversity-ecosystem function experiments. Journal of Vegetation Science, 25, 248-261.
The RAINFOR Plant Trait Database	Fyllas, N. M., S. Patino, T. R. Baker, G. Bielefeld Nardoto, L. A. Martinelli, C. A. Quesada, R. Paiva, M. Schwarz, V. Horna, L. M. Mercado, A. Santos, L. Arroyo, E. M. Jimenez, F. J. Luizao, D. A. Neill, N. Silva, A. Prieto, A. Rudas, M. Silviera, I. C. G. Vieira, G. Lopez-Gonzale, and J. Lloyd. 2009. Basin-wide variations in foliar properties of Amazonian forest: phylogeny, soils and climate Biogeosciences 6:2677-2708.
The VISTA Plant Trait Database	Garnier, E., S. Lavorel, P. Ansquer, H. Castro, P. Cruz, J. Dolezal, O. Eriksson, C. Fortunel, H. Freitas, C. Golodets, K. Grigulis, C. Jouany, E. Kazakou, J. Kigel, M. Kleyer, V. Lehsten, J. Leps, T. Meier, R. Pakeman, M. Papadimitriou, V. P. Papanastasis, H. Quested, F. Quetier, M. Robson, C. Roumet, G. Rusch, C. Skarpe, M. Sternberg, J.-P. Theau, A. Thebault, D. Vile, and M. P. Zarovali. 2007. Assessing the effects of land-use change on plant traits, communities and ecosystem functioning in grasslands: A standardized methodology and lessons from an application to 11 European sites. Annals of Botany 99:967-985.
PLANTSdata USDA	Green, W. 2009. USDA PLANTS Compilation, version 1, 09-02-02. (http://bricol.net/downloads/data/PLANTSdatabase/) NRCS: The PLANTS Database (http://plants.usda.gov, 1 Feb 2009). National Plant Data Center: Baton Rouge, LA 70874-74490 USA.
Chinese Leaf Traits Database	Han, W. X., J. Y. Fang, D. L. Guo, and Y. Zhang. 2005. Leaf nitrogen and phosphorus stoichiometry across 753 terrestrial plant species in China. New Phytologist 168:377-385.

Dataset	Reference
Chinese Leaf Traits Database	He, J. S., L. Wang, D. F. B. Flynn, X. P. Wang, W. H. Ma, and J. Y. Fang. 2008. Leaf nitrogen : phosphorus stoichiometry across Chinese grassland biomes. Oecologia 155:301-310.
Chinese Leaf Traits Database	He, J. S., Z. H. Wang, X. P. Wang, B. Schmid, W. Y. Zuo, M. Zhou, C. Y. Zheng, M. F. Wang, and J. Y. Fang. 2006. A test of the generality of leaf trait relationships on the Tibetan Plateau. New Phytologist 170:835-848.
Herbaceous Traits from the Öland Island Database	Hickler, T. 1999. Plant functional types and community characteristics along environmental gradients on Öland's Great Alvar (Sweden) Masters Thesis, University of Lund, Sweden.
Leaf Physiology Database	Kattge, J., W. Knorr, T. Raddatz, and C. Wirth. 2009. Quantifying photosynthetic capacity and its relationship to leaf nitrogen content for global-scale terrestrial biosphere models. Global Change Biology 15:976-991.
Leaf and Whole Plant Traits Database	Kazakou, E., D. Vile, B. Shipley, C. Gallet, and E. Garnier. 2006. Co-variations in litter decomposition, leaf traits and plant growth in species from a Mediterranean old-field succession. Functional Ecology 20:21-30.
KEW African Plant Traits Database	Kirkup, D., P. Malcolm, G. Christian, and A. Paton. 2005. Towards a digital African Flora. Taxon 54:457-466.
The LEDA Traitbase	Kleyer, M., R. M. Bekker, I. C. Knevel, J. P. Bakker, K. Thompson, M. Sonnenschein, P. Poschlod, J. M. van Groenendael, L. Klimes, J. Klimesova, S. Klotz, G. M. Rusch, Hermy, M. , D. Adriaens, G. Boedeltje, B. Bossuyt, A. Dannemann, P. Endels, L. Götzenberger, J. G. Hodgson, A.-K. Jackel, I. Kühn, D. Kunzmann, W. A. Ozinga, C. Römermann, M. Stadler, J. Schlegelmilch, H. J. Steendam, O. Tackenberg, B. Wilmann, J. H. C. Cornelissen, O. Eriksson, E. Garnier, and B. Peco. 2008. The LEDA Traitbase: a database of life-history traits of the Northwest European flora. Journal of Ecology 96:1266-1274.
Ponderosa Pine Forest Database	Laughlin, D. C., J. J. Leppert, M. M. Moore, and C. H. Sieg. 2010. A multi-trait test of the leaf-height-seed plant strategy scheme with 133 species from a pine forest flora. Functional Ecology 24:493-501.
Plant Physiology Database	Loveys, B. R., L. J. Atkinson, D. J. Sherlock, R. L. Roberts, A. H. Fitter, and O. K. Atkin. 2003. Thermal acclimation of leaf and root respiration: an investigation comparing inherently fast- and slow-growing plant species. Global Change Biology 9:895-910.
Fonseca/Wright New South Wales Database	McDonald, P. G., C. R. Fonseca, J. M. Overton, and M. Westoby. 2003. Leaf-size divergence along rainfall and soil-nutrient gradients: is the method of size reduction common among clades? Functional Ecology 17:50-57.
Leaf and Whole Plant Traits Database	McKenna, M. F. and B. Shipley. 1999. Interacting determinants of interspecific relative growth: Empirical patterns and a theoretical explanation. Ecoscience 6: 286-296.
ECOCRAFT	Medlyn, B. E. and P. G. Jarvis. 1999. Design and use of a database of model parameters from elevated [CO2] experiments. Ecological Modelling 124:69-83.

Dataset	Reference
ECOCRAFT	Medlyn, B. E., C. V. M. Barton, M. S. J. Broadmeadow, R. Ceulemans, P. DeAngelis, M. Forstreuter, M. Freeman, S. B. Jackson, S. Kellomaeki, E. Laitat, A. Rey, P. Roberntz, B. D. Sigurdsson, J. Strassemeyer, K. Wang, P. S. Curtis, and P. G. Jarvis. 2001. Stomatal Conductance of forest species after long-term exposure to elevated CO2 concentration: a synthesis. New Phytologist 149:247-264.
ECOCRAFT	Medlyn, B. E., F.-W. Badeck, D. G. G. De Pury, C. V. M. Barton, M. Broadmeadow, R. Ceulemans, P. De Angelis, M. Forstreuter, M. E. Jach, S. Kellomäki, E. Laitat, M. Marek, S. Philippot, A. Rey, J. Strassemeyer, K. Laitinen, R. Liozon, B. Portier, P. Roberntz, K. Wang, and P. G. Jarvis. 1999. Effects of elevated CO2 on photosynthesis in European forest species: a meta-analysis of model parameters. Plant, Cell and Environment 22:1475-1495.
Leaf and Whole Plant Traits Database	Meziane, D. and B. Shipley. 1999. Interacting components of interspecific relative growth rate: constancy and change under differing conditions of light and nutrient supply. Functional Ecology 13:611-622.
Leaf and Whole Plant Traits Database	Meziane, D. and B. Shipley. 1999. Interacting determinants of specific leaf area in 22 herbaceous species: effects of irradiance and nutrient availability. Plant Cell and Environment 22:447-459.
Global Seed Mass, Plant Height Database	Moles, A. T., D. D. Ackerly, C. O. Webb, J. C. Tweddle, J. B. Dickie, A. J. Pitman, and M. Westoby. 2005. Factors that shape seed mass evolution. Proceedings of the National Academy of Sciences of the United States of America 102:10540-10544.
Global Seed Mass, Plant Height Database	Moles, A. T., D. S. Falster, M. R. Leishman, and M. Westoby. 2004. Small-seeded species produce more seeds per square metre of canopy per year, but not per individual per lifetime. Journal of Ecology 92:384-396.
Global Leaf Robustness and Physiology Database	Niinemets, U. 1999. Components of leaf dry mass per area - thickness and density - alter leaf photosynthetic capacity in reverse directions in woody plants. New Phytologist 144:35-47.
Global Leaf Robustness and Physiology Database	Niinemets, U. 2001. Global-scale climatic controls of leaf dry mass per area, density, and thickness in trees and shrubs. Ecology 82:453-469.
Catalonian Mediterranean Forest Trait Database	Ogaya, R. and J. Penuelas. 2003. Comparative field study of Quercus ilex and Phillyrea latifolia: photosynthetic response to experimental drought conditions. Environmental and Experimental Botany 50:137-148.
Catalonian Mediterranean Forest Trait Database	Ogaya, R. and J. Penuelas. 2006. Contrasting foliar responses to drought in Quercus ilex and Phillyrea latifolia. Biologia Plantarum 50:373-382.

Dataset	Reference
Catalonian Mediterranean Forest Trait Database	Ogaya, R. and J. Penuelas. 2007. Tree growth, mortality, and above-ground biomass accumulation in a holm oak forest under a five-year experimental field drought. Plant Ecology 189:291-299.
Catalonian Mediterranean Forest Trait Database	Ogaya, R. and J. Penuelas. 2008. Changes in leaf delta C-13 and delta N-15 for three Mediterranean tree species in relation to soil water availability. Acta Oecologica-International Journal of Ecology 34:331-338.
Leaf Biomechanics Database	Onoda, Y., M. Westoby, P. B. Adler, A. M. F. Choong, F. J. Clissold, J. H. C. Cornelissen, S. Diaz, N. J. Dominy, A. Elgart, L. Enrico, P. V. A. Fine, J. J. Howard, A. Jalili, K. Kitajima, H. Kurokawa, C. McArthur, P. W. Lucas, L. Markesteijn, N. Perez-Harguindeguy, L. Poorter, L. Richards, L. S. Santiago, Jr. E. Sosinski, S. Van Bael, D. I. Warton, I. J. Wright, S. J. Wright, and N. Yamashita. 2011 . Global patterns of leaf mechanical properties. Ecology Letters 14:301-312.
The Netherlands Plant Traits Database	Ordonez, J. C., P. M. van Bodegom, J. P. M. Witte, R. P. Bartholomeus, H. F. van Dobben, and R. Aerts. 2010. Leaf habit and woodiness regulate different leaf economy traits at a given nutrient supply. Ecology 91:3218-3228.
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Sheffield Database	unpub.
Dispersal Traits Database	unpub.
Leaf and Whole Plant Traits Database	unpub.
Wetland Dunes Database	unpub.
Categorical Plant Traits Database	unpub.
Overton/Wright New Zealand Database	unpub.
Leaf Physiology Database	unpub.
Tundra Plant Traits Database	unpub.
Causasus Plant Traits Database	unpub.
Ukraine Wetlands Plant Traits Database	unpub.

Dataset	Reference
New South Wales Plant Traits Database	unpub.
Photosynthesis Traits Database	unpub.
Photosynthesis and Leaf Characteristics Database	unpub.
The Netherlands Plant Height Database	unpub.
Wetland Dunes Database	van Bodegom, P. M., B. K. Sorrell, A. Oosthoek, C. Bakke, and R. Aerts. 2008. Separating the effects of partial submergence and soil oxygen demand on plant physiology. Ecology 89:193-204.
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Dataset	Reference
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Panama Plant Traits Database	Wright, S. J., K. Kitajima, N. J. B. Kraft, P. B. Reich, I. J. Wright, D. E. Bunker, R. Condit, J. W. Dalling, S. J. Davies, S. Díaz, B. M. J. Engelbrecht, K. E. Harms, S. P. Hubbell, C. O. Marks, M. C. Ruiz-Jaen, C. M. Salvador, and A. E. Zanne. 2011 . Functional traits and the growth-mortality tradeoff in tropical trees. Ecology 91:3664-3674.
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1.4.2. Plant biomass properties

Aboveground community biomass was sampled in May 2011 and 2014 by cutting the vegetation at a height of 2–3 cm in four 0.5 × 0.5 m subplots in close proximity to the vegetation quadrat. In meadows, we sampled plant biomass at the same time as the first hay harvest by the farmer. In pastures and mown pastures, we temporarily fenced our subplots to ensure that the vegetation had not been grazed before plant biomass sampling. The biomass was dried at 80 °C for 48 hr, weighed, and ground to fine powder using cyclone mill (Cyclotec 1093, Foss, Höganäs, Sweden). Samples were analysed for the percent neutral detergent fibre (NDF), acid detergent fibre (ADF) and acid detergent lignin (ADL, lignin), as well as P and N content using near-infrared spectroscopy (NIRS). The concentrations were derived from previously established calibration models by recording a specific reflectance spectrum of each sample from 1250 to 2350 nm at intervals of 1 nm (algorithmically averaged over 24 measurements). For details see Klaus et al. (2016) and Kleinebecker, Klaus and Hölzel (2011). From these measures, cellulose (= ADF − ADL), hemicelluloses (= NDF − ADF) and the lignin to N ratio were calculated according to Kirchgeßner (2014).

1.5. Statistical analyses

1.5.1. Statistical modelling of changes in soil properties

In preliminary hierarchical regression model analyses we found that several variables were not significantly related to any soil microbial community and function variables. These were: measures of plant species richness, functional diversity (Rao's Q index), a composite measure of plant traits representing the fast-slow spectrum based upon the first axis scores of a principal component analysis of CWM SLA, CWM leaf P and CWM leaf N, plant functional group identity (abundance of legumes, grasses and forbs) and lignin:N ratio of plant biomass. These variables were omitted from the final modelling procedure to reduce its complexity.

1.5.2. Structural equation models

We tested two estimators, ML (maximum likelihood estimation) and the more robust towards non-normal distribution and heteroscedasticity estimator MLM (maximum likelihood estimation with robust standard errors and a Satorra-Bentler scaled test statistic (Rosseel, 2012)), on a subset of variables for each region from all three categories – biomass, enzyme activities and community composition (C_{mic}, N_{mic}, C_{mic}:N_{mic}, glucosidase, phosphatase, urease, bacterial PLFA and fungal PLFA). The two estimators (ML and MLM) gave the same outcome – CWM leaf P was the best mediator variable in the South-West and Central regions and unfortunately the covariance matrices of SEMs in the North-East regions differed significantly from the data for both estimators.

There were some small differences in the exact values calculated with the two estimators: comparing the results obtained by MLM to those of ML yielded an increase in the number of significant paths by <1% (both for standardized and unstandardized p-values) and, on average, standard errors were 2.5% higher for unstandardized and 2.7% lower for standardized errors, while z-values were higher by 2.5% (unstandardized) and 6.1% (standardized) when using MLM. Unstandardized regression coefficients and standardized correlation coefficients were identical in 100% of cases and R^2 values of the models in 99.7% of cases. As the results did not essentially differ from each other, we chose the default ML estimator for our SEMs.

1.6. References for Laboratory Analyses

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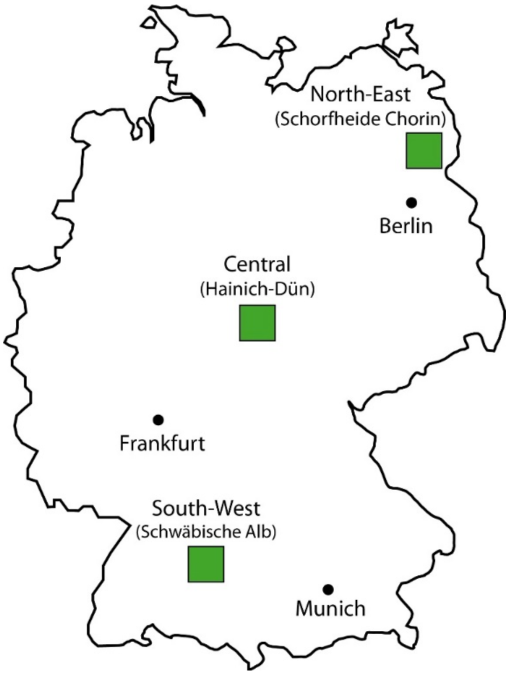


Figure S7-1: Location of the three investigated regions in Germany.

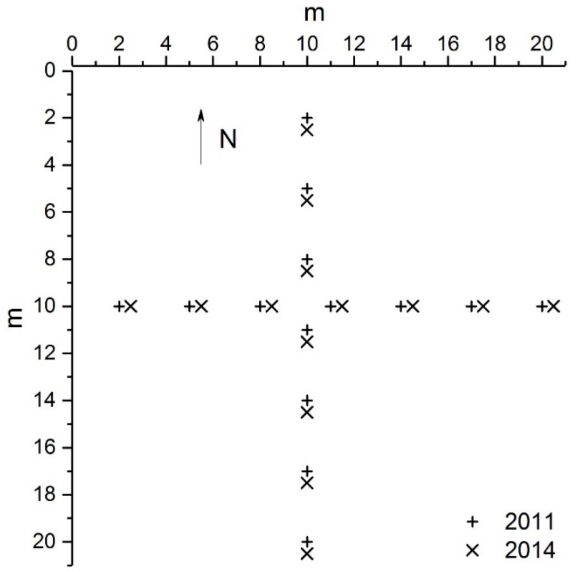
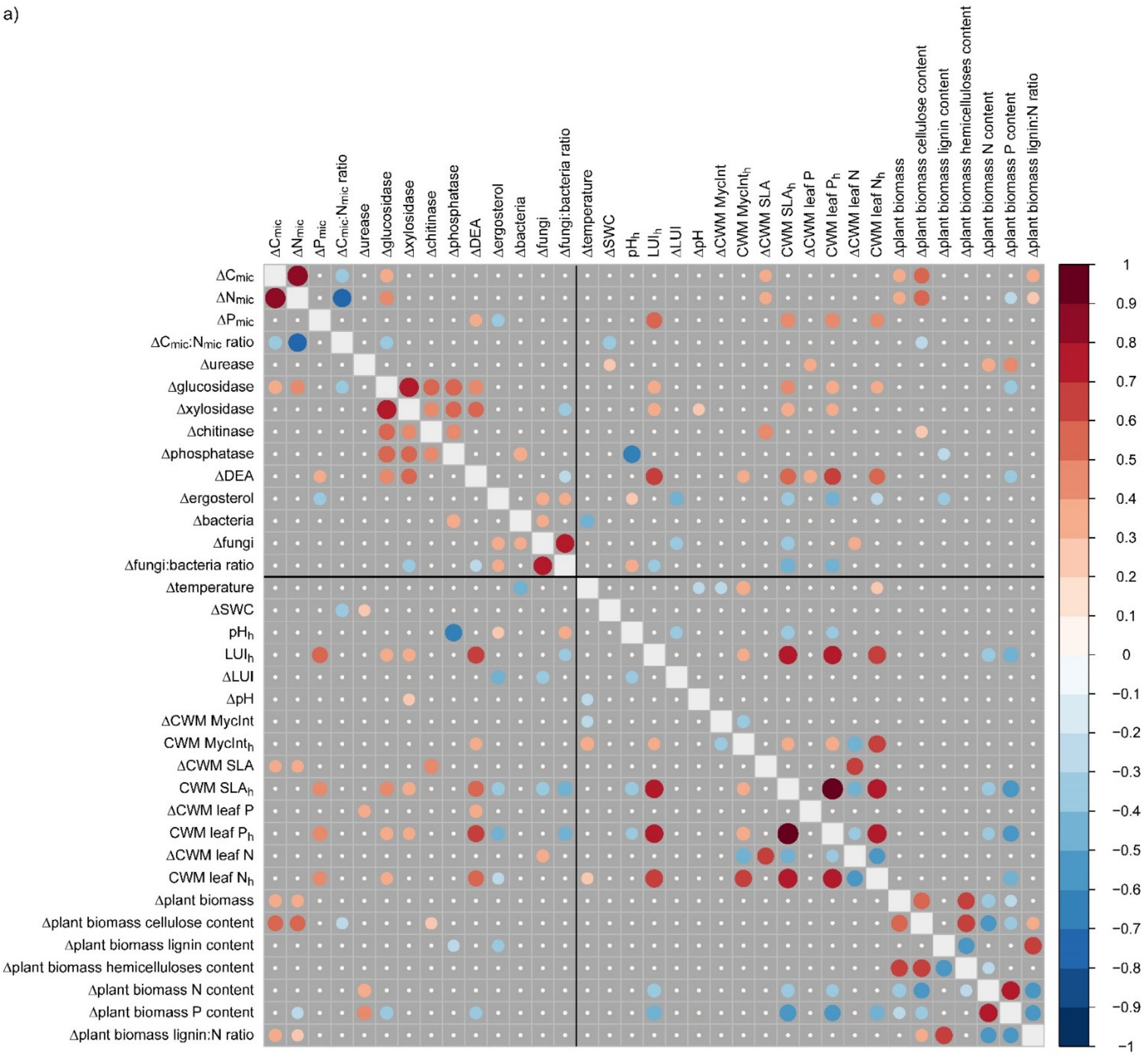
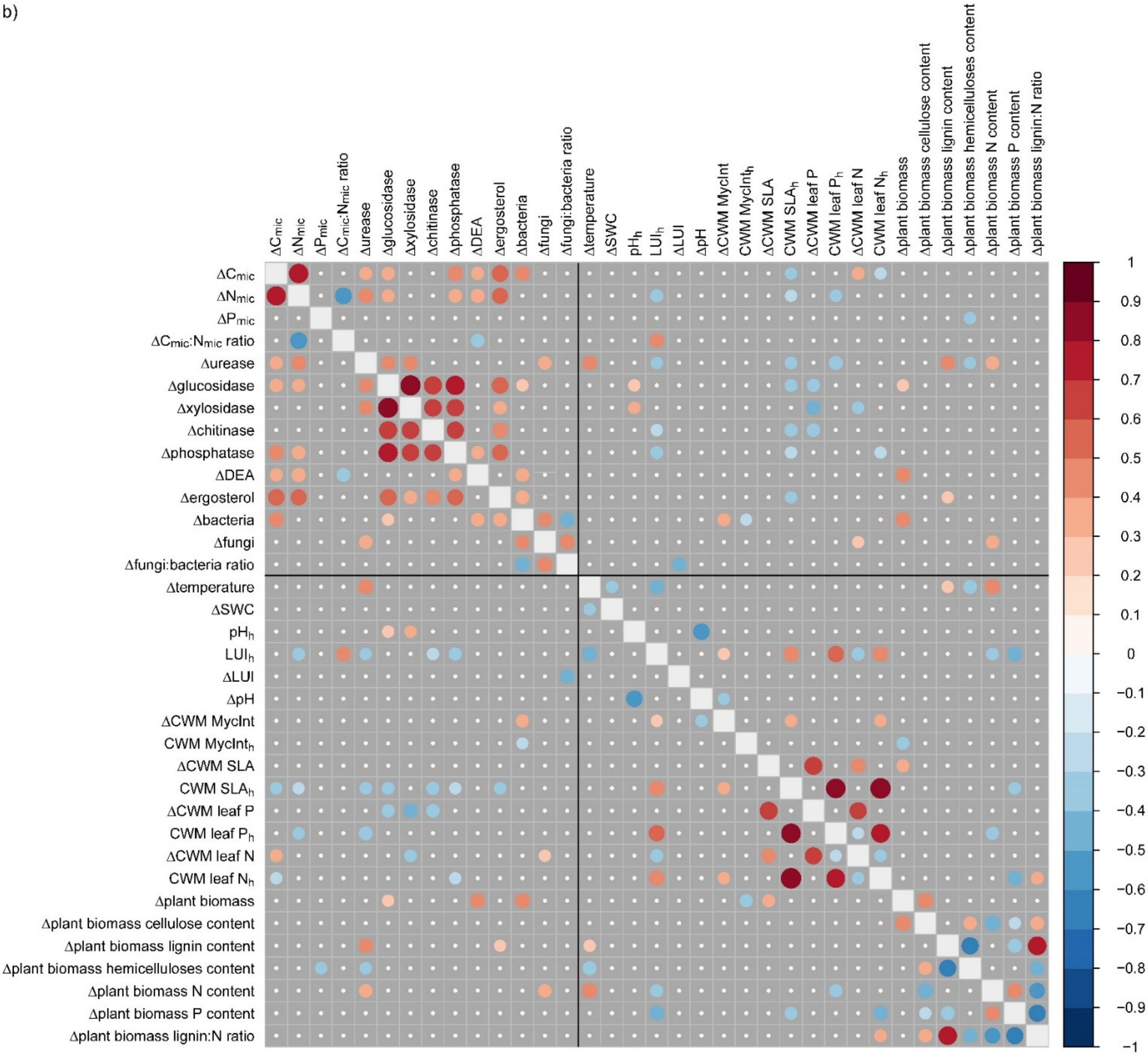


Figure S7-2: Sampling scheme for all grassland plots with sampling points of 2011 and 2014. In case obstacles such as shrubs or rocks inferred sampling at a selected spot, the sampling point was shifted along the transects by 1 m and the action protocolled.

a)


ΔC_{mic}
ΔN_{mic}
ΔP_{mic}
ΔC_{mic}:N_{mic} ratio
Δurease
Δglucosidase
Δxylosidase
Δchitinase
Δphosphatase
ΔDEA
Δergosterol
Δbacteria
Δfungi
Δfungi:bacteria ratio
Δtemperature
ΔSWC
pH_h
LUI_h
ΔLUI
ΔpH
ΔCWM MycInt
CWM $MycInt_h$
ΔCWM SLA
CWM SLA_h
ΔCWM leaf P
CWM leaf P_h
ΔCWM leaf N
CWM leaf N_h
Δplant biomass
Δplant biomass cellulose content
Δplant biomass lignin content
Δplant biomass hemicelluloses content
Δplant biomass N content
Δplant biomass P content
Δplant biomass lignin:N ratio
ΔC_{mic}
ΔN_{mic}
ΔP_{mic}
ΔC_{mic}:N_{mic} ratio
Δurease
Δglucosidase
Δxylosidase
Δchitinase
Δphosphatase
ΔDEA
Δergosterol
Δbacteria
Δfungi
Δfungi:bacteria ratio
Δtemperature
ΔSWC
pH_h
LUI_h
ΔLUI
ΔpH
ΔCWM MycInt
CWM $MycInt_h$
ΔCWM SLA
CWM SLA_h
ΔCWM leaf P
CWM leaf P_h
ΔCWM leaf N
CWM leaf N_h
Δplant biomass
Δplant biomass cellulose content
Δplant biomass lignin content
Δplant biomass hemicelluloses content
Δplant biomass N content
Δplant biomass P content
Δplant biomass lignin:N ratio
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
−0.1
−0.2
−0.3
−0.4
−0.5
−0.6
−0.7
−0.8
−0.9
−1

b)


ΔCmic
ΔNmic
ΔPmic
ΔCmic:Nmic ratio
Δurease
Δglucosidase
Δxylosidase
Δchitinase
Δphosphatase
ΔDEA
Δergosterol
Δbacteria
Δfungi
Δfungi:bacteria ratio
Δtemperature
ΔSWC
pHh
LUIh
ΔLUI
ΔpH
ΔCWM MycInt
CWM MycInth
ΔCWM SLA
CWM SLAh
ΔCWM leaf P
CWM leaf Ph
ΔCWM leaf N
CWM leaf Nh
Δplant biomass
Δplant biomass cellulose content
Δplant biomass lignin content
Δplant biomass hemicelluloses content
Δplant biomass N content
Δplant biomass P content
Δplant biomass lignin:N ratio
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
−0.1
−0.2
−0.3
−0.4
−0.5
−0.6
−0.7
−0.8
−0.9
−1

c)

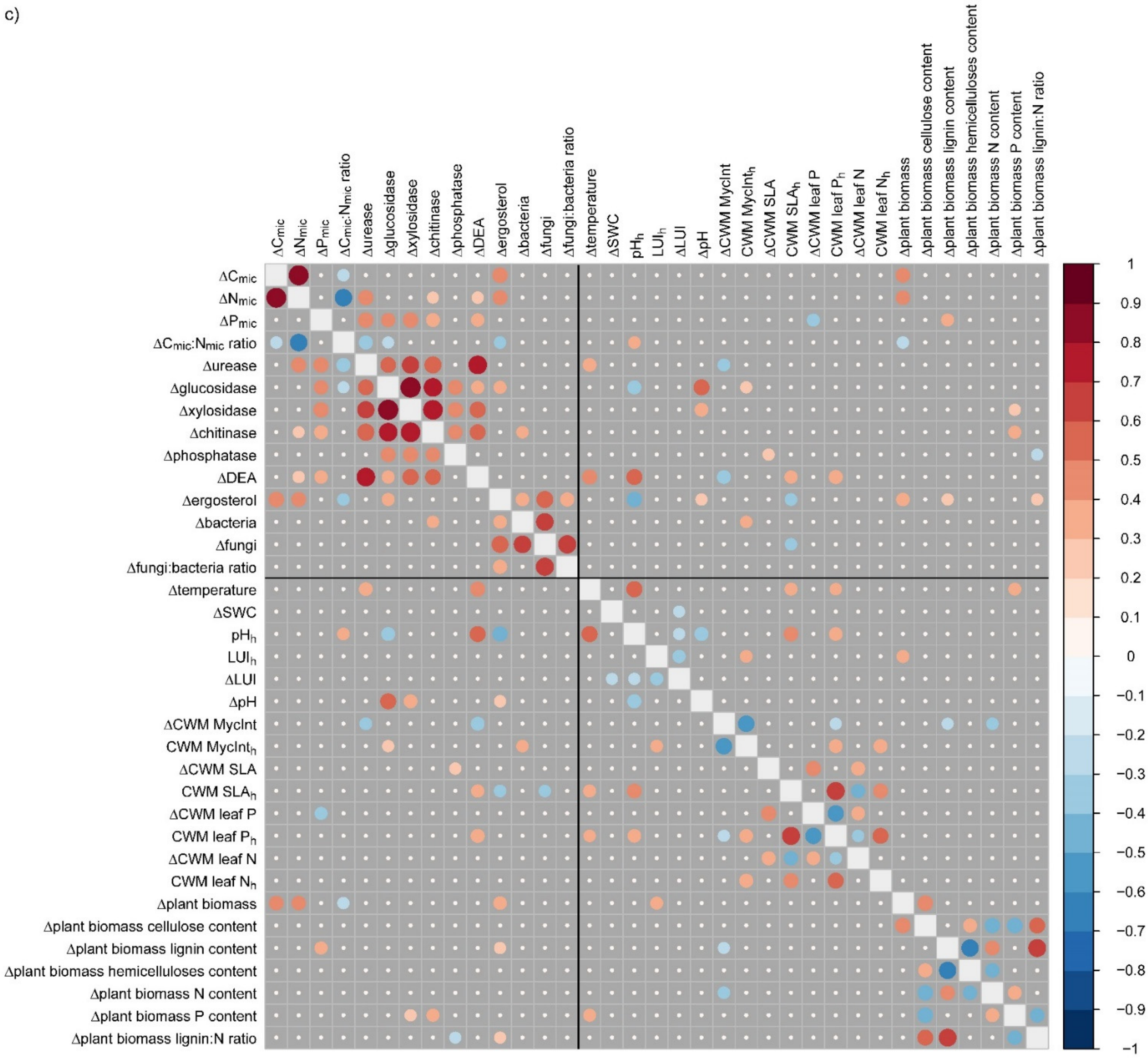


Figure S7-3: Spearman rank correlation coefficients (r) between fixed effects and response variables of linear models for the a) South-West, b) Central and c) North-East region. Only significant correlations are displayed.

Table S7-1: Hypothesized pathways in SEMs shown in Figures 1a and 1b. Land-use intensity influences soil microorganisms directly, but can also act indirectly as it affects properties of the microbial environment. Historic and change mediators were chosen as they were the most the most significant of the plausible mediator variables in hierarchical regression modelling. Effects can occur due to short term changes in the variables, but also via long-term legacy effects on changes in soil microorganisms (Δ). The nutrient content of a soil, for example, reflects past land-use intensity and influences the effect of new nutrient inputs by determining the level of nutrient limitation of soil biota and plants (Perring et al., 2016; Richter et al., 2000). In the case of grassland soil function for example, plant communities, and their functional properties, may take several years to fully respond to changes in land-use intensity (Poptcheva et al., 2009) (see following page).

Path			Hypotheses	References
LUI_h	←→	ΔLUI	Historic land-use can influence future change in land use (e.g. highly intensive sites may be more likely to see LUI declines)	Perring et al. (2016)
LUI	→	Plant biomass	Nutrient availability to plants is increased by fertilisation, leading to higher plant biomass production	Milton (1940); Klaus et al. (2011)
LUI	→	Plant biomass lignin content	Fertilised and frequently disturbed (via mowing and grazing) environments select for fast growing plants with less structural components incorporating lignin	Reich (2014)
LUI	→	CWM of plant functional leaf traits (leaf P)	Fertilisation shifts plant communities towards fast growing species with high leaf P content	Pfestorf et al. (2013); Busch et al. (2018)
LUI	→	CWM MycInt	Fertilisation leads to reduction in root mycorrhization	Gehring and Whitham (1994); Titus and Lepš (2000); Treseder (2004)
LUI	→	pH	N fertilization leads to acidification of soils	Bardgett and McAlister (1999)
LUI	→	Δmicrobial properties	Nutrient availability to microbes is increased by fertilisation, with effects on microbial communities including increases in the abundance of bacteria relative to fungi.	de Vries et al. (2012)
			Changes in nutrient status affect microbial physiology and metabolism altering microbial biomass and soil enzyme activities	Kandeler and Eder (1993); Bardgett and Leemans (1995); Donnison et al. (2000)
Plant biomass	→	Δmicrobial properties	Increase in plant biomass leads to increase in litter inputs and rhizodeposition, which are an important resources for soil microorganisms	Swinnen et al. (1995); Eisenhauer et al. (2017); Bardgett et al. (1998); Spohn et al. (2013)
Plant biomass lignin content	→	Δmicrobial properties	Plant litter with a high lignin input decomposes more slowly. Lignin rich inputs favour fungi over bacteria due to physiological differences.	Potthast et al. (2010); Sagova-Mareckova et al. (2011)
CWM of plant functional leaf traits (leaf P)	→	Δmicrobial properties	High quality litter inputs from plant communities possessing 'fast' traits favor bacteria over fungi	de Vries et al. (2012)
CWM MycInt	→	Δmicrobial properties	lower mycorrhization leads to lower total microbial biomass and less competition for nutrients between bacteria, saprotrophic fungi and mycorrhizal fungi	Tiunov and Scheu (2005)
pH	→	Δmicrobial properties	soil pH affects a wide range of microbial physiological process, including enzyme activities, and performance, affecting microbial community structure.	Fierer and Jackson (2006); Rousk et al. (2009); Fornara et al. (2011); Acosta-Martínez and Tabatabai (2011)

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Table S7-2: Characteristics of the three investigated regions with mean annual temperature (MAT), mean annual precipitation (MAP), elevation (m above sea level), areal spread of investigated sites, and soil types (and their number of occurrence) (Fischer et al., 2010), the latter determined after the World Reference Base of Soil Resources (IUSS Working Group WRB, 2015), as well as soil texture (Solly et al., 2014).

region	MAT [°C]	MAP [mm]	elevation [m a.s.l.]	area [km^2]	soil type (occurrence)	soil texture
South-West	6.0–7.0	700–1000	460–860	~422	Leptosol (33), Cambisol (17)	54 % clay, 41 % silt, 6 % sand
Central	6.5–8	500–800	285–550	~1300	Cambisol (28), Stagnosol (18),Vertisol (4)	42 % clay, 52 % silt, 6 % sand
North-East	8.0–8.5	500–600	3–140	~1300	Histosol (19), Luvisol (9), Gleysol (8), Albeluvisol (7), Cambisol (7)	17 % clay, 37 % silt, 45 % sand

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Table S7-3: Data used for the categories 'historic' and 'change'. 'Historic' data was calculated as means of several years and includes the background value of pH (only one year of data available), while 'change' describes the net difference between two years.

Category	Variable	Time frame
historic	pH (background value)	2011
	LUI	2006 – 2010
	CWM MycInt	2008 – 2011
	CWM SLA	2008 – 2011
	CWM leaf P	2008 – 2011
	CWM leaf N	2008 – 2011
change	Temperature	2011, 2014
	Soil water content	2011, 2014
	pH	2011, 2014
	LUI	2010, 2013
	CWM MycInt	2011, 2014
	CWM SLA	2011, 2014
	CWM leaf P	2011, 2014
	CWM leaf N	2011, 2014
	Plant biomass	2011, 2014
	Plant biomass cellulose content	2011, 2014
	Plant biomass hemicelluloses content	2011, 2014
	Plant biomass lignin content	2011, 2014
	Plant biomass N content	2011, 2014
	Plant biomass P content	2011, 2014
	Plant biomass lignin:N ratio	2011, 2014

Table S7-4: Overview of data from Schwäbische Alb (South-West), Hainich-Dün (Central) and Schorfheide-Chorin (North-East) (see following pages). Given are minimum (min), maximum (max), median, mean, standard deviation (SD) and number of samples (N).

				South-West					
		Variable	Unit	min	max	median	mean	SD	N
response variable (change between 2011 and 2014)	microbial biomass	Cmic	µg C g^{-1} soil DM	-266.28	211.40	-0.06	3.71	99.52	50
		Nmic	µg N g^{-1} soil DM	-64.83	51.81	7.22	6.97	22.51	50
		Cmic:Nmic ratio		-2.09	0.85	-0.32	-0.38	0.69	50
		Pmic	µg P g^{-1} soil DM	-33.33	66.59	2.89	8.25	22.71	39
	enzyme activiy	beta-glucosidase	nmol MUF g^{-1} h^{-1}	-224.99	1183.15	486.15	503.17	328.26	50
		beta-xylosidase	nmol MUF g^{-1} h^{-1}	1.13	332.38	146.54	154.21	70.80	50
		chitinase	nmol MUF g^{-1} h^{-1}	-280.31	438.38	249.72	232.42	136.60	47
		urease	µg N g^{-1} DM 2h^{-1}	-21.12	208.64	59.45	62.52	45.24	50
		DEA	µg N_2O-N + N_2-N g^{-1} soil DM h^{-1}	0.07	7.74	1.72	1.96	1.52	50
		phosphatase	nmol MUF g^{-1} h^{-1}	-171.94	2025.45	841.54	888.13	455.30	50
	microbial community	bacteria	nmol FAME g^{-1} soil DM	-39.79	95.55	10.19	8.74	27.41	50
		gram negative bacteria	nmol FAME g^{-1} soil DM	-4.54	20.16	3.82	4.09	4.21	50
		gram positive bacteria	nmol FAME g^{-1} soil DM	-36.22	69.04	0.04	1.43	20.39	50
		fungi	nmol FAME g^{-1} soil DM	-3.09	15.38	5.78	5.93	3.82	50
		fungi:bacteria ratio		-0.02	0.15	0.04	0.05	0.04	50
		ergosterol	µg g^{-1} soil DM	-2.45	9.93	3.17	3.22	3.00	50
		invertebrates	nmol FAME g^{-1} soil DM	-0.71	3.06	1.31	1.24	0.75	50
		sum microbial PLFA	nmol FAME g^{-1} soil DM	17.66	291.08	102.01	112.54	53.65	50
explanatory variables	abiotic factors	temperature change	°C	-2.04	1.04	-0.52	-0.49	0.66	49
		soil water content change	% vol. of water holding capacity	-19.89	8.46	-1.48	-2.99	5.82	49
		pH change	in $CaCl_2$	-0.35	0.24	-0.08	-0.09	0.11	50
		pH historic	in $CaCl_2$	5.08	7.30	6.15	6.26	0.55	50
	land-use intensity	LUI change	dimensionless	-1.12	0.74	0.01	0.00	0.44	50
		LUI historic	dimensionless	0.55	3.96	1.66	1.62	0.63	50
		mowing change	no. of cuts per year	-0.89	1.61	-0.03	0.00	0.44	50
		fertilization change	kg N ha^{-1} a^{-1}	-3.33	4.04	0.00	0.00	1.35	50
		grazing change	livestock units d ha^{-1} year^{-1}	-3.90	1.37	0.00	0.00	1.01	50
	plant functional traits	CWM MycInt change	% colonized root length	-22.92	13.95	-1.36	-1.46	6.61	48
		CWM MycInt historic	% colonized root length	36.36	57.35	49.85	49.16	5.01	50
		CWM SLA change	mm² g^{-1} DM	-4.43	2.42	-0.13	-0.36	1.69	48
		CWM SLA historic	mm² g^{-1} DM	19.91	30.29	26.53	25.55	3.08	50
		CWM leaf P change	mg P g^{-1} DM	-0.97	0.48	0.02	-0.01	0.26	48
		CWM leaf P historic	mg P g^{-1} DM	1.55	3.33	2.58	2.49	0.48	50
		CWM leaf N change	mg N g^{-1} DM	-7.03	3.70	-0.60	-0.60	2.32	48
		CWM leaf N historic	mg N g^{-1} DM	19.03	32.75	28.52	27.34	3.62	50

		Variable	Unit	South-West min	max	median	mean	SD	N
explanatory variables	plant biomass properties	plant biomass change	g m^{-2}	-74.45	602.95	124.23	164.37	145.01	50
		plant biomass cellulose content change	%	-2.60	8.65	1.53	2.08	2.93	48
		plant biomass hemicelluloses content change	%	-16.59	15.16	1.98	2.51	6.37	48
		plant biomass lignin content change	%	-1.27	2.75	0.43	0.51	0.99	48
		plant biomass lignin:N ratio change		-0.46	2.37	0.59	0.66	0.65	48
		plant biomass N content change	%	-1.06	0.31	-0.27	-0.29	0.34	48
		plant biomass P content change	%	-0.08	0.14	0.05	0.04	0.05	48
	excluded	fast-slow gradient change	site scores PC1	-3.38	2.37	-0.17	-0.19	1.10	48
		fast-slow gradient historic	site scores PC1	-2.61	4.57	-0.08	0.57	1.89	50
		Rao's Q change	index	-0.01	0.01	0.00	0.00	0.00	48
		Rao's Q historic	index	0.01	0.02	0.02	0.02	0.00	50
		number of species change	count	-6.00	21.00	4.00	4.42	4.43	48
		number of species historic	count	15.75	52.25	27.88	30.58	8.93	50
		number of grasses change	count	-6.00	8.00	0.00	0.20	2.62	49
		number of herbs change	count	-15.00	10.00	1.00	1.02	3.73	49
		number of legumes change	count	-3.00	2.00	0.00	-0.35	1.20	49
background variables (change between 2011 and 2014)		bulk density	g cm^{-3}	-0.196	0.892	0.075	0.083	0.144	49
		soil water content in samples	% g^{-1} soil DM	-27.109	33.061	15.099	14.479	10.607	50
		ammonium	µg N g^{-1} soil DM	-35.54	18.723	-5.487	-6.23	10.187	50
		nitrate	µg N g^{-1} soil DM	-38.008	14.17	-7.204	-8.619	10.277	50
		Nmin	µg N g^{-1} soil DM	-39.304	14.075	-16.569	-14.849	12.848	50
		Cmic:Ct ratio		-1.898	3.613	0.239	0.164	1.277	49
		C:N ratio		-0.743	0.531	0.009	-0.011	0.176	50
		EOC	µg C g^{-1} soil DM	-100.093	192.881	40.008	48.423	71.678	50
		EN	µg N g^{-1} soil DM	-22.174	22.931	-2.661	-2.832	8.802	50

						Central			
		Variable	Unit	min	max	median	mean	SD	N
response variable (change between 2011 and 2014)	microbial biomass	Cmic	μg C g^{-1} soil DM	-219.45	145.68	-43.10	-42.74	82.19	50
		Nmic	μg N g^{-1} soil DM	-68.30	17.58	-15.90	-16.91	17.32	50
		Cmic:Nmic ratio		-0.66	2.71	0.66	0.76	0.78	50
		Pmic	μg P g^{-1} soil DM	-44.05	51.55	-6.96	-6.16	21.19	45
	enzyme activiy	beta-glucosidase	nmol MUF g^{-1} h^{-1}	-914.27	1075.71	25.36	32.09	326.06	50
		beta-xylosidase	nmol MUF g^{-1} h^{-1}	-251.36	269.24	28.56	32.37	84.58	48
		chitinase	nmol MUF g^{-1} h^{-1}	-291.36	477.41	85.82	100.20	130.90	50
		urease	μg N g^{-1} DM 2h^{-1}	-224.06	39.28	-39.27	-42.49	62.81	45
		DEA	μg N_2O-N + N_2-N g^{-1} soil DM h^{-1}	-1.32	2.47	0.34	0.34	0.60	50
		phosphatase	nmol MUF g^{-1} h^{-1}	-579.22	874.99	101.98	73.69	244.47	50
	microbial community	bacteria	nmol FAME g^{-1} soil DM	-38.91	48.68	-2.35	-0.92	18.55	50
		gram negative bacteria	nmol FAME g^{-1} soil DM	-3.89	8.33	1.48	1.82	2.92	50
		gram positive bacteria	nmol FAME g^{-1} soil DM	-28.64	30.31	-1.20	-1.89	11.31	50
		fungi	nmol FAME g^{-1} soil DM	-4.50	5.60	2.00	2.09	2.16	50
		fungi:bacteria ratio		-0.02	0.12	0.03	0.04	0.03	50
		ergosterol	μg g^{-1} soil DM	-7.09	8.42	1.36	1.37	3.44	47
		invertebrates	nmol FAME g^{-1} soil DM	-0.95	1.91	0.08	0.20	0.55	50
		sum microbial PLFA	nmol FAME g^{-1} soil DM	-0.53	142.63	50.11	56.28	33.37	50
explanatory variables	abiotic factors	temperature change	°C	-1.91	9.80	0.17	0.39	1.61	48
		soil water content change	% vol. of water holding capacity	-10.20	22.97	5.46	4.92	6.01	49
		pH change	in $CaCl_2$	-0.28	0.31	-0.11	-0.08	0.12	50
		pH historic	in $CaCl_2$	5.02	7.45	7.09	6.89	0.51	50
	land-use intensity	LUI change	dimensionless	-0.77	1.21	-0.06	-0.02	0.40	50
		LUI historic	dimensionless	0.63	3.05	1.67	1.62	0.63	50
		mowing change	no. of cuts per year	-2.23	0.96	0.00	0.00	0.63	50
		fertilization change	kg N ha^{-1} a^{-1}	-2.81	3.05	0.00	0.00	1.05	50
		grazing change	livestock units d ha^{-1} year^{-1}	-2.81	6.56	-0.11	0.00	1.28	50
	plant functional traits	CWM MycInt change	% colonized root length	-24.73	14.05	0.79	0.10	7.11	50
		CWM MycInt historic	% colonized root length	39.72	58.53	52.23	51.43	4.36	50
		CWM SLA change	mm² g^{-1} DM	-4.41	3.95	0.23	0.37	1.53	50
		CWM SLA historic	mm² g^{-1} DM	21.61	29.51	26.37	25.95	1.88	50
		CWM leaf P change	mg P g^{-1} DM	-0.90	1.81	-0.12	-0.10	0.41	50
		CWM leaf P historic	mg P g^{-1} DM	1.73	3.67	2.60	2.59	0.42	50
		CWM leaf N change	mg N g^{-1} DM	-7.72	4.20	-0.12	-0.11	2.49	50
		CWM leaf N historic	mg N g^{-1} DM	21.17	31.92	28.30	28.38	2.79	50

		Variable	Unit	min	max	Central	mean	SD	N
						median			
explanatory variables	plant biomass properties	plant biomass change	g m^{-2}	-53.55	391.30	157.50	162.98	96.34	50
		plant biomass cellulose content change	%	-0.48	9.83	3.20	3.70	2.29	50
		plant biomass hemicelluloses content change	%	-10.53	11.58	-0.03	0.19	5.72	50
		plant biomass lignin content change	%	-1.82	3.92	0.63	0.67	1.30	50
		plant biomass lignin:N ratio change		-0.78	2.59	0.61	0.63	0.75	50
		plant biomass N content change	%	-1.21	0.63	-0.19	-0.22	0.38	50
		plant biomass P content change	%	-0.06	0.15	0.06	0.05	0.04	50
	excluded	fast-slow gradient change	site scores PC1	-3.70	3.61	-0.43	-0.21	1.52	50
		fast-slow gradient historic	site scores PC1	-2.67	3.29	0.15	0.16	1.46	50
		Rao's Q change	index	-0.01	0.01	0.00	0.00	0.00	50
		Rao's Q historic	index	0.01	0.02	0.02	0.02	0.00	50
		number of species change	count	-5.00	15.00	3.00	3.50	4.95	50
		number of species historic	count	13.25	61.75	27.88	29.81	10.80	50
		number of grasses change	count	-4.00	4.00	1.00	0.52	1.99	50
		number of herbs change	count	-4.00	10.00	3.00	2.84	3.44	50
		number of legumes change	count	-3.00	3.00	0.00	0.02	1.35	50
background variables (change between 2011 and 2014)		bulk density	g cm^{-3}	-0.274	0.39	0.068	0.066	0.108	47
		soil water content in samples	% g^{-1} soil DM	1.227	25.734	11.06	10.952	6.013	50
		ammonium	µg N g^{-1} soil DM	-6.891	23.306	3.589	3.906	5.931	50
		nitrate	µg N g^{-1} soil DM	-23.667	33.505	-2.33	0.032	12.095	50
		Nmin	µg N g^{-1} soil DM	-30.558	32.546	2.242	3.938	13.164	50
		Cmic:Ct ratio		-2.319	6.67	1.316	1.287	1.69	50
		C:N ratio		-0.895	0.274	-0.125	-0.201	0.255	50
		EOC	µg C g^{-1} soil DM	-147.669	119.939	-14.975	-24.206	57.62	50
		EN	µg N g^{-1} soil DM	-32.6	32.653	3.578	3.519	10.755	50

				North-East					
		Variable	**Unit**	**min**	**max**	**median**	**mean**	**SD**	**N**
response variable (change between 2011 and 2014)	microbial biomass	Cmic	µg C g^{-1} soil DM	-362.66	224.35	-54.55	-67.48	118.44	50
		Nmic	µg N g^{-1} soil DM	-67.22	62.88	-4.73	-2.87	25.63	50
		Cmic:Nmic ratio		-2.89	1.84	-0.45	-0.43	0.79	50
		Pmic	µg P g^{-1} soil DM	-39.51	51.01	-8.18	-2.25	20.39	46
	enzyme activiy	beta-glucosidase	nmol MUF g^{-1} h^{-1}	-990.61	1434.12	96.29	190.09	511.64	50
		beta-xylosidase	nmol MUF g^{-1} h^{-1}	-108.24	386.74	47.73	77.15	97.49	50
		chitinase	nmol MUF g^{-1} h^{-1}	-261.82	711.18	94.03	126.78	184.53	50
		urease	µg N g^{-1} DM $2h^{-1}$	-201.71	347.94	34.72	63.41	99.62	50
		DEA	µg N_2O-N + N_2-N g^{-1} soil DM h^{-1}	-0.26	4.99	1.38	1.43	1.21	50
		phosphatase	nmol MUF g^{-1} h^{-1}	-1043.77	5400.01	344.25	530.56	897.41	50
	microbial community	bacteria	nmol FAME g^{-1} soil DM	-82.71	43.32	4.93	2.46	23.17	50
		gram negative bacteria	nmol FAME g^{-1} soil DM	-10.14	7.24	-0.39	-0.16	2.97	50
		gram positive bacteria	nmol FAME g^{-1} soil DM	-47.80	28.71	3.84	1.59	14.19	50
		fungi	nmol FAME g^{-1} soil DM	-2.93	4.15	0.38	0.31	1.19	50
		fungi:bacteria ratio		-0.04	0.08	0.00	0.00	0.02	50
		ergosterol	µg g^{-1} soil DM	-6.78	24.62	1.56	2.04	4.57	50
		invertebrates	nmol FAME g^{-1} soil DM	-1.00	1.14	-0.08	-0.03	0.49	50
		sum microbial PLFA	nmol FAME g^{-1} soil DM	-63.58	150.52	36.14	50.72	43.28	50
explanatory variables	abiotic factors	temperature change	°C	-0.33	8.90	1.16	1.57	1.75	50
		soil water content change	% vol. of water holding capacity	-18.87	47.22	3.56	4.57	9.89	50
		pH change	in $CaCl_2$	-1.64	1.39	-0.09	0.00	0.37	50
		pH historic	in $CaCl_2$	4.58	7.43	6.43	6.39	0.91	50
	land-use intensity	LUI change	dimensionless	-2.02	2.72	0.06	-0.04	0.81	50
		LUI historic	dimensionless	0.92	2.93	1.40	1.63	0.58	50
		mowing change	no. of cuts per year	-1.06	2.38	0.00	0.00	0.74	50
		fertilization change	kg N ha^{-1} a^{-1}	-7.96	13.65	0.00	0.00	3.82	50
		grazing change	livestock units d ha^{-1} $year^{-1}$	-2.91	2.42	0.00	0.00	0.90	50
	plant functional traits	CWM MycInt change	% colonized root length	-29.46	15.99	2.67	0.29	8.33	50
		CWM MycInt historic	% colonized root length	27.45	67.58	49.48	48.80	7.79	50
		CWM SLA change	mm^2 g^{-1} DM	-5.05	5.03	0.41	0.56	1.84	50
		CWM SLA historic	mm^2 g^{-1} DM	23.06	31.11	27.48	27.45	1.89	50
		CWM leaf P change	mg P g^{-1} DM	-1.33	0.88	-0.15	-0.12	0.47	50
		CWM leaf P historic	mg P g^{-1} DM	2.18	4.20	2.92	2.94	0.43	50
		CWM leaf N change	mg N g^{-1} DM	-6.68	7.93	1.47	1.01	2.53	50
		CWM leaf N historic	mg N g^{-1} DM	22.32	35.15	29.31	29.04	2.51	50

		Variable	Unit	North-East					
				min	max	median	mean	SD	N
explanatory variables	plant biomass properties	plant biomass change	g m^{-2}	-81.55	611.85	173.75	174.82	157.66	49
		plant biomass cellulose content change	%	-3.54	10.07	1.85	2.12	2.55	49
		plant biomass hemicelluloses content change	%	-12.38	16.38	1.88	2.08	6.14	49
		plant biomass lignin content change	%	-2.59	2.98	0.88	0.72	1.26	49
		plant biomass lignin:N ratio change		-1.50	2.63	0.35	0.38	0.64	49
		plant biomass N content change	%	-1.26	1.39	-0.06	-0.05	0.55	49
		plant biomass P content change	%	-0.03	0.19	0.07	0.07	0.05	49
	excluded	fast-slow gradient change	site scores PC1	-2.96	4.36	0.21	0.39	1.56	50
		fast-slow gradient historic	site scores PC1	-3.13	2.86	-0.93	-0.74	1.38	50
		Rao's Q change	index	-0.01	0.01	0.00	0.00	0.00	50
		Rao's Q historic	index	0.01	0.03	0.02	0.02	0.00	50
		number of species change	count	-6.00	10.00	3.00	2.12	3.76	50
		number of species historic	count	13.00	27.25	19.00	19.20	3.45	50
		number of grasses change	count	-2.00	5.00	1.00	1.08	1.28	50
		number of herbs change	count	-6.00	5.00	0.00	0.16	2.74	50
		number of legumes change	count	-1.00	4.00	0.00	0.72	1.23	50
background variables (change between 2011 and 2014)		bulk density	g cm^{-3}	-0.166	0.33	0.069	0.073	0.098	50
		soil water content in samples	% g^{-1} soil DM	-15.16	28.367	7.054	7.136	7.7	50
		ammonium	µg N g^{-1} soil DM	-37.128	71.748	-1.612	-3.64	14.582	50
		nitrate	µg N g^{-1} soil DM	-30.739	73.36	0.408	4.132	18.193	50
		Nmin	µg N g^{-1} soil DM	-54.85	90.635	1.92	0.492	23.156	50
		Cmic:Ct ratio		-4.728	1.565	-0.818	-0.973	1.352	50
		C:N ratio		-0.824	1.545	-0.053	-0.067	0.337	50
		EOC	µg C g^{-1} soil DM	-335.436	223.978	-10.903	-23.174	96.42	50
		EN	µg N g^{-1} soil DM	-90.64	110.188	2.206	-1.054	23.351	50

Table S7-5: Hierarchical levels of multiple regression analyses (Δ = change, h = historic, bv = background value).

Level	overall description	fixed effects
Level 1	abiotic factors I	Δtemperature, Δsoil water content, pH_{bv}
Level 2	land-use intensity	LUI_h, ΔLUI
Level 3	abiotic factors II	ΔpH
Level 4	plant functional traits	ΔCWM MycInt, CWM $MycInt_h$, ΔCWM SLA, CWM SLA_h, ΔCWM leaf P, CWM leaf P_h, ΔCWM leaf N, CWM leaf N_h
Level 5	plant biomass properties	Δplant biomass, Δplant biomass cellulose content, Δplant biomass hemicelluloses content, Δplant biomass lignin content, Δplant biomass P content, Δplant biomass N content

Table S7-6.1: Model fits of SEMs in Schwäbische Alb (South-West), Hainich-Dün (Central) and Schorfheide-Chorin (North-East) (see following pages). Given are the model fit values for the five tested mediator types. Insignificant *p*-value of X^2 were highlighted in green and the model with the lowest AIC value in red. If the model with the lowest AIC value had a significant *p*-value of X^2, the model with the next lower AIC without a significant *p*-value of X^2 was chosen (according to the t-rule model fit based on chi-square tests could not be assessed for SEMs with plant biomass and lignin). ntotal = no. of samples, npar = no. of estimated parameters, df = degrees of freedom, *p* = *p*-value of X^2, rmsea = root means square error, rmsea.*p* = *p*-value of rmsea, AIC = Akaike's information criterion, O2E = ratio of observed samples:estimated parameters.

Region	MO variable	mediator	ntotal	npar	X^2	df	*p*	rmsea	rmsea.*p*	AIC	O2E
South-West	Cmic	**CWM leaf P**	48	12	6.31	3	0.10	0.15	0.13	-87.31	4.00
South-West	Cmic	CWM MycInt	48	12	9.23	3	0.03	0.21	0.04	-69.40	4.00
South-West	Cmic	Plant biomass	50	10	0.00	0	NA	0.00	NA	-55.85	5.00
South-West	Cmic	Lignin content	48	10	0.00	0	NA	0.00	NA	-26.80	4.80
South-West	Cmic	pH	50	12	8.72	3	0.03	0.20	0.05	-53.84	4.17
South-West	Nmic	**CWM leaf P**	48	12	6.31	3	0.10	0.15	0.13	-95.16	4.00
South-West	Nmic	CWM MycInt	48	12	9.23	3	0.03	0.21	0.04	-77.16	4.00
South-West	Nmic	Plant biomass	50	10	0.00	0	NA	0.00	NA	-63.13	5.00
South-West	Nmic	Lignin content	48	10	0.00	0	NA	0.00	NA	-35.05	4.80
South-West	Nmic	pH	50	12	8.72	3	0.03	0.20	0.05	-62.97	4.17
South-West	Cmic:Nmic ratio	**CWM leaf P**	48	12	6.31	3	0.10	0.15	0.13	-73.08	4.00
South-West	Cmic:Nmic ratio	CWM MycInt	48	12	9.23	3	0.03	0.21	0.04	-55.48	4.00
South-West	Cmic:Nmic ratio	Plant biomass	50	10	0.00	0	NA	0.00	NA	-36.64	5.00
South-West	Cmic:Nmic ratio	Lignin content	48	10	0.00	0	NA	0.00	NA	-15.55	4.80
South-West	Cmic:Nmic ratio	pH	50	12	8.72	3	0.03	0.20	0.05	-41.39	4.17
South-West	Pmic	**CWM leaf P**	37	12	4.66	3	0.20	0.12	0.23	-68.98	3.08
South-West	Pmic	CWM MycInt	37	12	10.53	3	0.01	0.26	0.02	-63.40	3.08
South-West	Pmic	Plant biomass	39	10	0.00	0	NA	0.00	NA	-28.16	3.90
South-West	Pmic	Lignin content	37	10	0.00	0	NA	0.00	NA	-11.24	3.70
South-West	Pmic	pH	39	12	9.99	3	0.02	0.24	0.03	-39.02	3.25
South-West	glucosidase	**CWM leaf P**	48	12	6.31	3	0.10	0.15	0.13	-85.80	4.00
South-West	glucosidase	CWM MycInt	48	12	9.23	3	0.03	0.21	0.04	-59.94	4.00
South-West	glucosidase	Plant biomass	50	10	0.00	0	NA	0.00	NA	-42.10	5.00
South-West	glucosidase	Lignin content	48	10	0.00	0	NA	0.00	NA	-20.73	4.80
South-West	glucosidase	pH	50	12	8.72	3	0.03	0.20	0.05	-48.66	4.17
South-West	xylosidase	**CWM leaf P**	48	12	6.31	3	0.10	0.15	0.13	-90.09	4.00
South-West	xylosidase	CWM MycInt	48	12	9.23	3	0.03	0.21	0.04	-65.13	4.00
South-West	xylosidase	Plant biomass	50	10	0.00	0	NA	0.00	NA	-47.35	5.00
South-West	xylosidase	Lignin content	48	10	0.00	0	NA	0.00	NA	-27.28	4.80
South-West	xylosidase	pH	50	12	8.72	3	0.03	0.20	0.05	-61.12	4.17
South-West	chitinase	**CWM leaf P**	45	12	4.56	3	0.21	0.11	0.25	-96.19	3.75
South-West	chitinase	CWM MycInt	45	12	9.53	3	0.02	0.22	0.04	-67.27	3.75
South-West	chitinase	Plant biomass	47	10	0.00	0	NA	0.00	NA	-49.85	4.70
South-West	chitinase	Lignin content	45	10	0.00	0	NA	0.00	NA	-30.85	4.50
South-West	chitinase	pH	47	12	7.58	3	0.06	0.18	0.08	-54.12	3.92
South-West	urease	**CWM leaf P**	48	12	6.31	3	0.10	0.15	0.13	-95.58	4.00
South-West	urease	CWM MycInt	48	12	9.23	3	0.03	0.21	0.04	-77.49	4.00
South-West	urease	Plant biomass	50	10	0.00	0	NA	0.00	NA	-51.71	5.00
South-West	urease	Lignin content	48	10	0.00	0	NA	0.00	NA	-31.69	4.80
South-West	urease	pH	50	12	8.72	3	0.03	0.20	0.05	-54.52	4.17
South-West	DEA	**CWM leaf P**	48	12	6.31	3	0.10	0.15	0.13	-106.19	4.00
South-West	DEA	CWM MycInt	48	12	9.23	3	0.03	0.21	0.04	-79.51	4.00
South-West	DEA	Plant biomass	50	10	0.00	0	NA	0.00	NA	-61.14	5.00
South-West	DEA	Lignin content	48	10	0.00	0	NA	0.00	NA	-40.52	4.80
South-West	DEA	pH	50	12	8.72	3	0.03	0.20	0.05	-66.45	4.17
South-West	phosphatase	**CWM leaf P**	48	12	6.31	3	0.10	0.15	0.13	-83.60	4.00
South-West	phosphatase	CWM MycInt	48	12	9.23	3	0.03	0.21	0.04	-65.88	4.00
South-West	phosphatase	Plant biomass	50	10	0.00	0	NA	0.00	NA	-46.12	5.00
South-West	phosphatase	Lignin content	48	10	0.00	0	NA	0.00	NA	-32.41	4.80
South-West	phosphatase	pH	50	12	8.72	3	0.03	0.20	0.05	-88.18	4.17
South-West	bacteria	**CWM leaf P**	48	12	6.31	3	0.10	0.15	0.13	-85.92	4.00
South-West	bacteria	CWM MycInt	48	12	9.23	3	0.03	0.21	0.04	-69.58	4.00
South-West	bacteria	Plant biomass	50	10	0.00	0	NA	0.00	NA	-48.27	5.00
South-West	bacteria	Lignin content	48	10	0.00	0	NA	0.00	NA	-27.34	4.80
South-West	bacteria	pH	50	12	8.72	3	0.03	0.20	0.05	-56.77	4.17
South-West	fungi	**CWM leaf P**	48	12	6.31	3	0.10	0.15	0.13	-87.28	4.00
South-West	fungi	CWM MycInt	48	12	9.23	3	0.03	0.21	0.04	-68.65	4.00
South-West	fungi	Plant biomass	50	10	0.00	0	NA	0.00	NA	-48.45	5.00
South-West	fungi	Lignin content	48	10	0.00	0	NA	0.00	NA	-27.44	4.80
South-West	fungi	pH	50	12	8.72	3	0.03	0.20	0.05	-52.31	4.17
South-West	fungi:bacteria ratio	**CWM leaf P**	48	12	6.31	3	0.10	0.15	0.13	-84.02	4.00
South-West	fungi:bacteria ratio	CWM MycInt	48	12	9.23	3	0.03	0.21	0.04	-60.38	4.00
South-West	fungi:bacteria ratio	Plant biomass	50	10	0.00	0	NA	0.00	NA	-41.75	5.00
South-West	fungi:bacteria ratio	Lignin content	48	10	0.00	0	NA	0.00	NA	-22.01	4.80
South-West	fungi:bacteria ratio	pH	50	12	8.72	3	0.03	0.20	0.05	-49.09	4.17
South-West	ergosterol	**CWM leaf P**	48	12	6.31	3	0.10	0.15	0.13	-82.95	4.00
South-West	ergosterol	CWM MycInt	48	12	9.23	3	0.03	0.21	0.04	-62.80	4.00
South-West	ergosterol	Plant biomass	50	10	0.00	0	NA	0.00	NA	-38.99	5.00
South-West	ergosterol	Lignin content	48	10	0.00	0	NA	0.00	NA	-19.77	4.80
South-West	ergosterol	pH	50	12	8.72	3	0.03	0.20	0.05	-43.20	4.17

Region	MO variable	mediator	ntotal	npar	X^2	df	*p*	rmsea	rmsea.*p*	AIC	O2E
Central	Cmic	**CWM leaf P**	50	12	3.44	3	0.33	0.05	0.38	-89.13	4.17
Central	Cmic	CWM MycInt	50	12	9.29	3	0.03	0.20	0.04	-38.43	4.17
Central	Cmic	Plant biomass	50	10	0.00	0	NA	0.00	NA	-19.96	5.00
Central	Cmic	Lignin content	50	10	0.00	0	NA	0.00	NA	-14.50	5.00
Central	Cmic	pH	50	12	21.62	3	0.00	0.35	0.00	-34.42	4.17
Central	Nmic	**CWM leaf P**	50	12	3.44	3	0.33	0.05	0.38	-107.87	4.17
Central	Nmic	CWM MycInt	50	12	9.29	3	0.03	0.20	0.04	-57.19	4.17
Central	Nmic	Plant biomass	50	10	0.00	0	NA	0.00	NA	-37.91	5.00
Central	Nmic	Lignin content	50	10	0.00	0	NA	0.00	NA	-33.75	5.00
Central	Nmic	pH	50	12	21.62	3	0.00	0.35	0.00	-51.88	4.17
Central	Cmic:Nmic ratio	**CWM leaf P**	50	12	3.44	3	0.33	0.05	0.38	-87.70	4.17
Central	Cmic:Nmic ratio	CWM MycInt	50	12	9.29	3	0.03	0.20	0.04	-37.50	4.17
Central	Cmic:Nmic ratio	Plant biomass	50	10	0.00	0	NA	0.00	NA	-19.42	5.00
Central	Cmic:Nmic ratio	Lignin content	50	10	0.00	0	NA	0.00	NA	-13.81	5.00
Central	Cmic:Nmic ratio	pH	50	12	21.62	3	0.00	0.35	0.00	-41.14	4.17
Central	Pmic	**CWM leaf P**	45	12	6.36	3	0.10	0.16	0.13	-75.18	3.75
Central	Pmic	CWM MycInt	45	12	9.61	3	0.02	0.22	0.03	-19.27	3.75
Central	Pmic	Plant biomass	45	10	0.00	0	NA	0.00	NA	-7.63	4.50
Central	Pmic	Lignin content	45	10	0.00	0	NA	0.00	NA	-3.07	4.50
Central	Pmic	pH	45	12	20.04	3	0.00	0.36	0.00	-19.06	3.75
Central	glucosidase	**CWM leaf P**	50	12	3.44	3	0.33	0.05	0.38	-138.60	4.17
Central	glucosidase	CWM MycInt	50	12	9.29	3	0.03	0.20	0.04	-72.80	4.17
Central	glucosidase	Plant biomass	50	10	0.00	0	NA	0.00	NA	-55.60	5.00
Central	glucosidase	Lignin content	50	10	0.00	0	NA	0.00	NA	-47.83	5.00
Central	glucosidase	pH	50	12	21.62	3	0.00	0.35	0.00	-66.96	4.17
Central	xylosidase	**CWM leaf P**	48	12	3.01	3	0.39	0.01	0.44	-127.99	4.00
Central	xylosidase	CWM MycInt	48	12	7.66	3	0.05	0.18	0.08	-72.95	4.00
Central	xylosidase	Plant biomass	48	10	0.00	0	NA	0.00	NA	-57.10	4.80
Central	xylosidase	Lignin content	48	10	0.00	0	NA	0.00	NA	-51.30	4.80
Central	xylosidase	pH	48	12	21.35	3	0.00	0.36	0.00	-65.43	4.00
Central	chitinase	**CWM leaf P**	50	12	3.44	3	0.33	0.05	0.38	-126.86	4.17
Central	chitinase	CWM MycInt	50	12	9.29	3	0.03	0.20	0.04	-67.61	4.17
Central	chitinase	Plant biomass	50	10	0.00	0	NA	0.00	NA	-51.47	5.00
Central	chitinase	Lignin content	50	10	0.00	0	NA	0.00	NA	-49.09	5.00
Central	chitinase	pH	50	12	21.62	3	0.00	0.35	0.00	-64.59	4.17
Central	urease	**CWM leaf P**	45	12	3.84	3	0.28	0.08	0.33	-72.35	3.75
Central	urease	CWM MycInt	45	12	12.33	3	0.01	0.26	0.01	-22.51	3.75
Central	urease	Plant biomass	45	10	0.00	0	NA	0.00	NA	-10.71	4.50
Central	urease	Lignin content	45	10	0.00	0	NA	0.00	NA	-12.25	4.50
Central	urease	pH	45	12	18.53	3	0.00	0.34	0.00	-21.60	3.75
Central	DEA	**CWM leaf P**	50	12	3.44	3	0.33	0.05	0.38	-125.66	4.17
Central	DEA	CWM MycInt	50	12	9.29	3	0.03	0.20	0.04	-73.03	4.17
Central	DEA	Plant biomass	50	10	0.00	0	NA	0.00	NA	-68.20	5.00
Central	DEA	Lignin content	50	10	0.00	0	NA	0.00	NA	-50.68	5.00
Central	DEA	pH	50	12	21.62	3	0.00	0.35	0.00	-69.63	4.17
Central	phosphatase	**CWM leaf P**	50	12	3.44	3	0.33	0.05	0.38	-121.60	4.17
Central	phosphatase	CWM MycInt	50	12	9.29	3	0.03	0.20	0.04	-67.66	4.17
Central	phosphatase	Plant biomass	50	10	0.00	0	NA	0.00	NA	-52.26	5.00
Central	phosphatase	Lignin content	50	10	0.00	0	NA	0.00	NA	-46.22	5.00
Central	phosphatase	pH	50	12	21.62	3	0.00	0.35	0.00	-67.40	4.17
Central	bacteria	**CWM leaf P**	50	12	3.44	3	0.33	0.05	0.38	-92.75	4.17
Central	bacteria	CWM MycInt	50	12	9.29	3	0.03	0.20	0.04	-50.43	4.17
Central	bacteria	Plant biomass	50	10	0.00	0	NA	0.00	NA	-32.84	5.00
Central	bacteria	Lignin content	50	10	0.00	0	NA	0.00	NA	-19.43	5.00
Central	bacteria	pH	50	12	21.62	3	0.00	0.35	0.00	-40.09	4.17
Central	fungi	**CWM leaf P**	50	12	3.44	3	0.33	0.05	0.38	-97.14	4.17
Central	fungi	CWM MycInt	50	12	9.29	3	0.03	0.20	0.04	-49.11	4.17
Central	fungi	Plant biomass	50	10	0.00	0	NA	0.00	NA	-30.82	5.00
Central	fungi	Lignin content	50	10	0.00	0	NA	0.00	NA	-23.52	5.00
Central	fungi	pH	50	12	21.62	3	0.00	0.35	0.00	-44.62	4.17
Central	fungi:bacteria ratio	**CWM leaf P**	50	12	3.44	3	0.33	0.05	0.38	-98.91	4.17
Central	fungi:bacteria ratio	CWM MycInt	50	12	9.29	3	0.03	0.20	0.04	-48.74	4.17
Central	fungi:bacteria ratio	Plant biomass	50	10	0.00	0	NA	0.00	NA	-30.68	5.00
Central	fungi:bacteria ratio	Lignin content	50	10	0.00	0	NA	0.00	NA	-25.76	5.00
Central	fungi:bacteria ratio	pH	50	12	21.62	3	0.00	0.35	0.00	-43.98	4.17
Central	ergosterol	**CWM leaf P**	47	12	3.53	3	0.32	0.06	0.37	-76.15	3.92
Central	ergosterol	CWM MycInt	47	12	10.12	3	0.02	0.22	0.03	-31.86	3.92
Central	ergosterol	Plant biomass	47	10	0.00	0	NA	0.00	NA	-16.24	4.70
Central	ergosterol	Lignin content	47	10	0.00	0	NA	0.00	NA	-13.43	4.70
Central	ergosterol	pH	47	12	24.77	3	0.00	0.39	0.00	-31.19	3.92

Region	MO variable	mediator	ntotal	npar	X^2	df	*p*	rmsea	rmsea.*p*	AIC	O2E
North-East	Cmic	CWM leaf P	50	12	27.36	3	0.00	0.40	0.00	-54.46	4.17
North-East	Cmic	CWM MycInt	50	12	29.64	3	0.00	0.42	0.00	-84.56	4.17
North-East	Cmic	Plant biomass	49	10	0.00	0	NA	0.00	NA	-44.38	4.90
North-East	Cmic	Lignin content	49	10	0.00	0	NA	0.00	NA	-35.53	4.90
North-East	Cmic	pH	50	12	11.30	3	0.01	0.24	0.02	-71.18	4.17
North-East	Nmic	CWM leaf P	50	12	27.36	3	0.00	0.40	0.00	-56.68	4.17
North-East	Nmic	CWM MycInt	50	12	29.64	3	0.00	0.42	0.00	-82.74	4.17
North-East	Nmic	Plant biomass	49	10	0.00	0	NA	0.00	NA	-43.18	4.90
North-East	Nmic	Lignin content	49	10	0.00	0	NA	0.00	NA	-37.43	4.90
North-East	Nmic	pH	50	12	11.30	3	0.01	0.24	0.02	-74.08	4.17
North-East	Cmic:Nmic ratio	CWM leaf P	50	12	27.36	3	0.00	0.40	0.00	-78.91	4.17
North-East	Cmic:Nmic ratio	CWM MycInt	50	12	29.64	3	0.00	0.42	0.00	-103.35	4.17
North-East	Cmic:Nmic ratio	Plant biomass	49	10	0.00	0	NA	0.00	NA	-60.00	4.90
North-East	Cmic:Nmic ratio	Lignin content	49	10	0.00	0	NA	0.00	NA	-57.93	4.90
North-East	Cmic:Nmic ratio	pH	50	12	11.30	3	0.01	0.24	0.02	-106.48	4.17
North-East	Pmic	CWM leaf P	46	12	24.31	3	0.00	0.39	0.00	-44.22	3.83
North-East	Pmic	CWM MycInt	46	12	28.49	3	0.00	0.43	0.00	-73.97	3.83
North-East	Pmic	Plant biomass	45	10	0.00	0	NA	0.00	NA	-24.47	4.50
North-East	Pmic	Lignin content	45	10	0.00	0	NA	0.00	NA	-25.38	4.50
North-East	Pmic	pH	46	12	10.01	3	0.02	0.23	0.03	-49.69	3.83
North-East	glucosidase	CWM leaf P	50	12	27.36	3	0.00	0.40	0.00	-51.42	4.17
North-East	glucosidase	CWM MycInt	50	12	29.64	3	0.00	0.42	0.00	-81.07	4.17
North-East	glucosidase	Plant biomass	49	10	0.00	0	NA	0.00	NA	-32.03	4.90
North-East	glucosidase	Lignin content	49	10	0.00	0	NA	0.00	NA	-32.96	4.90
North-East	glucosidase	pH	50	12	11.30	3	0.01	0.24	0.02	-82.23	4.17
North-East	xylosidase	CWM leaf P	50	12	27.36	3	0.00	0.40	0.00	-59.46	4.17
North-East	xylosidase	CWM MycInt	50	12	29.64	3	0.00	0.42	0.00	-89.46	4.17
North-East	xylosidase	Plant biomass	49	10	0.00	0	NA	0.00	NA	-39.67	4.90
North-East	xylosidase	Lignin content	49	10	0.00	0	NA	0.00	NA	-40.48	4.90
North-East	xylosidase	pH	50	12	11.30	3	0.01	0.24	0.02	-80.28	4.17
North-East	chitinase	CWM leaf P	50	12	27.36	3	0.00	0.40	0.00	-66.37	4.17
North-East	chitinase	CWM MycInt	50	12	29.64	3	0.00	0.42	0.00	-91.19	4.17
North-East	chitinase	Plant biomass	49	10	0.00	0	NA	0.00	NA	-44.14	4.90
North-East	chitinase	Lignin content	49	10	0.00	0	NA	0.00	NA	-44.90	4.90
North-East	chitinase	pH	50	12	11.30	3	0.01	0.24	0.02	-82.26	4.17
North-East	urease	CWM leaf P	50	12	27.36	3	0.00	0.40	0.00	-66.09	4.17
North-East	urease	CWM MycInt	50	12	29.64	3	0.00	0.42	0.00	-94.64	4.17
North-East	urease	Plant biomass	49	10	0.00	0	NA	0.00	NA	-45.81	4.90
North-East	urease	Lignin content	49	10	0.00	0	NA	0.00	NA	-46.62	4.90
North-East	urease	pH	50	12	11.30	3	0.01	0.24	0.02	-101.17	4.17
North-East	DEA	CWM leaf P	50	12	27.36	3	0.00	0.40	0.00	-45.36	4.17
North-East	DEA	CWM MycInt	50	12	29.64	3	0.00	0.42	0.00	-75.05	4.17
North-East	DEA	Plant biomass	49	10	0.00	0	NA	0.00	NA	-22.60	4.90
North-East	DEA	Lignin content	49	10	0.00	0	NA	0.00	NA	-23.22	4.90
North-East	DEA	pH	50	12	11.30	3	0.01	0.24	0.02	-79.56	4.17
North-East	phosphatase	CWM leaf P	50	12	27.36	3	0.00	0.40	0.00	-103.75	4.17
North-East	phosphatase	CWM MycInt	50	12	29.64	3	0.00	0.42	0.00	-124.61	4.17
North-East	phosphatase	Plant biomass	49	10	0.00	0	NA	0.00	NA	-77.17	4.90
North-East	phosphatase	Lignin content	49	10	0.00	0	NA	0.00	NA	-77.95	4.90
North-East	phosphatase	pH	50	12	11.30	3	0.01	0.24	0.02	-117.55	4.17
North-East	bacteria	CWM leaf P	50	12	27.36	3	0.00	0.40	0.00	-68.04	4.17
North-East	bacteria	CWM MycInt	50	12	29.64	3	0.00	0.42	0.00	-99.86	4.17
North-East	bacteria	Plant biomass	49	10	0.00	0	NA	0.00	NA	-48.55	4.90
North-East	bacteria	Lignin content	49	10	0.00	0	NA	0.00	NA	-46.73	4.90
North-East	bacteria	pH	50	12	11.30	3	0.01	0.24	0.02	-79.94	4.17
North-East	fungi	CWM leaf P	50	12	27.36	3	0.00	0.40	0.00	-77.01	4.17
North-East	fungi	CWM MycInt	50	12	29.64	3	0.00	0.42	0.00	-109.60	4.17
North-East	fungi	Plant biomass	49	10	0.00	0	NA	0.00	NA	-57.28	4.90
North-East	fungi	Lignin content	49	10	0.00	0	NA	0.00	NA	-57.83	4.90
North-East	fungi	pH	50	12	11.30	3	0.01	0.24	0.02	-91.74	4.17
North-East	fungi:bacteria ratio	CWM leaf P	50	12	27.36	3	0.00	0.40	0.00	-76.56	4.17
North-East	fungi:bacteria ratio	CWM MycInt	50	12	29.64	3	0.00	0.42	0.00	-100.54	4.17
North-East	fungi:bacteria ratio	Plant biomass	49	10	0.00	0	NA	0.00	NA	-59.57	4.90
North-East	fungi:bacteria ratio	Lignin content	49	10	0.00	0	NA	0.00	NA	-60.89	4.90
North-East	fungi:bacteria ratio	pH	50	12	11.30	3	0.01	0.24	0.02	-89.50	4.17
North-East	ergosterol	CWM leaf P	50	12	27.36	3	0.00	0.40	0.00	-95.11	4.17
North-East	ergosterol	CWM MycInt	50	12	29.64	3	0.00	0.42	0.00	-119.49	4.17
North-East	ergosterol	Plant biomass	49	10	0.00	0	NA	0.00	NA	-79.02	4.90
North-East	ergosterol	Lignin content	49	10	0.00	0	NA	0.00	NA	-74.93	4.90
North-East	ergosterol	pH	50	12	11.30	3	0.01	0.24	0.02	-121.36	4.17

Table S7-6.2: Estimates of SEMs in Schwäbische Alb (South-West), Hainich-Dün (Central) and Schorfheide-Chorin (North-East) (see following pages). Given are the unstandardized regression coefficients (est) with their standard error (se), z-value (z) and respective *p* -value (*p*), as well as the standardized correlation coefficients (est.std) with their standard error (se.std), z-value (z.std) and *p* -value (*p* .std) for each microbial variable (MO variable) and the five selected mediator variables (mediator). The single model paths are described by lhs = left hand side, op = operator, rhs = right hand side and if applicable the respective label of the path.

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*p*	est.std	se.std	z.std	*p*.std
South-West	Cmic	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	1.04	0.14	7.23	0.000	0.72	0.07	10.44	0.000
South-West	Cmic	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	0.06	0.11	0.57	0.570	0.08	0.14	0.57	0.569
South-West	Cmic	CWM_leaf_P	Cmic	~	CWM_leafP_historic	c	0.03	0.15	0.18	0.854	0.04	0.20	0.18	0.854
South-West	Cmic	CWM_leaf_P	Cmic	~	CWM_leafP_change	d	0.35	0.16	2.20	0.028	0.30	0.13	2.29	0.022
South-West	Cmic	CWM_leaf_P	Cmic	~	LUI_historic	e	0.12	0.22	0.54	0.592	0.11	0.20	0.54	0.591
South-West	Cmic	CWM_leaf_P	Cmic	~	LUI_change	f	-0.12	0.13	-0.95	0.341	-0.13	0.14	-0.96	0.337
South-West	Cmic	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	Cmic	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	4.90	0.000	0.48	0.10	4.80	0.000
South-West	Cmic	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.03	0.01	4.90	0.000	0.99	0.02	42.42	0.000
South-West	Cmic	CWM_leaf_P	Cmic	~~	Cmic		0.04	0.01	4.90	0.000	0.88	0.09	10.04	0.000
South-West	Cmic	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	Cmic	CWM_leaf_P	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	Cmic	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.03	0.16	0.18	0.855	0.03	0.14	0.18	0.855
South-West	Cmic	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.02	0.04	0.55	0.583	0.02	0.04	0.55	0.583
South-West	Cmic	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.15	0.15	0.96	0.336	0.13	0.14	0.97	0.333
South-West	Cmic	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.10	0.13	-0.74	0.458	-0.11	0.14	-0.75	0.456
South-West	Cmic	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.15	0.15	0.97	0.335	0.14	0.14	1.06	0.289
South-West	Cmic	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.10	0.13	-0.75	0.455	-0.12	0.14	-0.85	0.394
South-West	Cmic	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.38	0.18	2.09	0.037	0.29	0.13	2.18	0.029
South-West	Cmic	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.24	0.11	2.18	0.029	0.30	0.13	2.29	0.022
South-West	Cmic	CWM_MycInt	Cmic	~	CWM_MycInt_historic	c	0.04	0.12	0.30	0.761	0.04	0.14	0.30	0.761
South-West	Cmic	CWM_MycInt	Cmic	~	CWM_MycInt_change	d	0.39	0.17	2.37	0.018	0.33	0.13	2.49	0.013
South-West	Cmic	CWM_MycInt	Cmic	~	LUI_historic	e	0.21	0.16	1.34	0.180	0.19	0.14	1.36	0.174
South-West	Cmic	CWM_MycInt	Cmic	~	LUI_change	f	-0.18	0.13	-1.37	0.170	-0.19	0.14	-1.39	0.164
South-West	Cmic	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	Cmic	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	4.90	0.000	0.92	0.08	12.02	0.000
South-West	Cmic	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	4.90	0.000	0.91	0.08	11.52	0.000
South-West	Cmic	CWM_MycInt	Cmic	~~	Cmic		0.04	0.01	4.90	0.000	0.85	0.09	8.96	0.000
South-West	Cmic	CWM_MycInt	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	Cmic	CWM_MycInt	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	Cmic	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.05	0.30	0.764	0.01	0.04	0.30	0.764
South-West	Cmic	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.09	0.06	1.61	0.108	0.10	0.06	1.63	0.104
South-West	Cmic	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.23	0.15	1.49	0.137	0.20	0.13	1.52	0.130
South-West	Cmic	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.09	0.13	-0.66	0.510	-0.09	0.14	-0.66	0.508
South-West	Cmic	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.23	0.15	1.49	0.136	0.21	0.13	1.60	0.109
South-West	Cmic	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.09	0.13	-0.67	0.504	-0.12	0.14	-0.82	0.415
South-West	Cmic	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.16	1.17	0.244	0.16	0.14	1.18	0.238
South-West	Cmic	Plant_biomass	Plant_biomass	~	LUI_change	b	-0.04	0.13	-0.29	0.771	-0.04	0.14	-0.29	0.771
South-West	Cmic	Plant_biomass	Cmic	~	Plant_biomass	c	0.39	0.12	3.14	0.002	0.40	0.12	3.41	0.001
South-West	Cmic	Plant_biomass	Cmic	~	LUI_historic	e	0.14	0.15	0.95	0.344	0.12	0.13	0.95	0.341
South-West	Cmic	Plant_biomass	Cmic	~	LUI_change	f	-0.10	0.11	-0.88	0.378	-0.11	0.13	-0.89	0.376
South-West	Cmic	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	Cmic	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.04	0.01	5.00	0.000	0.97	0.05	20.22	0.000
South-West	Cmic	Plant_biomass	Cmic	~~	Cmic		0.03	0.01	5.00	0.000	0.79	0.10	7.65	0.000
South-West	Cmic	Plant_biomass	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	Cmic	Plant_biomass	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	Cmic	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.07	0.07	1.09	0.274	0.07	0.06	1.11	0.266
South-West	Cmic	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	-0.02	0.05	-0.29	0.772	-0.02	0.06	-0.29	0.771
South-West	Cmic	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.21	0.16	1.35	0.177	0.19	0.14	1.37	0.170
South-West	Cmic	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.11	0.12	-0.92	0.355	-0.13	0.14	-0.93	0.352
South-West	Cmic	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.21	0.16	1.36	0.175	0.21	0.14	1.52	0.128
South-West	Cmic	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.12	0.12	-0.94	0.349	-0.16	0.14	-1.13	0.259
South-West	Cmic	Lignin_content	Lignin_content	~	LUI_historic	a	0.03	0.19	0.13	0.895	0.02	0.15	0.13	0.895
South-West	Cmic	Lignin_content	Lignin_content	~	LUI_change	b	0.08	0.15	0.54	0.589	0.08	0.15	0.54	0.588
South-West	Cmic	Lignin_content	Cmic	~	Lignin_content	c	0.11	0.12	0.90	0.368	0.13	0.14	0.91	0.364
South-West	Cmic	Lignin_content	Cmic	~	LUI_historic	e	0.21	0.16	1.33	0.183	0.19	0.14	1.35	0.176
South-West	Cmic	Lignin_content	Cmic	~	LUI_change	f	-0.12	0.12	-0.96	0.338	-0.14	0.14	-0.97	0.334
South-West	Cmic	Lignin_content	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.95	0.342	-0.14	0.14	-0.98	0.329
South-West	Cmic	Lignin_content	Lignin_content	~~	Lignin_content		0.06	0.01	4.90	0.000	0.99	0.02	44.29	0.000
South-West	Cmic	Lignin_content	Cmic	~~	Cmic		0.04	0.01	4.90	0.000	0.93	0.07	12.77	0.000
South-West	Cmic	Lignin_content	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	Cmic	Lignin_content	LUI_change	~~	LUI_change		0.06	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	Cmic	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	0.13	0.897	0.00	0.02	0.13	0.897
South-West	Cmic	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.01	0.02	0.46	0.643	0.01	0.02	0.46	0.643
South-West	Cmic	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.21	0.16	1.34	0.181	0.19	0.14	1.36	0.173
South-West	Cmic	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.11	0.13	-0.88	0.377	-0.13	0.14	-0.89	0.373
South-West	Cmic	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.22	0.16	1.34	0.179	0.21	0.14	1.49	0.135
South-West	Cmic	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.11	0.13	-0.90	0.371	-0.15	0.14	-1.07	0.284
South-West	Cmic	pH	pH_historic	~	LUI_historic	a	-0.13	0.19	-0.67	0.505	-0.09	0.14	-0.67	0.504
South-West	Cmic	pH	pH_change	~	LUI_change	b	-0.01	0.12	-0.08	0.933	-0.01	0.14	-0.08	0.933
South-West	Cmic	pH	Cmic	~	pH_historic	c	0.01	0.11	0.09	0.926	0.01	0.13	0.09	0.926
South-West	Cmic	pH	Cmic	~	pH_change	d	0.28	0.14	2.01	0.044	0.26	0.13	2.08	0.038
South-West	Cmic	pH	Cmic	~	LUI_historic	e	0.25	0.15	1.66	0.097	0.22	0.13	1.70	0.090
South-West	Cmic	pH	Cmic	~	LUI_change	f	-0.10	0.12	-0.87	0.387	-0.12	0.13	-0.87	0.384
South-West	Cmic	pH	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	Cmic	pH	pH_historic	~~	pH_historic		0.06	0.01	5.00	0.000	0.99	0.03	37.71	0.000
South-West	Cmic	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	1.00	0.00	298.93	0.000
South-West	Cmic	pH	Cmic	~~	Cmic		0.04	0.01	5.00	0.000	0.86	0.09	9.58	0.000
South-West	Cmic	pH	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	Cmic	pH	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	Cmic	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	-0.09	0.927	0.00	0.01	-0.09	0.927
South-West	Cmic	pH	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.03	-0.08	0.933	0.00	0.04	-0.08	0.933
South-West	Cmic	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.25	0.15	1.66	0.097	0.22	0.13	1.69	0.090
South-West	Cmic	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.11	0.12	-0.86	0.392	-0.12	0.14	-0.86	0.389
South-West	Cmic	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.25	0.15	1.66	0.096	0.24	0.13	1.84	0.065
South-West	Cmic	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.11	0.12	-0.87	0.385	-0.15	0.14	-1.09	0.277

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*p*	est.std	se.std	z.std	*p*.std
South-West	Nmic	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	1.04	0.14	7.23	0.000	0.72	0.07	10.44	0.000
South-West	Nmic	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	0.06	0.11	0.57	0.570	0.08	0.14	0.57	0.569
South-West	Nmic	CWM_leaf_P	Nmic	~	CWM_leafP_historic	c	0.00	0.14	-0.01	0.989	0.00	0.19	-0.01	0.989
South-West	Nmic	CWM_leaf_P	Nmic	~	CWM_leafP_change	d	0.31	0.15	2.10	0.036	0.28	0.13	2.18	0.029
South-West	Nmic	CWM_leaf_P	Nmic	~	LUI_historic	e	0.21	0.20	1.04	0.299	0.20	0.19	1.05	0.295
South-West	Nmic	CWM_leaf_P	Nmic	~	LUI_change	f	-0.13	0.12	-1.10	0.270	-0.15	0.13	-1.11	0.265
South-West	Nmic	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	Nmic	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	4.90	0.000	0.48	0.10	4.80	0.000
South-West	Nmic	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.03	0.01	4.90	0.000	0.99	0.02	42.42	0.000
South-West	Nmic	CWM_leaf_P	Nmic	~~	Nmic		0.03	0.01	4.90	0.000	0.86	0.09	9.35	0.000
South-West	Nmic	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	Nmic	CWM_leaf_P	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	Nmic	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.15	-0.01	0.989	0.00	0.14	-0.01	0.989
South-West	Nmic	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.02	0.04	0.55	0.584	0.02	0.04	0.55	0.584
South-West	Nmic	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.21	0.14	1.48	0.139	0.20	0.13	1.51	0.132
South-West	Nmic	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.11	0.12	-0.90	0.370	-0.13	0.14	-0.90	0.366
South-West	Nmic	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.21	0.14	1.49	0.137	0.21	0.13	1.62	0.105
South-West	Nmic	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.11	0.12	-0.91	0.365	-0.15	0.14	-1.06	0.290
South-West	Nmic	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.38	0.18	2.09	0.037	0.29	0.13	2.18	0.029
South-West	Nmic	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.24	0.11	2.18	0.029	0.30	0.13	2.29	0.022
South-West	Nmic	CWM_MycInt	Nmic	~	CWM_MycInt_historic	c	-0.02	0.11	-0.19	0.853	-0.03	0.14	-0.19	0.853
South-West	Nmic	CWM_MycInt	Nmic	~	CWM_MycInt_change	d	0.32	0.15	2.09	0.037	0.29	0.13	2.16	0.031
South-West	Nmic	CWM_MycInt	Nmic	~	LUI_historic	e	0.28	0.15	1.95	0.052	0.27	0.13	2.01	0.045
South-West	Nmic	CWM_MycInt	Nmic	~	LUI_change	f	-0.18	0.12	-1.46	0.145	-0.20	0.14	-1.48	0.139
South-West	Nmic	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	Nmic	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	4.90	0.000	0.92	0.08	12.02	0.000
South-West	Nmic	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	4.90	0.000	0.91	0.08	11.52	0.000
South-West	Nmic	CWM_MycInt	Nmic	~~	Nmic		0.03	0.01	4.90	0.000	0.83	0.10	8.65	0.000
South-West	Nmic	CWM_MycInt	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	Nmic	CWM_MycInt	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	Nmic	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.04	-0.18	0.854	-0.01	0.04	-0.18	0.854
South-West	Nmic	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.08	0.05	1.51	0.131	0.09	0.06	1.53	0.127
South-West	Nmic	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.28	0.14	1.97	0.048	0.26	0.13	2.04	0.042
South-West	Nmic	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.10	0.12	-0.83	0.404	-0.12	0.14	-0.84	0.401
South-West	Nmic	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.28	0.14	1.98	0.048	0.28	0.13	2.15	0.032
South-West	Nmic	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.10	0.12	-0.85	0.398	-0.15	0.14	-1.03	0.302
South-West	Nmic	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.16	1.17	0.244	0.16	0.14	1.18	0.238
South-West	Nmic	Plant_biomass	Plant_biomass	~	LUI_change	b	-0.04	0.13	-0.29	0.771	-0.04	0.14	-0.29	0.771
South-West	Nmic	Plant_biomass	Nmic	~	Plant_biomass	c	0.33	0.12	2.86	0.004	0.37	0.12	3.05	0.002
South-West	Nmic	Plant_biomass	Nmic	~	LUI_historic	e	0.19	0.14	1.39	0.164	0.18	0.13	1.41	0.159
South-West	Nmic	Plant_biomass	Nmic	~	LUI_change	f	-0.08	0.11	-0.78	0.439	-0.10	0.13	-0.78	0.437
South-West	Nmic	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	Nmic	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.04	0.01	5.00	0.000	0.97	0.05	20.22	0.000
South-West	Nmic	Plant_biomass	Nmic	~~	Nmic		0.03	0.01	5.00	0.000	0.79	0.10	7.76	0.000
South-West	Nmic	Plant_biomass	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	Nmic	Plant_biomass	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	Nmic	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.06	0.06	1.08	0.280	0.06	0.05	1.10	0.271
South-West	Nmic	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	-0.01	0.04	-0.29	0.772	-0.02	0.05	-0.29	0.772
South-West	Nmic	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.25	0.14	1.75	0.081	0.24	0.13	1.80	0.073
South-West	Nmic	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.09	0.11	-0.83	0.408	-0.11	0.14	-0.83	0.405
South-West	Nmic	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.25	0.14	1.75	0.080	0.26	0.13	1.94	0.052
South-West	Nmic	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.10	0.11	-0.84	0.399	-0.15	0.14	-1.08	0.281
South-West	Nmic	Lignin_content	Lignin_content	~	LUI_historic	a	0.03	0.19	0.13	0.895	0.02	0.15	0.13	0.895
South-West	Nmic	Lignin_content	Lignin_content	~	LUI_change	b	0.08	0.15	0.54	0.589	0.08	0.15	0.54	0.588
South-West	Nmic	Lignin_content	Nmic	~	Lignin_content	c	0.09	0.11	0.79	0.432	0.11	0.14	0.79	0.429
South-West	Nmic	Lignin_content	Nmic	~	LUI_historic	e	0.24	0.15	1.65	0.099	0.23	0.14	1.70	0.090
South-West	Nmic	Lignin_content	Nmic	~	LUI_change	f	-0.10	0.11	-0.83	0.406	-0.12	0.14	-0.84	0.403
South-West	Nmic	Lignin_content	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.95	0.342	-0.14	0.14	-0.98	0.329
South-West	Nmic	Lignin_content	Lignin_content	~~	Lignin_content		0.06	0.01	4.90	0.000	0.99	0.02	44.29	0.000
South-West	Nmic	Lignin_content	Nmic	~~	Nmic		0.03	0.01	4.90	0.000	0.92	0.08	11.93	0.000
South-West	Nmic	Lignin_content	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	Nmic	Lignin_content	LUI_change	~~	LUI_change		0.06	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	Nmic	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	0.13	0.897	0.00	0.02	0.13	0.897
South-West	Nmic	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.01	0.02	0.45	0.656	0.01	0.02	0.45	0.656
South-West	Nmic	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.24	0.15	1.66	0.098	0.23	0.14	1.70	0.089
South-West	Nmic	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.09	0.11	-0.77	0.443	-0.11	0.14	-0.77	0.440
South-West	Nmic	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.24	0.15	1.66	0.097	0.25	0.14	1.83	0.068
South-West	Nmic	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.09	0.11	-0.78	0.435	-0.14	0.14	-0.99	0.323
South-West	Nmic	pH	pH_historic	~	LUI_historic	a	-0.13	0.19	-0.67	0.505	-0.09	0.14	-0.67	0.504
South-West	Nmic	pH	pH_change	~	LUI_change	b	-0.01	0.12	-0.08	0.933	-0.01	0.14	-0.08	0.933
South-West	Nmic	pH	Nmic	~	pH_historic	c	-0.05	0.10	-0.48	0.633	-0.06	0.13	-0.48	0.633
South-West	Nmic	pH	Nmic	~	pH_change	d	0.26	0.13	2.02	0.044	0.26	0.13	2.08	0.038
South-West	Nmic	pH	Nmic	~	LUI_historic	e	0.28	0.14	1.99	0.046	0.26	0.13	2.05	0.040
South-West	Nmic	pH	Nmic	~	LUI_change	f	-0.11	0.11	-0.98	0.327	-0.13	0.13	-0.99	0.324
South-West	Nmic	pH	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	Nmic	pH	pH_historic	~~	pH_historic		0.06	0.01	5.00	0.000	0.99	0.03	37.71	0.000
South-West	Nmic	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	1.00	0.00	298.94	0.000
South-West	Nmic	pH	Nmic	~~	Nmic		0.03	0.01	5.00	0.000	0.83	0.10	8.72	0.000
South-West	Nmic	pH	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	Nmic	pH	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	Nmic	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.02	0.39	0.698	0.01	0.02	0.39	0.698
South-West	Nmic	pH	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.03	-0.08	0.933	0.00	0.04	-0.08	0.933
South-West	Nmic	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.28	0.14	2.04	0.041	0.27	0.13	2.11	0.035
South-West	Nmic	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.11	0.11	-0.97	0.334	-0.13	0.13	-0.97	0.330
South-West	Nmic	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.28	0.14	2.05	0.041	0.29	0.13	2.28	0.023
South-West	Nmic	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.11	0.11	-0.98	0.326	-0.17	0.14	-1.24	0.215

Region	**MO variable**	**mediator**	**lhs**	**op**	**rhs**	**label**	**est**	**se**	**z**	***p***	**est.std**	**se.std**	**z.std**	***p*.std**
South-West	Cmic:Nmic ratio	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	1.04	0.14	7.23	0.000	0.72	0.07	10.44	0.000
South-West	Cmic:Nmic ratio	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	0.06	0.11	0.57	0.570	0.08	0.14	0.57	0.569
South-West	Cmic:Nmic ratio	CWM_leaf_P	RatioCmic_Nmic	~	CWM_leafP_historic	c	0.07	0.18	0.40	0.691	0.08	0.20	0.40	0.690
South-West	Cmic:Nmic ratio	CWM_leaf_P	RatioCmic_Nmic	~	CWM_leafP_change	d	-0.17	0.19	-0.93	0.353	-0.13	0.14	-0.94	0.349
South-West	Cmic:Nmic ratio	CWM_leaf_P	RatioCmic_Nmic	~	LUI_historic	e	-0.34	0.25	-1.33	0.185	-0.27	0.20	-1.35	0.177
South-West	Cmic:Nmic ratio	CWM_leaf_P	RatioCmic_Nmic	~	LUI_change	f	-0.01	0.15	-0.06	0.951	-0.01	0.14	-0.06	0.951
South-West	Cmic:Nmic ratio	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	Cmic:Nmic ratio	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	4.90	0.000	0.48	0.10	4.80	0.000
South-West	Cmic:Nmic ratio	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.03	0.01	4.90	0.000	0.99	0.02	42.42	0.000
South-West	Cmic:Nmic ratio	CWM_leaf_P	RatioCmic_Nmic	~~	RatioCmic_Nmic		0.05	0.01	4.90	0.000	0.94	0.07	13.81	0.000
South-West	Cmic:Nmic ratio	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	Cmic:Nmic ratio	CWM_leaf_P	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	Cmic:Nmic ratio	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.07	0.18	0.40	0.691	0.06	0.15	0.40	0.691
South-West	Cmic:Nmic ratio	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	-0.01	0.02	-0.48	0.628	-0.01	0.02	-0.49	0.627
South-West	Cmic:Nmic ratio	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.26	0.18	-1.50	0.135	-0.21	0.14	-1.53	0.127
South-West	Cmic:Nmic ratio	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.02	0.15	-0.14	0.892	-0.02	0.14	-0.14	0.892
South-West	Cmic:Nmic ratio	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.26	0.18	-1.50	0.135	-0.21	0.14	-1.52	0.128
South-West	Cmic:Nmic ratio	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.02	0.15	-0.13	0.899	0.01	0.14	0.04	0.972
South-West	Cmic:Nmic ratio	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.38	0.18	2.09	0.037	0.29	0.13	2.18	0.029
South-West	Cmic:Nmic ratio	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.24	0.11	2.18	0.029	0.30	0.13	2.29	0.022
South-West	Cmic:Nmic ratio	CWM_MycInt	RatioCmic_Nmic	~	CWM_MycInt_historic	c	0.10	0.14	0.74	0.460	0.11	0.14	0.74	0.458
South-West	Cmic:Nmic ratio	CWM_MycInt	RatioCmic_Nmic	~	CWM_MycInt_change	d	-0.17	0.19	-0.90	0.371	-0.13	0.14	-0.90	0.367
South-West	Cmic:Nmic ratio	CWM_MycInt	RatioCmic_Nmic	~	LUI_historic	e	-0.34	0.18	-1.86	0.063	-0.27	0.14	-1.92	0.055
South-West	Cmic:Nmic ratio	CWM_MycInt	RatioCmic_Nmic	~	LUI_change	f	0.02	0.15	0.16	0.875	0.02	0.15	0.16	0.875
South-West	Cmic:Nmic ratio	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	Cmic:Nmic ratio	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	4.90	0.000	0.92	0.08	12.02	0.000
South-West	Cmic:Nmic ratio	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	4.90	0.000	0.91	0.08	11.52	0.000
South-West	Cmic:Nmic ratio	CWM_MycInt	RatioCmic_Nmic	~~	RatioCmic_Nmic		0.05	0.01	4.90	0.000	0.92	0.08	12.15	0.000
South-West	Cmic:Nmic ratio	CWM_MycInt	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	Cmic:Nmic ratio	CWM_MycInt	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	Cmic:Nmic ratio	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.04	0.06	0.70	0.486	0.03	0.04	0.70	0.485
South-West	Cmic:Nmic ratio	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	-0.04	0.05	-0.83	0.407	-0.04	0.05	-0.83	0.405
South-West	Cmic:Nmic ratio	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.30	0.18	-1.71	0.088	-0.24	0.14	-1.76	0.079
South-West	Cmic:Nmic ratio	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.02	0.15	-0.11	0.909	-0.02	0.14	-0.11	0.909
South-West	Cmic:Nmic ratio	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.30	0.18	-1.71	0.088	-0.24	0.14	-1.76	0.079
South-West	Cmic:Nmic ratio	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.02	0.15	-0.10	0.917	0.01	0.14	0.08	0.936
South-West	Cmic:Nmic ratio	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.16	1.17	0.244	0.16	0.14	1.18	0.238
South-West	Cmic:Nmic ratio	Plant_biomass	Plant_biomass	~	LUI_change	b	-0.04	0.13	-0.29	0.771	-0.04	0.14	-0.29	0.771
South-West	Cmic:Nmic ratio	Plant_biomass	RatioCmic_Nmic	~	Plant_biomass	c	-0.24	0.15	-1.62	0.106	-0.22	0.13	-1.65	0.098
South-West	Cmic:Nmic ratio	Plant_biomass	RatioCmic_Nmic	~	LUI_historic	e	-0.22	0.18	-1.26	0.208	-0.17	0.14	-1.28	0.202
South-West	Cmic:Nmic ratio	Plant_biomass	RatioCmic_Nmic	~	LUI_change	f	-0.07	0.14	-0.50	0.621	-0.07	0.14	-0.50	0.620
South-West	Cmic:Nmic ratio	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	Cmic:Nmic ratio	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.04	0.01	5.00	0.000	0.97	0.05	20.22	0.000
South-West	Cmic:Nmic ratio	Plant_biomass	RatioCmic_Nmic	~~	RatioCmic_Nmic		0.05	0.01	5.00	0.000	0.91	0.08	11.70	0.000
South-West	Cmic:Nmic ratio	Plant_biomass	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	Cmic:Nmic ratio	Plant_biomass	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	Cmic:Nmic ratio	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	-0.05	0.05	-0.95	0.345	-0.04	0.04	-0.96	0.338
South-West	Cmic:Nmic ratio	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.01	0.03	0.29	0.775	0.01	0.03	0.29	0.775
South-West	Cmic:Nmic ratio	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.27	0.18	-1.50	0.133	-0.21	0.14	-1.54	0.125
South-West	Cmic:Nmic ratio	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.06	0.14	-0.42	0.676	-0.06	0.14	-0.42	0.676
South-West	Cmic:Nmic ratio	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.27	0.18	-1.50	0.133	-0.20	0.14	-1.49	0.138
South-West	Cmic:Nmic ratio	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.06	0.14	-0.41	0.685	-0.03	0.14	-0.19	0.846
South-West	Cmic:Nmic ratio	Lignin_content	Lignin_content	~	LUI_historic	a	0.03	0.19	0.13	0.895	0.02	0.15	0.13	0.895
South-West	Cmic:Nmic ratio	Lignin_content	Lignin_content	~	LUI_change	b	0.08	0.15	0.54	0.589	0.08	0.15	0.54	0.588
South-West	Cmic:Nmic ratio	Lignin_content	RatioCmic_Nmic	~	Lignin_content	c	-0.01	0.14	-0.08	0.935	-0.01	0.14	-0.08	0.935
South-West	Cmic:Nmic ratio	Lignin_content	RatioCmic_Nmic	~	LUI_historic	e	-0.24	0.18	-1.32	0.185	-0.19	0.14	-1.35	0.178
South-West	Cmic:Nmic ratio	Lignin_content	RatioCmic_Nmic	~	LUI_change	f	-0.07	0.14	-0.51	0.609	-0.07	0.14	-0.51	0.608
South-West	Cmic:Nmic ratio	Lignin_content	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.95	0.342	-0.14	0.14	-0.98	0.329
South-West	Cmic:Nmic ratio	Lignin_content	Lignin_content	~~	Lignin_content		0.06	0.01	4.90	0.000	0.99	0.02	44.29	0.000
South-West	Cmic:Nmic ratio	Lignin_content	RatioCmic_Nmic	~~	RatioCmic_Nmic		0.05	0.01	4.90	0.000	0.96	0.05	17.84	0.000
South-West	Cmic:Nmic ratio	Lignin_content	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	Cmic:Nmic ratio	Lignin_content	LUI_change	~~	LUI_change		0.06	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	Cmic:Nmic ratio	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.00	-0.07	0.945	0.00	0.00	-0.07	0.945
South-West	Cmic:Nmic ratio	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	-0.08	0.936	0.00	0.01	-0.08	0.936
South-West	Cmic:Nmic ratio	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.24	0.18	-1.33	0.185	-0.19	0.14	-1.35	0.177
South-West	Cmic:Nmic ratio	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.07	0.14	-0.52	0.603	-0.07	0.14	-0.52	0.603
South-West	Cmic:Nmic ratio	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.24	0.18	-1.32	0.185	-0.18	0.14	-1.28	0.199
South-West	Cmic:Nmic ratio	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.07	0.14	-0.51	0.610	-0.05	0.14	-0.33	0.739
South-West	Cmic:Nmic ratio	pH	pH_historic	~	LUI_historic	a	-0.13	0.19	-0.67	0.505	-0.09	0.14	-0.67	0.504
South-West	Cmic:Nmic ratio	pH	pH_change	~	LUI_change	b	-0.01	0.12	-0.08	0.933	-0.01	0.14	-0.08	0.933
South-West	Cmic:Nmic ratio	pH	RatioCmic_Nmic	~	pH_historic	c	0.21	0.13	1.65	0.099	0.22	0.13	1.69	0.091
South-West	Cmic:Nmic ratio	pH	RatioCmic_Nmic	~	pH_change	d	-0.20	0.16	-1.24	0.216	-0.16	0.13	-1.25	0.211
South-West	Cmic:Nmic ratio	pH	RatioCmic_Nmic	~	LUI_historic	e	-0.25	0.17	-1.47	0.142	-0.20	0.13	-1.50	0.135
South-West	Cmic:Nmic ratio	pH	RatioCmic_Nmic	~	LUI_change	f	0.02	0.13	0.14	0.890	0.02	0.13	0.14	0.890
South-West	Cmic:Nmic ratio	pH	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	Cmic:Nmic ratio	pH	pH_historic	~~	pH_historic		0.06	0.01	5.00	0.000	0.99	0.03	37.71	0.000
South-West	Cmic:Nmic ratio	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	1.00	0.00	298.93	0.000
South-West	Cmic:Nmic ratio	pH	RatioCmic_Nmic	~~	RatioCmic_Nmic		0.05	0.01	5.00	0.000	0.88	0.09	10.15	0.000
South-West	Cmic:Nmic ratio	pH	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	Cmic:Nmic ratio	pH	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	Cmic:Nmic ratio	pH	LUI_hist_in	:=	a*c	LUI_hist_in	-0.03	0.04	-0.62	0.537	-0.02	0.03	-0.62	0.534
South-West	Cmic:Nmic ratio	pH	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.02	0.08	0.933	0.00	0.02	0.08	0.933
South-West	Cmic:Nmic ratio	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.28	0.18	-1.59	0.112	-0.22	0.13	-1.63	0.104
South-West	Cmic:Nmic ratio	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.02	0.14	0.15	0.880	0.02	0.14	0.15	0.880
South-West	Cmic:Nmic ratio	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.28	0.18	-1.59	0.112	-0.22	0.13	-1.67	0.096
South-West	Cmic:Nmic ratio	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.02	0.14	0.16	0.870	0.05	0.14	0.38	0.702

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*p*	est.std	se.std	z.std	*p*.std
South-West	Pmic	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	1.01	0.15	6.72	0.000	0.74	0.07	10.00	0.000
South-West	Pmic	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	0.12	0.12	1.02	0.308	0.17	0.16	1.03	0.301
South-West	Pmic	CWM_leaf_P	Pmic	~	CWM_leafP_historic	c	0.00	0.16	0.00	0.999	0.00	0.21	0.00	0.999
South-West	Pmic	CWM_leaf_P	Pmic	~	CWM_leafP_change	d	-0.08	0.17	-0.47	0.641	-0.07	0.15	-0.47	0.640
South-West	Pmic	CWM_leaf_P	Pmic	~	LUI_historic	e	0.49	0.21	2.29	0.022	0.49	0.20	2.42	0.015
South-West	Pmic	CWM_leaf_P	Pmic	~	LUI_change	f	0.07	0.12	0.56	0.575	0.08	0.15	0.56	0.575
South-West	Pmic	CWM_leaf_P	LUI_historic	~~	LUI_change	g	0.00	0.01	-0.38	0.701	-0.06	0.16	-0.39	0.699
South-West	Pmic	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	4.30	0.000	0.45	0.11	4.10	0.000
South-West	Pmic	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.03	0.01	4.30	0.000	0.97	0.05	18.40	0.000
South-West	Pmic	CWM_leaf_P	Pmic	~~	Pmic		0.03	0.01	4.30	0.000	0.76	0.12	6.18	0.000
South-West	Pmic	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.04	0.01	4.30	0.000	1.00	0.00	NA	NA
South-West	Pmic	CWM_leaf_P	LUI_change	~~	LUI_change		0.06	0.01	4.30	0.000	1.00	0.00	NA	NA
South-West	Pmic	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.16	0.00	0.999	0.00	0.16	0.00	0.999
South-West	Pmic	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	-0.01	0.02	-0.42	0.671	-0.01	0.03	-0.43	0.671
South-West	Pmic	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.49	0.14	3.41	0.001	0.49	0.13	3.89	0.000
South-West	Pmic	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.06	0.12	0.49	0.625	0.07	0.14	0.49	0.625
South-West	Pmic	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.49	0.14	3.41	0.001	0.48	0.13	3.85	0.000
South-West	Pmic	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.06	0.12	0.48	0.634	0.04	0.16	0.24	0.810
South-West	Pmic	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.28	0.19	1.50	0.134	0.24	0.16	1.55	0.122
South-West	Pmic	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.18	0.11	1.67	0.095	0.27	0.15	1.73	0.083
South-West	Pmic	CWM_MycInt	Pmic	~	CWM_MycInt_historic	c	0.01	0.12	0.06	0.950	0.01	0.15	0.06	0.950
South-West	Pmic	CWM_MycInt	Pmic	~	CWM_MycInt_change	d	0.22	0.18	1.22	0.224	0.18	0.15	1.23	0.219
South-West	Pmic	CWM_MycInt	Pmic	~	LUI_historic	e	0.46	0.15	3.17	0.002	0.47	0.13	3.53	0.000
South-West	Pmic	CWM_MycInt	Pmic	~	LUI_change	f	0.02	0.12	0.15	0.885	0.02	0.15	0.15	0.885
South-West	Pmic	CWM_MycInt	LUI_historic	~~	LUI_change	g	0.00	0.01	-0.38	0.701	-0.06	0.16	-0.39	0.699
South-West	Pmic	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	4.30	0.000	0.94	0.07	12.70	0.000
South-West	Pmic	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.02	0.01	4.30	0.000	0.93	0.08	11.48	0.000
South-West	Pmic	CWM_MycInt	Pmic	~~	Pmic		0.03	0.01	4.30	0.000	0.75	0.12	6.17	0.000
South-West	Pmic	CWM_MycInt	LUI_historic	~~	LUI_historic		0.04	0.01	4.30	0.000	1.00	0.00	NA	NA
South-West	Pmic	CWM_MycInt	LUI_change	~~	LUI_change		0.06	0.01	4.30	0.000	1.00	0.00	NA	NA
South-West	Pmic	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.04	0.06	0.950	0.00	0.04	0.06	0.950
South-West	Pmic	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.04	0.04	0.98	0.325	0.05	0.05	0.99	0.322
South-West	Pmic	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.46	0.14	3.28	0.001	0.47	0.13	3.69	0.000
South-West	Pmic	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.06	0.12	0.47	0.635	0.07	0.15	0.48	0.635
South-West	Pmic	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.46	0.14	3.28	0.001	0.46	0.13	3.64	0.000
South-West	Pmic	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.06	0.12	0.46	0.643	0.04	0.16	0.24	0.810
South-West	Pmic	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.29	0.17	1.69	0.091	0.26	0.15	1.75	0.080
South-West	Pmic	Plant_biomass	Plant_biomass	~	LUI_change	b	-0.03	0.14	-0.19	0.852	-0.03	0.16	-0.19	0.852
South-West	Pmic	Plant_biomass	Pmic	~	Plant_biomass	c	0.21	0.15	1.44	0.151	0.21	0.14	1.46	0.145
South-West	Pmic	Plant_biomass	Pmic	~	LUI_historic	e	0.47	0.17	2.85	0.004	0.41	0.13	3.08	0.002
South-West	Pmic	Plant_biomass	Pmic	~	LUI_change	f	-0.06	0.13	-0.46	0.645	-0.06	0.14	-0.46	0.645
South-West	Pmic	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.68	0.499	-0.11	0.16	-0.69	0.492
South-West	Pmic	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.04	0.01	4.42	0.000	0.93	0.08	11.70	0.000
South-West	Pmic	Plant_biomass	Pmic	~~	Pmic		0.04	0.01	4.42	0.000	0.74	0.12	6.08	0.000
South-West	Pmic	Plant_biomass	LUI_historic	~~	LUI_historic		0.04	0.01	4.42	0.000	1.00	0.00	NA	NA
South-West	Pmic	Plant_biomass	LUI_change	~~	LUI_change		0.06	0.01	4.42	0.000	1.00	0.00	NA	NA
South-West	Pmic	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.06	0.06	1.09	0.274	0.05	0.05	1.12	0.264
South-West	Pmic	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	-0.01	0.03	-0.19	0.853	-0.01	0.03	-0.19	0.853
South-West	Pmic	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.54	0.17	3.26	0.001	0.46	0.13	3.66	0.000
South-West	Pmic	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.06	0.13	-0.49	0.623	-0.07	0.14	-0.49	0.623
South-West	Pmic	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.54	0.17	3.26	0.001	0.47	0.13	3.76	0.000
South-West	Pmic	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.07	0.13	-0.51	0.609	-0.12	0.16	-0.76	0.447
South-West	Pmic	Lignin_content	Lignin_content	~	LUI_historic	a	-0.08	0.20	-0.38	0.701	-0.06	0.16	-0.39	0.700
South-West	Pmic	Lignin_content	Lignin_content	~	LUI_change	b	0.17	0.16	1.09	0.277	0.18	0.16	1.10	0.270
South-West	Pmic	Lignin_content	Pmic	~	Lignin_content	c	0.04	0.14	0.31	0.757	0.05	0.15	0.31	0.757
South-West	Pmic	Lignin_content	Pmic	~	LUI_historic	e	0.50	0.17	3.04	0.002	0.45	0.13	3.39	0.001
South-West	Pmic	Lignin_content	Pmic	~	LUI_change	f	-0.06	0.13	-0.45	0.653	-0.07	0.15	-0.45	0.653
South-West	Pmic	Lignin_content	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.59	0.553	-0.10	0.16	-0.60	0.548
South-West	Pmic	Lignin_content	Lignin_content	~~	Lignin_content		0.06	0.01	4.30	0.000	0.96	0.06	15.79	0.000
South-West	Pmic	Lignin_content	Pmic	~~	Pmic		0.04	0.01	4.30	0.000	0.79	0.12	6.66	0.000
South-West	Pmic	Lignin_content	LUI_historic	~~	LUI_historic		0.04	0.01	4.30	0.000	1.00	0.00	NA	NA
South-West	Pmic	Lignin_content	LUI_change	~~	LUI_change		0.06	0.01	4.30	0.000	1.00	0.00	NA	NA
South-West	Pmic	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	-0.24	0.810	0.00	0.01	-0.24	0.810
South-West	Pmic	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.01	0.02	0.30	0.766	0.01	0.03	0.30	0.766
South-West	Pmic	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.50	0.17	3.02	0.003	0.45	0.13	3.37	0.001
South-West	Pmic	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.05	0.13	-0.40	0.689	-0.06	0.15	-0.40	0.688
South-West	Pmic	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.50	0.17	3.02	0.003	0.45	0.13	3.44	0.001
South-West	Pmic	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.06	0.13	-0.42	0.675	-0.10	0.16	-0.63	0.529
South-West	Pmic	pH	pH_historic	~	LUI_historic	a	-0.26	0.21	-1.25	0.213	-0.20	0.15	-1.27	0.204
South-West	Pmic	pH	pH_change	~	LUI_change	b	0.08	0.11	0.70	0.484	0.11	0.16	0.70	0.481
South-West	Pmic	pH	Pmic	~	pH_historic	c	-0.11	0.13	-0.90	0.370	-0.13	0.14	-0.90	0.367
South-West	Pmic	pH	Pmic	~	pH_change	d	-0.02	0.19	-0.08	0.939	-0.01	0.14	-0.08	0.939
South-West	Pmic	pH	Pmic	~	LUI_historic	e	0.50	0.17	2.99	0.003	0.43	0.13	3.28	0.001
South-West	Pmic	pH	Pmic	~	LUI_change	f	-0.11	0.13	-0.85	0.394	-0.12	0.14	-0.86	0.392
South-West	Pmic	pH	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.68	0.499	-0.11	0.16	-0.69	0.492
South-West	Pmic	pH	pH_historic	~~	pH_historic		0.06	0.01	4.42	0.000	0.96	0.06	15.97	0.000
South-West	Pmic	pH	pH_change	~~	pH_change		0.03	0.01	4.42	0.000	0.99	0.04	28.04	0.000
South-West	Pmic	pH	Pmic	~~	Pmic		0.04	0.01	4.42	0.000	0.75	0.12	6.30	0.000
South-West	Pmic	pH	LUI_historic	~~	LUI_historic		0.04	0.01	4.42	0.000	1.00	0.00	NA	NA
South-West	Pmic	pH	LUI_change	~~	LUI_change		0.06	0.01	4.42	0.000	1.00	0.00	NA	NA
South-West	Pmic	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.03	0.04	0.73	0.467	0.03	0.03	0.74	0.463
South-West	Pmic	pH	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.02	-0.08	0.939	0.00	0.02	-0.08	0.939
South-West	Pmic	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.53	0.17	3.19	0.001	0.45	0.13	3.57	0.000
South-West	Pmic	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.11	0.13	-0.87	0.387	-0.12	0.14	-0.87	0.384
South-West	Pmic	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.53	0.17	3.20	0.001	0.47	0.13	3.70	0.000
South-West	Pmic	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.12	0.13	-0.89	0.375	-0.17	0.15	-1.10	0.270

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*p*	est.std	se.std	z.std	*p*.std
South-West	beta-glucosidase	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	1.04	0.14	7.23	0.000	0.72	0.07	10.44	0.000
South-West	beta-glucosidase	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	0.06	0.11	0.57	0.570	0.08	0.14	0.57	0.569
South-West	beta-glucosidase	CWM_leaf_P	Glucosidase	~	CWM_leafP_historic	c	0.42	0.15	2.71	0.007	0.48	0.17	2.84	0.005
South-West	beta-glucosidase	CWM_leaf_P	Glucosidase	~	CWM_leafP_change	d	0.33	0.16	2.04	0.042	0.25	0.12	2.08	0.038
South-West	beta-glucosidase	CWM_leaf_P	Glucosidase	~	LUI_historic	e	-0.16	0.22	-0.73	0.466	-0.13	0.18	-0.73	0.465
South-West	beta-glucosidase	CWM_leaf_P	Glucosidase	~	LUI_change	f	-0.28	0.13	-2.24	0.025	-0.27	0.12	-2.30	0.021
South-West	beta-glucosidase	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	beta-glucosidase	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	4.90	0.000	0.48	0.10	4.80	0.000
South-West	beta-glucosidase	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.03	0.01	4.90	0.000	0.99	0.02	42.42	0.000
South-West	beta-glucosidase	CWM_leaf_P	Glucosidase	~~	Glucosidase		0.04	0.01	4.90	0.000	0.71	0.11	6.59	0.000
South-West	beta-glucosidase	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	beta-glucosidase	CWM_leaf_P	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	beta-glucosidase	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.43	0.17	2.54	0.011	0.34	0.13	2.65	0.008
South-West	beta-glucosidase	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.02	0.04	0.55	0.585	0.02	0.04	0.55	0.586
South-West	beta-glucosidase	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.27	0.17	1.64	0.102	0.22	0.13	1.67	0.095
South-West	beta-glucosidase	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.26	0.13	-2.00	0.046	-0.25	0.12	-2.05	0.040
South-West	beta-glucosidase	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.27	0.17	1.65	0.100	0.24	0.13	1.86	0.063
South-West	beta-glucosidase	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.27	0.13	-2.01	0.045	-0.28	0.13	-2.22	0.026
South-West	beta-glucosidase	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.38	0.18	2.09	0.037	0.29	0.13	2.18	0.029
South-West	beta-glucosidase	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.24	0.11	2.18	0.029	0.30	0.13	2.29	0.022
South-West	beta-glucosidase	CWM_MycInt	Glucosidase	~	CWM_MycInt_historic	c	0.11	0.13	0.79	0.427	0.11	0.14	0.80	0.425
South-West	beta-glucosidase	CWM_MycInt	Glucosidase	~	CWM_MycInt_change	d	-0.07	0.18	-0.38	0.706	-0.05	0.14	-0.38	0.706
South-West	beta-glucosidase	CWM_MycInt	Glucosidase	~	LUI_historic	e	0.29	0.18	1.67	0.095	0.24	0.14	1.71	0.087
South-West	beta-glucosidase	CWM_MycInt	Glucosidase	~	LUI_change	f	-0.16	0.14	-1.08	0.279	-0.15	0.14	-1.09	0.274
South-West	beta-glucosidase	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	beta-glucosidase	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	4.90	0.000	0.92	0.08	12.02	0.000
South-West	beta-glucosidase	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	4.90	0.000	0.91	0.08	11.52	0.000
South-West	beta-glucosidase	CWM_MycInt	Glucosidase	~~	Glucosidase		0.05	0.01	4.90	0.000	0.87	0.09	9.78	0.000
South-West	beta-glucosidase	CWM_MycInt	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	beta-glucosidase	CWM_MycInt	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	beta-glucosidase	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.04	0.05	0.74	0.458	0.03	0.04	0.75	0.455
South-West	beta-glucosidase	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	-0.02	0.04	-0.37	0.710	-0.02	0.04	-0.37	0.710
South-West	beta-glucosidase	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.33	0.17	1.97	0.049	0.27	0.13	2.04	0.041
South-West	beta-glucosidase	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.17	0.14	-1.25	0.211	-0.17	0.13	-1.27	0.205
South-West	beta-glucosidase	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.33	0.17	1.97	0.048	0.29	0.13	2.19	0.029
South-West	beta-glucosidase	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.17	0.14	-1.26	0.207	-0.20	0.14	-1.46	0.144
South-West	beta-glucosidase	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.16	1.17	0.244	0.16	0.14	1.18	0.238
South-West	beta-glucosidase	Plant_biomass	Plant_biomass	~	LUI_change	b	-0.04	0.13	-0.29	0.771	-0.04	0.14	-0.29	0.771
South-West	beta-glucosidase	Plant_biomass	Glucosidase	~	Plant_biomass	c	0.25	0.14	1.73	0.083	0.23	0.13	1.77	0.077
South-West	beta-glucosidase	Plant_biomass	Glucosidase	~	LUI_historic	e	0.30	0.17	1.83	0.068	0.24	0.13	1.87	0.061
South-West	beta-glucosidase	Plant_biomass	Glucosidase	~	LUI_change	f	-0.17	0.13	-1.30	0.192	-0.17	0.13	-1.32	0.187
South-West	beta-glucosidase	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	beta-glucosidase	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.04	0.01	5.00	0.000	0.97	0.05	20.22	0.000
South-West	beta-glucosidase	Plant_biomass	Glucosidase	~~	Glucosidase		0.04	0.01	5.00	0.000	0.83	0.10	8.49	0.000
South-West	beta-glucosidase	Plant_biomass	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	beta-glucosidase	Plant_biomass	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	beta-glucosidase	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.05	0.05	0.97	0.334	0.04	0.04	0.98	0.327
South-West	beta-glucosidase	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	-0.01	0.03	-0.29	0.774	-0.01	0.03	-0.29	0.774
South-West	beta-glucosidase	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.35	0.17	2.07	0.038	0.28	0.13	2.15	0.031
South-West	beta-glucosidase	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.18	0.13	-1.34	0.181	-0.18	0.13	-1.36	0.175
South-West	beta-glucosidase	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.35	0.17	2.08	0.037	0.30	0.13	2.37	0.018
South-West	beta-glucosidase	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.18	0.13	-1.36	0.175	-0.22	0.14	-1.63	0.102
South-West	beta-glucosidase	Lignin_content	Lignin_content	~	LUI_historic	a	0.03	0.19	0.13	0.895	0.02	0.15	0.13	0.895
South-West	beta-glucosidase	Lignin_content	Lignin_content	~	LUI_change	b	0.08	0.15	0.54	0.589	0.08	0.15	0.54	0.588
South-West	beta-glucosidase	Lignin_content	Glucosidase	~	Lignin_content	c	-0.04	0.13	-0.34	0.734	-0.05	0.14	-0.34	0.734
South-West	beta-glucosidase	Lignin_content	Glucosidase	~	LUI_historic	e	0.34	0.17	2.03	0.043	0.28	0.13	2.10	0.035
South-West	beta-glucosidase	Lignin_content	Glucosidase	~	LUI_change	f	-0.16	0.13	-1.24	0.216	-0.17	0.14	-1.25	0.210
South-West	beta-glucosidase	Lignin_content	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.95	0.342	-0.14	0.14	-0.98	0.329
South-West	beta-glucosidase	Lignin_content	Lignin_content	~~	Lignin_content		0.06	0.01	4.90	0.000	0.99	0.02	44.29	0.000
South-West	beta-glucosidase	Lignin_content	Glucosidase	~~	Glucosidase		0.05	0.01	4.90	0.000	0.88	0.09	9.94	0.000
South-West	beta-glucosidase	Lignin_content	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	beta-glucosidase	Lignin_content	LUI_change	~~	LUI_change		0.06	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	beta-glucosidase	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	-0.12	0.902	0.00	0.01	-0.12	0.903
South-West	beta-glucosidase	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	-0.29	0.774	0.00	0.01	-0.29	0.774
South-West	beta-glucosidase	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.34	0.17	2.02	0.044	0.28	0.13	2.10	0.036
South-West	beta-glucosidase	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.17	0.13	-1.27	0.206	-0.17	0.14	-1.28	0.200
South-West	beta-glucosidase	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.34	0.17	2.03	0.043	0.30	0.13	2.28	0.022
South-West	beta-glucosidase	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.17	0.13	-1.28	0.200	-0.21	0.14	-1.53	0.126
South-West	beta-glucosidase	pH	pH_historic	~	LUI_historic	a	-0.13	0.19	-0.67	0.505	-0.09	0.14	-0.67	0.504
South-West	beta-glucosidase	pH	pH_change	~	LUI_change	b	-0.01	0.12	-0.08	0.933	-0.01	0.14	-0.08	0.933
South-West	beta-glucosidase	pH	Glucosidase	~	pH_historic	c	-0.27	0.12	-2.25	0.025	-0.27	0.12	-2.31	0.021
South-West	beta-glucosidase	pH	Glucosidase	~	pH_change	d	0.20	0.15	1.33	0.183	0.16	0.12	1.34	0.179
South-West	beta-glucosidase	pH	Glucosidase	~	LUI_historic	e	0.32	0.16	2.03	0.042	0.25	0.12	2.08	0.037
South-West	beta-glucosidase	pH	Glucosidase	~	LUI_change	f	-0.28	0.13	-2.22	0.027	-0.27	0.12	-2.28	0.023
South-West	beta-glucosidase	pH	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	beta-glucosidase	pH	pH_historic	~~	pH_historic		0.06	0.01	5.00	0.000	0.99	0.03	37.71	0.000
South-West	beta-glucosidase	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	1.00	0.00	298.93	0.000
South-West	beta-glucosidase	pH	Glucosidase	~~	Glucosidase		0.04	0.01	5.00	0.000	0.73	0.11	6.91	0.000
South-West	beta-glucosidase	pH	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	beta-glucosidase	pH	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	beta-glucosidase	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.03	0.05	0.64	0.523	0.03	0.04	0.65	0.519
South-West	beta-glucosidase	pH	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.02	-0.08	0.933	0.00	0.02	-0.08	0.933
South-West	beta-glucosidase	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.36	0.17	2.15	0.032	0.28	0.12	2.23	0.026
South-West	beta-glucosidase	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.28	0.13	-2.19	0.028	-0.27	0.12	-2.26	0.024
South-West	beta-glucosidase	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.36	0.17	2.16	0.031	0.32	0.13	2.51	0.012
South-West	beta-glucosidase	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.28	0.13	-2.21	0.027	-0.31	0.12	-2.55	0.011

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*p*	est.std	se.std	z.std	*p*.std
South-West	beta-xylosidase	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	1.04	0.14	7.23	0.000	0.72	0.07	10.44	0.000
South-West	beta-xylosidase	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	0.06	0.11	0.57	0.570	0.08	0.14	0.57	0.569
South-West	beta-xylosidase	CWM_leaf_P	Xylosidase	~	CWM_leafP_historic	c	0.42	0.15	2.87	0.004	0.51	0.17	3.04	0.002
South-West	beta-xylosidase	CWM_leaf_P	Xylosidase	~	CWM_leafP_change	d	0.13	0.16	0.85	0.398	0.10	0.12	0.85	0.396
South-West	beta-xylosidase	CWM_leaf_P	Xylosidase	~	LUI_historic	e	-0.17	0.21	-0.77	0.439	-0.14	0.18	-0.78	0.437
South-West	beta-xylosidase	CWM_leaf_P	Xylosidase	~	LUI_change	f	-0.29	0.12	-2.37	0.018	-0.29	0.12	-2.45	0.014
South-West	beta-xylosidase	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	beta-xylosidase	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	4.90	0.000	0.48	0.10	4.80	0.000
South-West	beta-xylosidase	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.03	0.01	4.90	0.000	0.99	0.02	42.42	0.000
South-West	beta-xylosidase	CWM_leaf_P	Xylosidase	~~	Xylosidase		0.04	0.01	4.90	0.000	0.72	0.11	6.66	0.000
South-West	beta-xylosidase	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	beta-xylosidase	CWM_leaf_P	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	beta-xylosidase	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.44	0.17	2.67	0.008	0.37	0.13	2.82	0.005
South-West	beta-xylosidase	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.01	0.02	0.47	0.637	0.01	0.02	0.47	0.638
South-West	beta-xylosidase	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.28	0.16	1.72	0.086	0.23	0.13	1.76	0.078
South-West	beta-xylosidase	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.28	0.12	-2.29	0.022	-0.28	0.12	-2.37	0.018
South-West	beta-xylosidase	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.28	0.16	1.73	0.084	0.26	0.13	1.96	0.050
South-West	beta-xylosidase	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.28	0.12	-2.31	0.021	-0.31	0.12	-2.55	0.011
South-West	beta-xylosidase	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.38	0.18	2.09	0.037	0.29	0.13	2.18	0.029
South-West	beta-xylosidase	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.24	0.11	2.18	0.029	0.30	0.13	2.29	0.022
South-West	beta-xylosidase	CWM_MycInt	Xylosidase	~	CWM_MycInt_historic	c	0.05	0.13	0.42	0.672	0.06	0.14	0.42	0.672
South-West	beta-xylosidase	CWM_MycInt	Xylosidase	~	CWM_MycInt_change	d	-0.07	0.17	-0.41	0.683	-0.06	0.14	-0.41	0.682
South-West	beta-xylosidase	CWM_MycInt	Xylosidase	~	LUI_historic	e	0.28	0.17	1.72	0.085	0.24	0.14	1.77	0.077
South-West	beta-xylosidase	CWM_MycInt	Xylosidase	~	LUI_change	f	-0.17	0.14	-1.24	0.216	-0.18	0.14	-1.25	0.210
South-West	beta-xylosidase	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	beta-xylosidase	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	4.90	0.000	0.92	0.08	12.02	0.000
South-West	beta-xylosidase	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	4.90	0.000	0.91	0.08	11.52	0.000
South-West	beta-xylosidase	CWM_MycInt	Xylosidase	~~	Xylosidase		0.04	0.01	4.90	0.000	0.88	0.09	9.86	0.000
South-West	beta-xylosidase	CWM_MycInt	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	beta-xylosidase	CWM_MycInt	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	beta-xylosidase	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.02	0.05	0.41	0.679	0.02	0.04	0.42	0.678
South-West	beta-xylosidase	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	-0.02	0.04	-0.40	0.688	-0.02	0.04	-0.40	0.687
South-West	beta-xylosidase	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.30	0.16	1.92	0.055	0.26	0.13	1.98	0.047
South-West	beta-xylosidase	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.19	0.13	-1.42	0.155	-0.19	0.13	-1.45	0.148
South-West	beta-xylosidase	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.31	0.16	1.92	0.054	0.28	0.13	2.14	0.032
South-West	beta-xylosidase	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.19	0.13	-1.43	0.152	-0.22	0.14	-1.64	0.102
South-West	beta-xylosidase	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.16	1.17	0.244	0.16	0.14	1.18	0.238
South-West	beta-xylosidase	Plant_biomass	Plant_biomass	~	LUI_change	b	-0.04	0.13	-0.29	0.771	-0.04	0.14	-0.29	0.771
South-West	beta-xylosidase	Plant_biomass	Xylosidase	~	Plant_biomass	c	-0.03	0.14	-0.23	0.818	-0.03	0.14	-0.23	0.818
South-West	beta-xylosidase	Plant_biomass	Xylosidase	~	LUI_historic	e	0.31	0.16	1.96	0.050	0.27	0.13	2.02	0.043
South-West	beta-xylosidase	Plant_biomass	Xylosidase	~	LUI_change	f	-0.16	0.12	-1.33	0.183	-0.18	0.13	-1.35	0.176
South-West	beta-xylosidase	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	beta-xylosidase	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.04	0.01	5.00	0.000	0.97	0.05	20.22	0.000
South-West	beta-xylosidase	Plant_biomass	Xylosidase	~~	Xylosidase		0.04	0.01	5.00	0.000	0.89	0.09	10.43	0.000
South-West	beta-xylosidase	Plant_biomass	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	beta-xylosidase	Plant_biomass	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	beta-xylosidase	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.03	-0.23	0.821	-0.01	0.02	-0.23	0.821
South-West	beta-xylosidase	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	0.18	0.857	0.00	0.01	0.18	0.857
South-West	beta-xylosidase	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.30	0.16	1.94	0.052	0.26	0.13	2.01	0.044
South-West	beta-xylosidase	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.16	0.12	-1.32	0.186	-0.18	0.13	-1.34	0.179
South-West	beta-xylosidase	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.30	0.16	1.95	0.051	0.29	0.13	2.22	0.026
South-West	beta-xylosidase	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.16	0.12	-1.34	0.180	-0.22	0.14	-1.61	0.108
South-West	beta-xylosidase	Lignin_content	Lignin_content	~	LUI_historic	a	0.03	0.19	0.13	0.895	0.02	0.15	0.13	0.895
South-West	beta-xylosidase	Lignin_content	Lignin_content	~	LUI_change	b	0.08	0.15	0.54	0.589	0.08	0.15	0.54	0.588
South-West	beta-xylosidase	Lignin_content	Xylosidase	~	Lignin_content	c	0.00	0.12	0.02	0.984	0.00	0.14	0.02	0.984
South-West	beta-xylosidase	Lignin_content	Xylosidase	~	LUI_historic	e	0.30	0.16	1.92	0.055	0.26	0.13	1.99	0.047
South-West	beta-xylosidase	Lignin_content	Xylosidase	~	LUI_change	f	-0.16	0.12	-1.27	0.205	-0.18	0.14	-1.29	0.199
South-West	beta-xylosidase	Lignin_content	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.95	0.342	-0.14	0.14	-0.98	0.329
South-West	beta-xylosidase	Lignin_content	Lignin_content	~~	Lignin_content		0.06	0.01	4.90	0.000	0.99	0.02	44.29	0.000
South-West	beta-xylosidase	Lignin_content	Xylosidase	~~	Xylosidase		0.04	0.01	4.90	0.000	0.89	0.09	10.31	0.000
South-West	beta-xylosidase	Lignin_content	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	beta-xylosidase	Lignin_content	LUI_change	~~	LUI_change		0.06	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	beta-xylosidase	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.00	0.02	0.984	0.00	0.00	0.02	0.984
South-West	beta-xylosidase	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	0.02	0.984	0.00	0.01	0.02	0.984
South-West	beta-xylosidase	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.30	0.16	1.92	0.054	0.26	0.13	1.99	0.047
South-West	beta-xylosidase	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.16	0.12	-1.27	0.204	-0.17	0.14	-1.29	0.198
South-West	beta-xylosidase	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.31	0.16	1.93	0.054	0.29	0.13	2.18	0.030
South-West	beta-xylosidase	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.16	0.12	-1.29	0.198	-0.21	0.14	-1.53	0.126
South-West	beta-xylosidase	pH	pH_historic	~	LUI_historic	a	-0.13	0.19	-0.67	0.505	-0.09	0.14	-0.67	0.504
South-West	beta-xylosidase	pH	pH_change	~	LUI_change	b	-0.01	0.12	-0.08	0.933	-0.01	0.14	-0.08	0.933
South-West	beta-xylosidase	pH	Xylosidase	~	pH_historic	c	-0.20	0.11	-1.89	0.058	-0.22	0.12	-1.92	0.054
South-West	beta-xylosidase	pH	Xylosidase	~	pH_change	d	0.37	0.13	2.80	0.005	0.33	0.11	2.91	0.004
South-West	beta-xylosidase	pH	Xylosidase	~	LUI_historic	e	0.31	0.14	2.22	0.026	0.26	0.12	2.28	0.023
South-West	beta-xylosidase	pH	Xylosidase	~	LUI_change	f	-0.23	0.11	-2.09	0.037	-0.25	0.12	-2.13	0.033
South-West	beta-xylosidase	pH	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	beta-xylosidase	pH	pH_historic	~~	pH_historic		0.06	0.01	5.00	0.000	0.99	0.03	37.71	0.000
South-West	beta-xylosidase	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	1.00	0.00	298.93	0.000
South-West	beta-xylosidase	pH	Xylosidase	~~	Xylosidase		0.03	0.01	5.00	0.000	0.68	0.11	6.42	0.000
South-West	beta-xylosidase	pH	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	beta-xylosidase	pH	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	beta-xylosidase	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.03	0.04	0.63	0.530	0.02	0.03	0.63	0.527
South-West	beta-xylosidase	pH	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.04	-0.08	0.933	0.00	0.05	-0.08	0.933
South-West	beta-xylosidase	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.34	0.15	2.33	0.020	0.28	0.12	2.40	0.016
South-West	beta-xylosidase	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.23	0.12	-1.98	0.048	-0.25	0.12	-2.03	0.042
South-West	beta-xylosidase	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.34	0.15	2.34	0.019	0.32	0.12	2.68	0.007
South-West	beta-xylosidase	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.24	0.12	-2.00	0.046	-0.29	0.13	-2.32	0.021

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*p*	est.std	se.std	z.std	*p* .std
South-West	chitinase	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	1.04	0.15	7.09	0.000	0.73	0.07	10.31	0.000
South-West	chitinase	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.05	0.10	-0.51	0.607	-0.08	0.15	-0.52	0.606
South-West	chitinase	CWM_leaf_P	Chitinase	~	CWM_leafP_historic	c	0.04	0.15	0.27	0.789	0.06	0.21	0.27	0.789
South-West	chitinase	CWM_leaf_P	Chitinase	~	CWM_leafP_change	d	0.01	0.19	0.06	0.952	0.01	0.15	0.06	0.952
South-West	chitinase	CWM_leaf_P	Chitinase	~	LUI_historic	e	-0.05	0.22	-0.24	0.808	-0.05	0.22	-0.24	0.808
South-West	chitinase	CWM_leaf_P	Chitinase	~	LUI_change	f	-0.14	0.13	-1.11	0.268	-0.17	0.15	-1.12	0.262
South-West	chitinase	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.07	0.285	-0.16	0.15	-1.11	0.267
South-West	chitinase	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.04	0.01	4.74	0.000	0.47	0.10	4.62	0.000
South-West	chitinase	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.02	0.01	4.74	0.000	0.99	0.02	43.86	0.000
South-West	chitinase	CWM_leaf_P	Chitinase	~~	Chitinase		0.04	0.01	4.74	0.000	0.97	0.05	19.80	0.000
South-West	chitinase	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.04	0.01	4.74	0.000	1.00	0.00	NA	NA
South-West	chitinase	CWM_leaf_P	LUI_change	~~	LUI_change		0.05	0.01	4.74	0.000	1.00	0.00	NA	NA
South-West	chitinase	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.04	0.16	0.27	0.789	0.04	0.16	0.27	0.789
South-West	chitinase	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	-0.06	0.952	0.00	0.01	-0.06	0.952
South-West	chitinase	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.01	0.15	-0.07	0.943	-0.01	0.15	-0.07	0.943
South-West	chitinase	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.14	0.13	-1.12	0.265	-0.17	0.15	-1.13	0.258
South-West	chitinase	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.01	0.15	-0.07	0.948	0.02	0.15	0.11	0.914
South-West	chitinase	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.14	0.13	-1.12	0.264	-0.16	0.15	-1.13	0.257
South-West	chitinase	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.40	0.19	2.14	0.032	0.30	0.14	2.25	0.025
South-West	chitinase	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.18	0.11	1.67	0.095	0.24	0.14	1.72	0.086
South-West	chitinase	CWM_MycInt	Chitinase	~	CWM_MycInt_historic	c	-0.10	0.12	-0.84	0.403	-0.13	0.15	-0.84	0.400
South-West	chitinase	CWM_MycInt	Chitinase	~	CWM_MycInt_change	d	-0.11	0.17	-0.63	0.529	-0.10	0.15	-0.63	0.527
South-West	chitinase	CWM_MycInt	Chitinase	~	LUI_historic	e	0.02	0.16	0.13	0.897	0.02	0.16	0.13	0.897
South-West	chitinase	CWM_MycInt	Chitinase	~	LUI_change	f	-0.10	0.13	-0.76	0.447	-0.12	0.15	-0.77	0.445
South-West	chitinase	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.07	0.285	-0.16	0.15	-1.11	0.267
South-West	chitinase	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.06	0.01	4.74	0.000	0.91	0.08	11.04	0.000
South-West	chitinase	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	4.74	0.000	0.94	0.07	13.90	0.000
South-West	chitinase	CWM_MycInt	Chitinase	~~	Chitinase		0.04	0.01	4.74	0.000	0.96	0.06	16.44	0.000
South-West	chitinase	CWM_MycInt	LUI_historic	~~	LUI_historic		0.04	0.01	4.74	0.000	1.00	0.00	NA	NA
South-West	chitinase	CWM_MycInt	LUI_change	~~	LUI_change		0.05	0.01	4.74	0.000	1.00	0.00	NA	NA
South-West	chitinase	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	-0.04	0.05	-0.78	0.436	-0.04	0.05	-0.78	0.433
South-West	chitinase	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	-0.02	0.03	-0.59	0.556	-0.02	0.04	-0.59	0.554
South-West	chitinase	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.02	0.15	-0.13	0.899	-0.02	0.15	-0.13	0.899
South-West	chitinase	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.12	0.13	-0.93	0.351	-0.14	0.15	-0.94	0.346
South-West	chitinase	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.02	0.15	-0.12	0.903	0.00	0.15	0.02	0.982
South-West	chitinase	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.12	0.13	-0.93	0.351	-0.14	0.15	-0.93	0.351
South-West	chitinase	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.18	0.17	1.08	0.279	0.16	0.15	1.10	0.273
South-West	chitinase	Plant_biomass	Plant_biomass	~	LUI_change	b	-0.03	0.13	-0.24	0.809	-0.04	0.15	-0.24	0.809
South-West	chitinase	Plant_biomass	Chitinase	~	Plant_biomass	c	0.11	0.13	0.84	0.399	0.12	0.14	0.85	0.396
South-West	chitinase	Plant_biomass	Chitinase	~	LUI_historic	e	-0.03	0.15	-0.19	0.853	-0.03	0.15	-0.19	0.853
South-West	chitinase	Plant_biomass	Chitinase	~	LUI_change	f	-0.12	0.12	-0.97	0.332	-0.14	0.15	-0.98	0.327
South-West	chitinase	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.29	0.198	-0.19	0.14	-1.36	0.174
South-West	chitinase	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.04	0.01	4.85	0.000	0.97	0.05	20.30	0.000
South-West	chitinase	Plant_biomass	Chitinase	~~	Chitinase		0.03	0.01	4.85	0.000	0.96	0.05	18.18	0.000
South-West	chitinase	Plant_biomass	LUI_historic	~~	LUI_historic		0.04	0.01	4.85	0.000	1.00	0.00	NA	NA
South-West	chitinase	Plant_biomass	LUI_change	~~	LUI_change		0.05	0.01	4.85	0.000	1.00	0.00	NA	NA
South-West	chitinase	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.02	0.03	0.67	0.506	0.02	0.03	0.67	0.504
South-West	chitinase	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.02	-0.23	0.816	0.00	0.02	-0.23	0.816
South-West	chitinase	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.01	0.15	-0.05	0.957	-0.01	0.15	-0.05	0.957
South-West	chitinase	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.12	0.12	-0.99	0.321	-0.15	0.15	-1.00	0.316
South-West	chitinase	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.01	0.15	-0.05	0.962	0.02	0.15	0.14	0.891
South-West	chitinase	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.12	0.12	-1.00	0.320	-0.15	0.14	-1.01	0.312
South-West	chitinase	Lignin_content	Lignin_content	~	LUI_historic	a	-0.03	0.20	-0.16	0.876	-0.02	0.15	-0.16	0.876
South-West	chitinase	Lignin_content	Lignin_content	~	LUI_change	b	0.03	0.16	0.19	0.854	0.03	0.15	0.19	0.853
South-West	chitinase	Lignin_content	Chitinase	~	Lignin_content	c	-0.08	0.11	-0.74	0.459	-0.11	0.15	-0.75	0.456
South-West	chitinase	Lignin_content	Chitinase	~	LUI_historic	e	0.02	0.15	0.11	0.909	0.02	0.15	0.11	0.909
South-West	chitinase	Lignin_content	Chitinase	~	LUI_change	f	-0.12	0.12	-1.00	0.320	-0.15	0.15	-1.01	0.315
South-West	chitinase	Lignin_content	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.21	0.228	-0.18	0.14	-1.27	0.205
South-West	chitinase	Lignin_content	Lignin_content	~~	Lignin_content		0.06	0.01	4.74	0.000	1.00	0.01	84.30	0.000
South-West	chitinase	Lignin_content	Chitinase	~~	Chitinase		0.03	0.01	4.74	0.000	0.96	0.06	17.66	0.000
South-West	chitinase	Lignin_content	LUI_historic	~~	LUI_historic		0.04	0.01	4.74	0.000	1.00	0.00	NA	NA
South-West	chitinase	Lignin_content	LUI_change	~~	LUI_change		0.06	0.01	4.74	0.000	1.00	0.00	NA	NA
South-West	chitinase	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	0.15	0.879	0.00	0.02	0.15	0.879
South-West	chitinase	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	-0.18	0.858	0.00	0.02	-0.18	0.858
South-West	chitinase	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.02	0.15	0.13	0.896	0.02	0.15	0.13	0.896
South-West	chitinase	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.12	0.12	-1.01	0.313	-0.15	0.15	-1.02	0.307
South-West	chitinase	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.02	0.15	0.14	0.891	0.05	0.15	0.32	0.751
South-West	chitinase	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.12	0.12	-1.01	0.311	-0.16	0.15	-1.06	0.288
South-West	chitinase	pH	pH_historic	~	LUI_historic	a	-0.08	0.19	-0.44	0.661	-0.06	0.15	-0.44	0.660
South-West	chitinase	pH	pH_change	~	LUI_change	b	-0.02	0.13	-0.15	0.884	-0.02	0.15	-0.15	0.884
South-West	chitinase	pH	Chitinase	~	pH_historic	c	-0.26	0.10	-2.46	0.014	-0.33	0.13	-2.58	0.010
South-West	chitinase	pH	Chitinase	~	pH_change	d	0.09	0.13	0.72	0.473	0.10	0.13	0.72	0.472
South-West	chitinase	pH	Chitinase	~	LUI_historic	e	-0.04	0.14	-0.29	0.775	-0.04	0.14	-0.29	0.775
South-West	chitinase	pH	Chitinase	~	LUI_change	f	-0.21	0.11	-1.89	0.059	-0.25	0.13	-1.94	0.052
South-West	chitinase	pH	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.29	0.198	-0.19	0.14	-1.36	0.174
South-West	chitinase	pH	pH_historic	~~	pH_historic		0.06	0.01	4.85	0.000	1.00	0.02	53.70	0.000
South-West	chitinase	pH	pH_change	~~	pH_change		0.04	0.01	4.85	0.000	1.00	0.01	160.82	0.000
South-West	chitinase	pH	Chitinase	~~	Chitinase		0.03	0.01	4.85	0.000	0.82	0.10	8.29	0.000
South-West	chitinase	pH	LUI_historic	~~	LUI_historic		0.04	0.01	4.85	0.000	1.00	0.00	NA	NA
South-West	chitinase	pH	LUI_change	~~	LUI_change		0.05	0.01	4.85	0.000	1.00	0.00	NA	NA
South-West	chitinase	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.02	0.05	0.43	0.666	0.02	0.05	0.43	0.665
South-West	chitinase	pH	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	-0.14	0.886	0.00	0.01	-0.14	0.886
South-West	chitinase	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.02	0.15	-0.13	0.901	-0.02	0.14	-0.13	0.901
South-West	chitinase	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.21	0.11	-1.89	0.058	-0.26	0.13	-1.95	0.051
South-West	chitinase	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.02	0.15	-0.11	0.910	0.03	0.15	0.22	0.830
South-West	chitinase	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.21	0.11	-1.90	0.058	-0.25	0.13	-1.96	0.051

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*p*	est.std	se.std	z.std	*p*.std
South-West	urease	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	1.04	0.14	7.23	0.000	0.72	0.07	10.44	0.000
South-West	urease	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	0.06	0.11	0.57	0.570	0.08	0.14	0.57	0.569
South-West	urease	CWM_leaf_P	Urease	~	CWM_leafP_historic	c	-0.30	0.14	-2.13	0.033	-0.40	0.18	-2.22	0.027
South-West	urease	CWM_leaf_P	Urease	~	CWM_leafP_change	d	0.26	0.15	1.79	0.074	0.24	0.13	1.83	0.067
South-West	urease	CWM_leaf_P	Urease	~	LUI_historic	e	0.10	0.20	0.47	0.637	0.09	0.19	0.47	0.637
South-West	urease	CWM_leaf_P	Urease	~	LUI_change	f	0.02	0.12	0.15	0.880	0.02	0.13	0.15	0.880
South-West	urease	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	urease	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	4.90	0.000	0.48	0.10	4.80	0.000
South-West	urease	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.03	0.01	4.90	0.000	0.99	0.02	42.42	0.000
South-West	urease	CWM_leaf_P	Urease	~~	Urease		0.03	0.01	4.90	0.000	0.82	0.10	8.40	0.000
South-West	urease	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	urease	CWM_leaf_P	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	urease	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	-0.31	0.15	-2.05	0.041	-0.29	0.14	-2.12	0.034
South-West	urease	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.02	0.03	0.54	0.589	0.02	0.04	0.54	0.587
South-West	urease	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.21	0.15	-1.46	0.143	-0.20	0.14	-1.49	0.136
South-West	urease	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.03	0.12	0.29	0.773	0.04	0.14	0.29	0.773
South-West	urease	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.21	0.15	-1.47	0.143	-0.21	0.13	-1.54	0.125
South-West	urease	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.04	0.12	0.30	0.766	0.06	0.14	0.45	0.651
South-West	urease	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.38	0.18	2.09	0.037	0.29	0.13	2.18	0.029
South-West	urease	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.24	0.11	2.18	0.029	0.30	0.13	2.29	0.022
South-West	urease	CWM_MycInt	Urease	~	CWM_MycInt_historic	c	-0.31	0.11	-2.82	0.005	-0.39	0.13	-3.03	0.002
South-West	urease	CWM_MycInt	Urease	~	CWM_MycInt_change	d	0.05	0.15	0.30	0.765	0.04	0.14	0.30	0.765
South-West	urease	CWM_MycInt	Urease	~	LUI_historic	e	-0.06	0.15	-0.40	0.688	-0.06	0.14	-0.40	0.688
South-West	urease	CWM_MycInt	Urease	~	LUI_change	f	-0.01	0.12	-0.11	0.915	-0.02	0.14	-0.11	0.915
South-West	urease	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	urease	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	4.90	0.000	0.92	0.08	12.02	0.000
South-West	urease	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	4.90	0.000	0.91	0.08	11.52	0.000
South-West	urease	CWM_MycInt	Urease	~~	Urease		0.03	0.01	4.90	0.000	0.83	0.10	8.48	0.000
South-West	urease	CWM_MycInt	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	urease	CWM_MycInt	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	urease	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	-0.12	0.07	-1.68	0.094	-0.11	0.06	-1.73	0.083
South-West	urease	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.01	0.04	0.30	0.767	0.01	0.04	0.30	0.767
South-West	urease	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.18	0.15	-1.17	0.242	-0.17	0.14	-1.19	0.236
South-West	urease	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.00	0.11	-0.02	0.985	0.00	0.13	-0.02	0.985
South-West	urease	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.18	0.15	-1.17	0.242	-0.17	0.14	-1.19	0.234
South-West	urease	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.00	0.11	-0.01	0.991	0.02	0.13	0.13	0.900
South-West	urease	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.16	1.17	0.244	0.16	0.14	1.18	0.238
South-West	urease	Plant_biomass	Plant_biomass	~	LUI_change	b	-0.04	0.13	-0.29	0.771	-0.04	0.14	-0.29	0.771
South-West	urease	Plant_biomass	Urease	~	Plant_biomass	c	-0.09	0.13	-0.70	0.481	-0.10	0.14	-0.71	0.479
South-West	urease	Plant_biomass	Urease	~	LUI_historic	e	-0.18	0.15	-1.18	0.238	-0.17	0.14	-1.20	0.232
South-West	urease	Plant_biomass	Urease	~	LUI_change	f	0.01	0.12	0.06	0.954	0.01	0.14	0.06	0.954
South-West	urease	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	urease	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.04	0.01	5.00	0.000	0.97	0.05	20.22	0.000
South-West	urease	Plant_biomass	Urease	~~	Urease		0.04	0.01	5.00	0.000	0.96	0.06	16.87	0.000
South-West	urease	Plant_biomass	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	urease	Plant_biomass	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	urease	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	-0.02	0.03	-0.60	0.547	-0.02	0.03	-0.61	0.545
South-West	urease	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	0.27	0.788	0.00	0.02	0.27	0.788
South-West	urease	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.20	0.15	-1.31	0.192	-0.18	0.14	-1.33	0.184
South-West	urease	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.01	0.12	0.09	0.931	0.01	0.14	0.09	0.931
South-West	urease	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.20	0.15	-1.31	0.191	-0.19	0.14	-1.36	0.175
South-West	urease	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.01	0.12	0.10	0.923	0.04	0.14	0.28	0.782
South-West	urease	Lignin_content	Lignin_content	~	LUI_historic	a	0.03	0.19	0.13	0.895	0.02	0.15	0.13	0.895
South-West	urease	Lignin_content	Lignin_content	~	LUI_change	b	0.08	0.15	0.54	0.589	0.08	0.15	0.54	0.588
South-West	urease	Lignin_content	Urease	~	Lignin_content	c	0.01	0.11	0.10	0.921	0.01	0.14	0.10	0.921
South-West	urease	Lignin_content	Urease	~	LUI_historic	e	-0.23	0.15	-1.52	0.129	-0.22	0.14	-1.55	0.120
South-West	urease	Lignin_content	Urease	~	LUI_change	f	0.02	0.12	0.15	0.883	0.02	0.14	0.15	0.883
South-West	urease	Lignin_content	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.95	0.342	-0.14	0.14	-0.98	0.329
South-West	urease	Lignin_content	Lignin_content	~~	Lignin_content		0.06	0.01	4.90	0.000	0.99	0.02	44.29	0.000
South-West	urease	Lignin_content	Urease	~~	Urease		0.04	0.01	4.90	0.000	0.95	0.06	15.74	0.000
South-West	urease	Lignin_content	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	urease	Lignin_content	LUI_change	~~	LUI_change		0.06	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	urease	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.00	0.08	0.937	0.00	0.00	0.08	0.937
South-West	urease	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	0.10	0.923	0.00	0.01	0.10	0.923
South-West	urease	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.23	0.15	-1.52	0.130	-0.22	0.14	-1.55	0.121
South-West	urease	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.02	0.12	0.16	0.877	0.02	0.14	0.16	0.877
South-West	urease	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.23	0.15	-1.52	0.129	-0.22	0.14	-1.59	0.112
South-West	urease	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.02	0.12	0.17	0.867	0.05	0.14	0.36	0.719
South-West	urease	pH	pH_historic	~	LUI_historic	a	-0.13	0.19	-0.67	0.505	-0.09	0.14	-0.67	0.504
South-West	urease	pH	pH_change	~	LUI_change	b	-0.01	0.12	-0.08	0.933	-0.01	0.14	-0.08	0.933
South-West	urease	pH	Urease	~	pH_historic	c	0.03	0.11	0.31	0.758	0.04	0.14	0.31	0.758
South-West	urease	pH	Urease	~	pH_change	d	-0.02	0.14	-0.11	0.917	-0.02	0.14	-0.11	0.917
South-West	urease	pH	Urease	~	LUI_historic	e	-0.19	0.15	-1.27	0.205	-0.18	0.14	-1.29	0.198
South-West	urease	pH	Urease	~	LUI_change	f	0.02	0.12	0.20	0.844	0.03	0.14	0.20	0.844
South-West	urease	pH	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	urease	pH	pH_historic	~~	pH_historic		0.06	0.01	5.00	0.000	0.99	0.03	37.71	0.000
South-West	urease	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	1.00	0.00	298.93	0.000
South-West	urease	pH	Urease	~~	Urease		0.04	0.01	5.00	0.000	0.96	0.05	18.21	0.000
South-West	urease	pH	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	urease	pH	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	urease	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	-0.28	0.780	0.00	0.01	-0.28	0.780
South-West	urease	pH	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.00	0.07	0.948	0.00	0.00	0.07	0.948
South-West	urease	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.20	0.15	-1.30	0.193	-0.18	0.14	-1.32	0.186
South-West	urease	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.02	0.12	0.20	0.843	0.03	0.14	0.20	0.843
South-West	urease	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.20	0.15	-1.30	0.192	-0.19	0.14	-1.37	0.171
South-West	urease	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.02	0.12	0.21	0.835	0.06	0.14	0.39	0.698

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*p*	est.std	se.std	z.std	*p*.std
South-West	DEA	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	1.04	0.14	7.23	0.000	0.72	0.07	10.44	0.000
South-West	DEA	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	0.06	0.11	0.57	0.570	0.08	0.14	0.57	0.569
South-West	DEA	CWM_leaf_P	DEA	~	CWM_leafP_historic	c	0.34	0.13	2.70	0.007	0.46	0.16	2.82	0.005
South-West	DEA	CWM_leaf_P	DEA	~	CWM_leafP_change	d	0.34	0.13	2.56	0.010	0.30	0.11	2.64	0.008
South-West	DEA	CWM_leaf_P	DEA	~	LUI_historic	e	0.07	0.18	0.37	0.715	0.06	0.17	0.37	0.715
South-West	DEA	CWM_leaf_P	DEA	~	LUI_change	f	0.09	0.10	0.83	0.409	0.10	0.12	0.83	0.407
South-West	DEA	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	DEA	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	4.90	0.000	0.48	0.10	4.80	0.000
South-West	DEA	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.03	0.01	4.90	0.000	0.99	0.02	42.42	0.000
South-West	DEA	CWM_leaf_P	DEA	~~	DEA		0.03	0.01	4.90	0.000	0.66	0.11	6.11	0.000
South-West	DEA	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	DEA	CWM_leaf_P	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	DEA	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.35	0.14	2.53	0.012	0.33	0.12	2.65	0.008
South-West	DEA	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.02	0.04	0.55	0.579	0.02	0.04	0.56	0.578
South-West	DEA	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.42	0.13	3.10	0.002	0.39	0.12	3.33	0.001
South-West	DEA	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.11	0.11	0.97	0.330	0.12	0.13	0.98	0.328
South-West	DEA	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.42	0.13	3.09	0.002	0.38	0.12	3.18	0.001
South-West	DEA	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.10	0.11	0.96	0.339	0.08	0.14	0.56	0.573
South-West	DEA	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.38	0.18	2.09	0.037	0.29	0.13	2.18	0.029
South-West	DEA	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.24	0.11	2.18	0.029	0.30	0.13	2.29	0.022
South-West	DEA	CWM_MycInt	DEA	~	CWM_MycInt_historic	c	0.14	0.11	1.30	0.194	0.17	0.13	1.31	0.189
South-West	DEA	CWM_MycInt	DEA	~	CWM_MycInt_change	d	-0.01	0.15	-0.10	0.924	-0.01	0.13	-0.10	0.924
South-West	DEA	CWM_MycInt	DEA	~	LUI_historic	e	0.42	0.14	2.97	0.003	0.39	0.12	3.18	0.001
South-West	DEA	CWM_MycInt	DEA	~	LUI_change	f	0.18	0.12	1.54	0.125	0.20	0.13	1.56	0.120
South-West	DEA	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	DEA	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	4.90	0.000	0.92	0.08	12.02	0.000
South-West	DEA	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	4.90	0.000	0.91	0.08	11.52	0.000
South-West	DEA	CWM_MycInt	DEA	~~	DEA		0.03	0.01	4.90	0.000	0.76	0.11	7.07	0.000
South-West	DEA	CWM_MycInt	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	DEA	CWM_MycInt	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	DEA	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.05	0.05	1.10	0.270	0.05	0.04	1.12	0.263
South-West	DEA	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.04	-0.10	0.924	0.00	0.04	-0.10	0.924
South-West	DEA	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.48	0.14	3.43	0.001	0.44	0.12	3.79	0.000
South-West	DEA	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.18	0.11	1.58	0.114	0.20	0.13	1.60	0.109
South-West	DEA	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.48	0.14	3.43	0.001	0.42	0.12	3.52	0.000
South-West	DEA	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.17	0.11	1.56	0.119	0.15	0.14	1.07	0.286
South-West	DEA	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.16	1.17	0.244	0.16	0.14	1.18	0.238
South-West	DEA	Plant_biomass	Plant_biomass	~	LUI_change	b	-0.04	0.13	-0.29	0.771	-0.04	0.14	-0.29	0.771
South-West	DEA	Plant_biomass	DEA	~	Plant_biomass	c	0.04	0.12	0.33	0.740	0.04	0.13	0.33	0.740
South-West	DEA	Plant_biomass	DEA	~	LUI_historic	e	0.48	0.14	3.46	0.001	0.44	0.12	3.81	0.000
South-West	DEA	Plant_biomass	DEA	~	LUI_change	f	0.18	0.11	1.67	0.095	0.21	0.12	1.70	0.089
South-West	DEA	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	DEA	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.04	0.01	5.00	0.000	0.97	0.05	20.22	0.000
South-West	DEA	Plant_biomass	DEA	~~	DEA		0.03	0.01	5.00	0.000	0.78	0.10	7.54	0.000
South-West	DEA	Plant_biomass	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	DEA	Plant_biomass	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	DEA	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.02	0.32	0.750	0.01	0.02	0.32	0.750
South-West	DEA	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	-0.22	0.827	0.00	0.01	-0.22	0.827
South-West	DEA	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.48	0.14	3.56	0.000	0.45	0.11	3.94	0.000
South-West	DEA	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.18	0.11	1.66	0.097	0.21	0.12	1.68	0.092
South-West	DEA	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.48	0.14	3.55	0.000	0.42	0.12	3.59	0.000
South-West	DEA	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.17	0.11	1.63	0.103	0.14	0.14	1.03	0.301
South-West	DEA	Lignin_content	Lignin_content	~	LUI_historic	a	0.03	0.19	0.13	0.895	0.02	0.15	0.13	0.895
South-West	DEA	Lignin_content	Lignin_content	~	LUI_change	b	0.08	0.15	0.54	0.589	0.08	0.15	0.54	0.588
South-West	DEA	Lignin_content	DEA	~	Lignin_content	c	0.07	0.10	0.68	0.498	0.09	0.13	0.68	0.497
South-West	DEA	Lignin_content	DEA	~	LUI_historic	e	0.46	0.14	3.33	0.001	0.43	0.12	3.65	0.000
South-West	DEA	Lignin_content	DEA	~	LUI_change	f	0.18	0.11	1.65	0.100	0.21	0.13	1.68	0.094
South-West	DEA	Lignin_content	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.95	0.342	-0.14	0.14	-0.98	0.329
South-West	DEA	Lignin_content	Lignin_content	~~	Lignin_content		0.06	0.01	4.90	0.000	0.99	0.02	44.29	0.000
South-West	DEA	Lignin_content	DEA	~~	DEA		0.03	0.01	4.90	0.000	0.78	0.11	7.46	0.000
South-West	DEA	Lignin_content	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	DEA	Lignin_content	LUI_change	~~	LUI_change		0.06	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	DEA	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	0.13	0.897	0.00	0.01	0.13	0.897
South-West	DEA	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.01	0.01	0.42	0.673	0.01	0.02	0.42	0.672
South-West	DEA	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.46	0.14	3.33	0.001	0.43	0.12	3.66	0.000
South-West	DEA	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.18	0.11	1.70	0.090	0.22	0.13	1.73	0.084
South-West	DEA	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.46	0.14	3.32	0.001	0.40	0.12	3.31	0.001
South-West	DEA	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.18	0.11	1.67	0.095	0.16	0.14	1.14	0.255
South-West	DEA	pH	pH_historic	~	LUI_historic	a	-0.13	0.19	-0.67	0.505	-0.09	0.14	-0.67	0.504
South-West	DEA	pH	pH_change	~	LUI_change	b	-0.01	0.12	-0.08	0.933	-0.01	0.14	-0.08	0.933
South-West	DEA	pH	DEA	~	pH_historic	c	0.15	0.10	1.50	0.135	0.18	0.12	1.51	0.131
South-West	DEA	pH	DEA	~	pH_change	d	0.09	0.12	0.75	0.451	0.09	0.12	0.76	0.450
South-West	DEA	pH	DEA	~	LUI_historic	e	0.53	0.13	3.93	0.000	0.48	0.11	4.36	0.000
South-West	DEA	pH	DEA	~	LUI_change	f	0.24	0.10	2.27	0.023	0.27	0.12	2.33	0.020
South-West	DEA	pH	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	DEA	pH	pH_historic	~~	pH_historic		0.06	0.01	5.00	0.000	0.99	0.03	37.71	0.000
South-West	DEA	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	1.00	0.00	298.93	0.000
South-West	DEA	pH	DEA	~~	DEA		0.03	0.01	5.00	0.000	0.71	0.11	6.63	0.000
South-West	DEA	pH	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	DEA	pH	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	DEA	pH	LUI_hist_in	:=	a*c	LUI_hist_in	-0.02	0.03	-0.61	0.543	-0.02	0.03	-0.61	0.544
South-West	DEA	pH	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	-0.08	0.934	0.00	0.01	-0.08	0.934
South-West	DEA	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.51	0.14	3.73	0.000	0.46	0.11	4.13	0.000
South-West	DEA	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.24	0.11	2.25	0.025	0.27	0.12	2.31	0.021
South-West	DEA	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.51	0.14	3.72	0.000	0.42	0.12	3.61	0.000
South-West	DEA	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.23	0.11	2.22	0.026	0.21	0.13	1.54	0.124

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*p*	est.std	se.std	z.std	*p*.std
South-West	phosphatase	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	1.04	0.14	7.23	0.000	0.72	0.07	10.44	0.000
South-West	phosphatase	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	0.06	0.11	0.57	0.570	0.08	0.14	0.57	0.569
South-West	phosphatase	CWM_leaf_P	Phosphatase	~	CWM_leafP_historic	c	0.17	0.16	1.08	0.283	0.22	0.20	1.09	0.277
South-West	phosphatase	CWM_leaf_P	Phosphatase	~	CWM_leafP_change	d	-0.04	0.17	-0.25	0.800	-0.04	0.14	-0.25	0.800
South-West	phosphatase	CWM_leaf_P	Phosphatase	~	LUI_historic	e	0.01	0.23	0.06	0.951	0.01	0.20	0.06	0.951
South-West	phosphatase	CWM_leaf_P	Phosphatase	~	LUI_change	f	-0.06	0.13	-0.46	0.642	-0.07	0.14	-0.47	0.642
South-West	phosphatase	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	phosphatase	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	4.90	0.000	0.48	0.10	4.80	0.000
South-West	phosphatase	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.03	0.01	4.90	0.000	0.99	0.02	42.42	0.000
South-West	phosphatase	CWM_leaf_P	Phosphatase	~~	Phosphatase		0.04	0.01	4.90	0.000	0.94	0.07	14.17	0.000
South-West	phosphatase	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	phosphatase	CWM_leaf_P	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	phosphatase	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.18	0.17	1.06	0.288	0.16	0.15	1.08	0.282
South-West	phosphatase	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	-0.23	0.817	0.00	0.01	-0.23	0.817
South-West	phosphatase	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.19	0.16	1.19	0.235	0.17	0.14	1.21	0.228
South-West	phosphatase	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.06	0.13	-0.49	0.627	-0.07	0.14	-0.49	0.626
South-West	phosphatase	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.19	0.16	1.19	0.234	0.18	0.14	1.27	0.204
South-West	phosphatase	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.06	0.13	-0.49	0.622	-0.09	0.14	-0.62	0.534
South-West	phosphatase	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.38	0.18	2.09	0.037	0.29	0.13	2.18	0.029
South-West	phosphatase	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.24	0.11	2.18	0.029	0.30	0.13	2.29	0.022
South-West	phosphatase	CWM_MycInt	Phosphatase	~	CWM_MycInt_historic	c	-0.19	0.13	-1.49	0.137	-0.22	0.14	-1.52	0.129
South-West	phosphatase	CWM_MycInt	Phosphatase	~	CWM_MycInt_change	d	-0.08	0.17	-0.46	0.644	-0.07	0.15	-0.46	0.643
South-West	phosphatase	CWM_MycInt	Phosphatase	~	LUI_historic	e	0.26	0.16	1.56	0.118	0.23	0.14	1.60	0.109
South-West	phosphatase	CWM_MycInt	Phosphatase	~	LUI_change	f	0.01	0.14	0.08	0.935	0.01	0.15	0.08	0.935
South-West	phosphatase	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	phosphatase	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	4.90	0.000	0.92	0.08	12.02	0.000
South-West	phosphatase	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	4.90	0.000	0.91	0.08	11.52	0.000
South-West	phosphatase	CWM_MycInt	Phosphatase	~~	Phosphatase		0.04	0.01	4.90	0.000	0.93	0.07	12.70	0.000
South-West	phosphatase	CWM_MycInt	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	phosphatase	CWM_MycInt	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	phosphatase	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	-0.07	0.06	-1.21	0.226	-0.06	0.05	-1.22	0.221
South-West	phosphatase	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	-0.02	0.04	-0.45	0.651	-0.02	0.05	-0.45	0.650
South-West	phosphatase	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.19	0.16	1.16	0.245	0.17	0.14	1.18	0.239
South-West	phosphatase	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.01	0.13	-0.06	0.953	-0.01	0.14	-0.06	0.953
South-West	phosphatase	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.19	0.16	1.16	0.245	0.17	0.14	1.19	0.233
South-West	phosphatase	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.01	0.13	-0.07	0.948	-0.03	0.14	-0.19	0.846
South-West	phosphatase	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.16	1.17	0.244	0.16	0.14	1.18	0.238
South-West	phosphatase	Plant_biomass	Plant_biomass	~	LUI_change	b	-0.04	0.13	-0.29	0.771	-0.04	0.14	-0.29	0.771
South-West	phosphatase	Plant_biomass	Phosphatase	~	Plant_biomass	c	-0.07	0.14	-0.52	0.602	-0.07	0.14	-0.52	0.601
South-West	phosphatase	Plant_biomass	Phosphatase	~	LUI_historic	e	0.20	0.16	1.24	0.215	0.18	0.14	1.26	0.208
South-West	phosphatase	Plant_biomass	Phosphatase	~	LUI_change	f	-0.03	0.12	-0.22	0.825	-0.03	0.14	-0.22	0.825
South-West	phosphatase	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	phosphatase	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.04	0.01	5.00	0.000	0.97	0.05	20.22	0.000
South-West	phosphatase	Plant_biomass	Phosphatase	~~	Phosphatase		0.04	0.01	5.00	0.000	0.97	0.05	19.05	0.000
South-West	phosphatase	Plant_biomass	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	phosphatase	Plant_biomass	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	phosphatase	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.03	-0.48	0.634	-0.01	0.03	-0.48	0.633
South-West	phosphatase	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	0.25	0.799	0.00	0.01	0.25	0.799
South-West	phosphatase	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.18	0.16	1.17	0.243	0.16	0.14	1.18	0.237
South-West	phosphatase	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.03	0.12	-0.20	0.842	-0.03	0.14	-0.20	0.842
South-West	phosphatase	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.19	0.16	1.17	0.243	0.17	0.14	1.23	0.220
South-West	phosphatase	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.03	0.12	-0.21	0.834	-0.05	0.14	-0.37	0.710
South-West	phosphatase	Lignin_content	Lignin_content	~	LUI_historic	a	0.03	0.19	0.13	0.895	0.02	0.15	0.13	0.895
South-West	phosphatase	Lignin_content	Lignin_content	~	LUI_change	b	0.08	0.15	0.54	0.589	0.08	0.15	0.54	0.588
South-West	phosphatase	Lignin_content	Phosphatase	~	Lignin_content	c	-0.27	0.11	-2.37	0.018	-0.32	0.13	-2.50	0.012
South-West	phosphatase	Lignin_content	Phosphatase	~	LUI_historic	e	0.20	0.15	1.35	0.176	0.18	0.13	1.37	0.170
South-West	phosphatase	Lignin_content	Phosphatase	~	LUI_change	f	0.00	0.12	0.01	0.990	0.00	0.14	0.01	0.990
South-West	phosphatase	Lignin_content	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.95	0.342	-0.14	0.14	-0.98	0.329
South-West	phosphatase	Lignin_content	Lignin_content	~~	Lignin_content		0.06	0.01	4.90	0.000	0.99	0.02	44.29	0.000
South-West	phosphatase	Lignin_content	Phosphatase	~~	Phosphatase		0.04	0.01	4.90	0.000	0.87	0.09	9.44	0.000
South-West	phosphatase	Lignin_content	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	phosphatase	Lignin_content	LUI_change	~~	LUI_change		0.06	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	phosphatase	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.05	-0.13	0.896	-0.01	0.05	-0.13	0.896
South-West	phosphatase	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	-0.02	0.04	-0.53	0.598	-0.03	0.05	-0.53	0.597
South-West	phosphatase	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.20	0.16	1.24	0.216	0.18	0.14	1.26	0.209
South-West	phosphatase	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.02	0.12	-0.16	0.870	-0.02	0.14	-0.16	0.870
South-West	phosphatase	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.20	0.16	1.24	0.216	0.18	0.14	1.29	0.196
South-West	phosphatase	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.02	0.12	-0.17	0.863	-0.05	0.14	-0.33	0.739
South-West	phosphatase	pH	pH_historic	~	LUI_historic	a	-0.13	0.19	-0.67	0.505	-0.09	0.14	-0.67	0.504
South-West	phosphatase	pH	pH_change	~	LUI_change	b	-0.01	0.12	-0.08	0.933	-0.01	0.14	-0.08	0.933
South-West	phosphatase	pH	Phosphatase	~	pH_historic	c	-0.66	0.08	-8.31	0.000	-0.72	0.06	-11.21	0.000
South-West	phosphatase	pH	Phosphatase	~	pH_change	d	-0.02	0.10	-0.17	0.869	-0.01	0.09	-0.17	0.869
South-West	phosphatase	pH	Phosphatase	~	LUI_historic	e	0.05	0.11	0.48	0.634	0.04	0.09	0.48	0.635
South-West	phosphatase	pH	Phosphatase	~	LUI_change	f	-0.28	0.08	-3.38	0.001	-0.30	0.09	-3.34	0.001
South-West	phosphatase	pH	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	phosphatase	pH	pH_historic	~~	pH_historic		0.06	0.01	5.00	0.000	0.99	0.03	37.71	0.000
South-West	phosphatase	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	1.00	0.00	298.93	0.000
South-West	phosphatase	pH	Phosphatase	~~	Phosphatase		0.02	0.00	5.00	0.000	0.37	0.08	4.64	0.000
South-West	phosphatase	pH	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	phosphatase	pH	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	phosphatase	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.08	0.13	0.66	0.507	0.07	0.10	0.67	0.503
South-West	phosphatase	pH	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.00	0.08	0.941	0.00	0.00	0.08	0.941
South-West	phosphatase	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.13	0.16	0.82	0.414	0.11	0.13	0.82	0.410
South-West	phosphatase	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.28	0.08	-3.38	0.001	-0.30	0.09	-3.33	0.001
South-West	phosphatase	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.14	0.16	0.83	0.408	0.15	0.14	1.11	0.268
South-West	phosphatase	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.28	0.08	-3.39	0.001	-0.31	0.09	-3.49	0.000

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*p*	est.std	se.std	z.std	*p*.std
South-West	bacteria	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	1.04	0.14	7.23	0.000	0.72	0.07	10.44	0.000
South-West	bacteria	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	0.06	0.11	0.57	0.570	0.08	0.14	0.57	0.569
South-West	bacteria	CWM_leaf_P	bactotal	~	CWM_leafP_historic	c	0.14	0.15	0.89	0.373	0.18	0.20	0.90	0.370
South-West	bacteria	CWM_leaf_P	bactotal	~	CWM_leafP_change	d	0.11	0.16	0.65	0.517	0.09	0.14	0.65	0.515
South-West	bacteria	CWM_leaf_P	bactotal	~	LUI_historic	e	-0.05	0.22	-0.22	0.828	-0.04	0.20	-0.22	0.828
South-West	bacteria	CWM_leaf_P	bactotal	~	LUI_change	f	-0.16	0.13	-1.23	0.217	-0.17	0.14	-1.25	0.210
South-West	bacteria	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	bacteria	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	4.90	0.000	0.48	0.10	4.80	0.000
South-West	bacteria	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.03	0.01	4.90	0.000	0.99	0.02	42.42	0.000
South-West	bacteria	CWM_leaf_P	bactotal	~~	bactotal		0.04	0.01	4.90	0.000	0.94	0.07	13.96	0.000
South-West	bacteria	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	bacteria	CWM_leaf_P	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	bacteria	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.14	0.16	0.88	0.377	0.13	0.15	0.89	0.373
South-West	bacteria	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.01	0.02	0.43	0.669	0.01	0.02	0.43	0.669
South-West	bacteria	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.09	0.16	0.61	0.545	0.09	0.14	0.61	0.544
South-West	bacteria	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.15	0.13	-1.18	0.238	-0.17	0.14	-1.20	0.231
South-West	bacteria	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.10	0.16	0.61	0.542	0.11	0.14	0.74	0.460
South-West	bacteria	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.15	0.13	-1.19	0.236	-0.18	0.14	-1.27	0.203
South-West	bacteria	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.38	0.18	2.09	0.037	0.29	0.13	2.18	0.029
South-West	bacteria	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.24	0.11	2.18	0.029	0.30	0.13	2.29	0.022
South-West	bacteria	CWM_MycInt	bactotal	~	CWM_MycInt_historic	c	-0.17	0.12	-1.45	0.147	-0.21	0.14	-1.48	0.140
South-West	bacteria	CWM_MycInt	bactotal	~	CWM_MycInt_change	d	0.10	0.16	0.58	0.563	0.08	0.15	0.58	0.562
South-West	bacteria	CWM_MycInt	bactotal	~	LUI_historic	e	0.19	0.16	1.20	0.232	0.17	0.14	1.21	0.226
South-West	bacteria	CWM_MycInt	bactotal	~	LUI_change	f	-0.12	0.13	-0.94	0.346	-0.14	0.15	-0.95	0.342
South-West	bacteria	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	bacteria	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	4.90	0.000	0.92	0.08	12.02	0.000
South-West	bacteria	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	4.90	0.000	0.91	0.08	11.52	0.000
South-West	bacteria	CWM_MycInt	bactotal	~~	bactotal		0.04	0.01	4.90	0.000	0.92	0.07	12.68	0.000
South-West	bacteria	CWM_MycInt	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	bacteria	CWM_MycInt	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	bacteria	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	-0.07	0.06	-1.19	0.234	-0.06	0.05	-1.20	0.229
South-West	bacteria	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.02	0.04	0.56	0.576	0.03	0.05	0.56	0.575
South-West	bacteria	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.12	0.16	0.80	0.425	0.11	0.14	0.80	0.422
South-West	bacteria	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.10	0.12	-0.80	0.421	-0.11	0.14	-0.81	0.419
South-West	bacteria	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.12	0.15	0.80	0.423	0.13	0.14	0.90	0.370
South-West	bacteria	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.10	0.12	-0.81	0.418	-0.13	0.14	-0.90	0.366
South-West	bacteria	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.16	1.17	0.244	0.16	0.14	1.18	0.238
South-West	bacteria	Plant_biomass	Plant_biomass	~	LUI_change	b	-0.04	0.13	-0.29	0.771	-0.04	0.14	-0.29	0.771
South-West	bacteria	Plant_biomass	bactotal	~	Plant_biomass	c	-0.08	0.13	-0.62	0.537	-0.09	0.14	-0.62	0.536
South-West	bacteria	Plant_biomass	bactotal	~	LUI_historic	e	0.12	0.16	0.76	0.449	0.11	0.14	0.76	0.447
South-West	bacteria	Plant_biomass	bactotal	~	LUI_change	f	-0.10	0.12	-0.82	0.412	-0.12	0.14	-0.83	0.409
South-West	bacteria	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	bacteria	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.04	0.01	5.00	0.000	0.97	0.05	20.22	0.000
South-West	bacteria	Plant_biomass	bactotal	~~	bactotal		0.04	0.01	5.00	0.000	0.97	0.05	19.84	0.000
South-West	bacteria	Plant_biomass	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	bacteria	Plant_biomass	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	bacteria	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	-0.02	0.03	-0.55	0.585	-0.01	0.03	-0.55	0.584
South-West	bacteria	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	0.26	0.792	0.00	0.01	0.26	0.792
South-West	bacteria	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.10	0.16	0.66	0.508	0.09	0.14	0.67	0.506
South-West	bacteria	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.10	0.12	-0.79	0.428	-0.11	0.14	-0.80	0.425
South-West	bacteria	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.10	0.16	0.67	0.505	0.11	0.14	0.79	0.431
South-West	bacteria	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.10	0.12	-0.80	0.424	-0.13	0.14	-0.90	0.366
South-West	bacteria	Lignin_content	Lignin_content	~	LUI_historic	a	0.03	0.19	0.13	0.895	0.02	0.15	0.13	0.895
South-West	bacteria	Lignin_content	Lignin_content	~	LUI_change	b	0.08	0.15	0.54	0.589	0.08	0.15	0.54	0.588
South-West	bacteria	Lignin_content	bactotal	~	Lignin_content	c	-0.12	0.12	-0.98	0.326	-0.14	0.14	-0.99	0.321
South-West	bacteria	Lignin_content	bactotal	~	LUI_historic	e	0.10	0.16	0.64	0.525	0.09	0.14	0.64	0.524
South-West	bacteria	Lignin_content	bactotal	~	LUI_change	f	-0.08	0.12	-0.68	0.494	-0.10	0.14	-0.69	0.492
South-West	bacteria	Lignin_content	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.95	0.342	-0.14	0.14	-0.98	0.329
South-West	bacteria	Lignin_content	Lignin_content	~~	Lignin_content		0.06	0.01	4.90	0.000	0.99	0.02	44.29	0.000
South-West	bacteria	Lignin_content	bactotal	~~	bactotal		0.04	0.01	4.90	0.000	0.96	0.06	17.00	0.000
South-West	bacteria	Lignin_content	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	bacteria	Lignin_content	LUI_change	~~	LUI_change		0.06	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	bacteria	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	-0.13	0.896	0.00	0.02	-0.13	0.896
South-West	bacteria	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	-0.01	0.02	-0.47	0.636	-0.01	0.02	-0.48	0.635
South-West	bacteria	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.10	0.16	0.61	0.541	0.09	0.14	0.61	0.540
South-West	bacteria	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.09	0.12	-0.76	0.450	-0.11	0.14	-0.76	0.448
South-West	bacteria	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.10	0.16	0.62	0.539	0.10	0.14	0.72	0.470
South-West	bacteria	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.09	0.12	-0.76	0.447	-0.12	0.14	-0.85	0.395
South-West	bacteria	pH	pH_historic	~	LUI_historic	a	-0.13	0.19	-0.67	0.505	-0.09	0.14	-0.67	0.504
South-West	bacteria	pH	pH_change	~	LUI_change	b	-0.01	0.12	-0.08	0.933	-0.01	0.14	-0.08	0.933
South-West	bacteria	pH	bactotal	~	pH_historic	c	-0.20	0.11	-1.87	0.062	-0.24	0.13	-1.92	0.055
South-West	bacteria	pH	bactotal	~	pH_change	d	0.21	0.14	1.57	0.116	0.20	0.13	1.60	0.109
South-West	bacteria	pH	bactotal	~	LUI_historic	e	0.09	0.15	0.62	0.536	0.08	0.13	0.62	0.535
South-West	bacteria	pH	bactotal	~	LUI_change	f	-0.17	0.12	-1.48	0.138	-0.20	0.13	-1.51	0.132
South-West	bacteria	pH	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	bacteria	pH	pH_historic	~~	pH_historic		0.06	0.01	5.00	0.000	0.99	0.03	37.71	0.000
South-West	bacteria	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	1.00	0.00	298.93	0.000
South-West	bacteria	pH	bactotal	~~	bactotal		0.04	0.01	5.00	0.000	0.84	0.09	9.09	0.000
South-West	bacteria	pH	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	bacteria	pH	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	bacteria	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.03	0.04	0.63	0.531	0.02	0.04	0.63	0.528
South-West	bacteria	pH	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.03	-0.08	0.933	0.00	0.03	-0.08	0.933
South-West	bacteria	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.12	0.15	0.77	0.442	0.10	0.14	0.77	0.439
South-West	bacteria	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.17	0.12	-1.47	0.143	-0.20	0.13	-1.49	0.135
South-West	bacteria	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.12	0.15	0.78	0.437	0.13	0.14	0.98	0.326
South-West	bacteria	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.17	0.12	-1.47	0.141	-0.21	0.13	-1.62	0.105

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*p*	est.std	se.std	z.std	*p*.std
South-West	fungi:bacteria ratio	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	1.04	0.14	7.23	0.000	0.72	0.07	10.44	0.000
South-West	fungi:bacteria ratio	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	0.06	0.11	0.57	0.570	0.08	0.14	0.57	0.569
South-West	fungi:bacteria ratio	CWM_leaf_P	fungi_bac	~	CWM_leafP_historic	c	-0.42	0.16	-2.65	0.008	-0.49	0.17	-2.81	0.005
South-West	fungi:bacteria ratio	CWM_leaf_P	fungi_bac	~	CWM_leafP_change	d	-0.19	0.17	-1.15	0.249	-0.15	0.13	-1.16	0.246
South-West	fungi:bacteria ratio	CWM_leaf_P	fungi_bac	~	LUI_historic	e	0.06	0.23	0.27	0.784	0.05	0.18	0.28	0.784
South-West	fungi:bacteria ratio	CWM_leaf_P	fungi_bac	~	LUI_change	f	0.03	0.13	0.24	0.808	0.03	0.13	0.24	0.808
South-West	fungi:bacteria ratio	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	fungi:bacteria ratio	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	4.90	0.000	0.48	0.10	4.80	0.000
South-West	fungi:bacteria ratio	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.03	0.01	4.90	0.000	0.99	0.02	42.42	0.000
South-West	fungi:bacteria ratio	CWM_leaf_P	fungi_bac	~~	fungi_bac		0.04	0.01	4.90	0.000	0.77	0.11	7.36	0.000
South-West	fungi:bacteria ratio	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	fungi:bacteria ratio	CWM_leaf_P	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	fungi:bacteria ratio	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	-0.43	0.17	-2.49	0.013	-0.35	0.13	-2.63	0.009
South-West	fungi:bacteria ratio	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	-0.01	0.02	-0.51	0.611	-0.01	0.02	-0.51	0.610
South-West	fungi:bacteria ratio	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.37	0.17	-2.19	0.028	-0.30	0.13	-2.30	0.022
South-West	fungi:bacteria ratio	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.02	0.13	0.15	0.883	0.02	0.13	0.15	0.883
South-West	fungi:bacteria ratio	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.37	0.17	-2.20	0.028	-0.30	0.13	-2.33	0.020
South-West	fungi:bacteria ratio	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.02	0.13	0.16	0.872	0.05	0.14	0.40	0.692
South-West	fungi:bacteria ratio	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.38	0.18	2.09	0.037	0.29	0.13	2.18	0.029
South-West	fungi:bacteria ratio	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.24	0.11	2.18	0.029	0.30	0.13	2.29	0.022
South-West	fungi:bacteria ratio	CWM_MycInt	fungi_bac	~	CWM_MycInt_historic	c	0.11	0.13	0.84	0.401	0.12	0.14	0.85	0.398
South-West	fungi:bacteria ratio	CWM_MycInt	fungi_bac	~	CWM_MycInt_change	d	0.20	0.18	1.12	0.263	0.16	0.14	1.13	0.258
South-West	fungi:bacteria ratio	CWM_MycInt	fungi_bac	~	LUI_historic	e	-0.44	0.17	-2.55	0.011	-0.36	0.13	-2.71	0.007
South-West	fungi:bacteria ratio	CWM_MycInt	fungi_bac	~	LUI_change	f	-0.14	0.14	-0.96	0.337	-0.14	0.14	-0.97	0.334
South-West	fungi:bacteria ratio	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	fungi:bacteria ratio	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	4.90	0.000	0.92	0.08	12.02	0.000
South-West	fungi:bacteria ratio	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	4.90	0.000	0.91	0.08	11.52	0.000
South-West	fungi:bacteria ratio	CWM_MycInt	fungi_bac	~~	fungi_bac		0.05	0.01	4.90	0.000	0.86	0.09	9.29	0.000
South-West	fungi:bacteria ratio	CWM_MycInt	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	fungi:bacteria ratio	CWM_MycInt	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	fungi:bacteria ratio	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.04	0.05	0.78	0.436	0.03	0.04	0.78	0.434
South-West	fungi:bacteria ratio	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.05	0.05	1.00	0.319	0.05	0.05	1.00	0.315
South-West	fungi:bacteria ratio	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.40	0.17	-2.40	0.017	-0.33	0.13	-2.53	0.011
South-West	fungi:bacteria ratio	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.09	0.14	-0.65	0.518	-0.09	0.14	-0.65	0.517
South-West	fungi:bacteria ratio	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.40	0.17	-2.40	0.017	-0.32	0.13	-2.45	0.014
South-West	fungi:bacteria ratio	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.09	0.14	-0.63	0.527	-0.05	0.14	-0.35	0.724
South-West	fungi:bacteria ratio	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.16	1.17	0.244	0.16	0.14	1.18	0.238
South-West	fungi:bacteria ratio	Plant_biomass	Plant_biomass	~	LUI_change	b	-0.04	0.13	-0.29	0.771	-0.04	0.14	-0.29	0.771
South-West	fungi:bacteria ratio	Plant_biomass	fungi_bac	~	Plant_biomass	c	-0.01	0.14	-0.04	0.969	-0.01	0.14	-0.04	0.969
South-West	fungi:bacteria ratio	Plant_biomass	fungi_bac	~	LUI_historic	e	-0.41	0.17	-2.46	0.014	-0.34	0.13	-2.60	0.009
South-West	fungi:bacteria ratio	Plant_biomass	fungi_bac	~	LUI_change	f	-0.08	0.13	-0.63	0.531	-0.09	0.13	-0.63	0.529
South-West	fungi:bacteria ratio	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	fungi:bacteria ratio	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.04	0.01	5.00	0.000	0.97	0.05	20.22	0.000
South-West	fungi:bacteria ratio	Plant_biomass	fungi_bac	~~	fungi_bac		0.04	0.01	5.00	0.000	0.89	0.08	10.57	0.000
South-West	fungi:bacteria ratio	Plant_biomass	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	fungi:bacteria ratio	Plant_biomass	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	fungi:bacteria ratio	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.03	-0.04	0.969	0.00	0.02	-0.04	0.969
South-West	fungi:bacteria ratio	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	0.04	0.969	0.00	0.01	0.04	0.969
South-West	fungi:bacteria ratio	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.41	0.17	-2.50	0.013	-0.34	0.13	-2.65	0.008
South-West	fungi:bacteria ratio	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.08	0.13	-0.63	0.531	-0.08	0.13	-0.63	0.530
South-West	fungi:bacteria ratio	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.41	0.17	-2.50	0.013	-0.32	0.13	-2.56	0.010
South-West	fungi:bacteria ratio	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.08	0.13	-0.61	0.544	-0.04	0.14	-0.25	0.806
South-West	fungi:bacteria ratio	Lignin_content	Lignin_content	~	LUI_historic	a	0.03	0.19	0.13	0.895	0.02	0.15	0.13	0.895
South-West	fungi:bacteria ratio	Lignin_content	Lignin_content	~	LUI_change	b	0.08	0.15	0.54	0.589	0.08	0.15	0.54	0.588
South-West	fungi:bacteria ratio	Lignin_content	fungi_bac	~	Lignin_content	c	-0.07	0.13	-0.56	0.573	-0.08	0.14	-0.57	0.572
South-West	fungi:bacteria ratio	Lignin_content	fungi_bac	~	LUI_historic	e	-0.40	0.17	-2.38	0.017	-0.33	0.13	-2.51	0.012
South-West	fungi:bacteria ratio	Lignin_content	fungi_bac	~	LUI_change	f	-0.08	0.13	-0.64	0.521	-0.09	0.14	-0.64	0.520
South-West	fungi:bacteria ratio	Lignin_content	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.95	0.342	-0.14	0.14	-0.98	0.329
South-West	fungi:bacteria ratio	Lignin_content	Lignin_content	~~	Lignin_content		0.06	0.01	4.90	0.000	0.99	0.02	44.29	0.000
South-West	fungi:bacteria ratio	Lignin_content	fungi_bac	~~	fungi_bac		0.05	0.01	4.90	0.000	0.89	0.09	10.27	0.000
South-West	fungi:bacteria ratio	Lignin_content	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	fungi:bacteria ratio	Lignin_content	LUI_change	~~	LUI_change		0.06	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	fungi:bacteria ratio	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	-0.13	0.898	0.00	0.01	-0.13	0.898
South-West	fungi:bacteria ratio	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	-0.01	0.02	-0.39	0.696	-0.01	0.02	-0.39	0.696
South-West	fungi:bacteria ratio	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.40	0.17	-2.38	0.017	-0.33	0.13	-2.52	0.012
South-West	fungi:bacteria ratio	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.09	0.13	-0.69	0.493	-0.09	0.14	-0.69	0.491
South-West	fungi:bacteria ratio	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.40	0.17	-2.38	0.017	-0.32	0.13	-2.42	0.015
South-West	fungi:bacteria ratio	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.09	0.13	-0.67	0.504	-0.05	0.14	-0.34	0.734
South-West	fungi:bacteria ratio	pH	pH_historic	~	LUI_historic	a	-0.13	0.19	-0.67	0.505	-0.09	0.14	-0.67	0.504
South-West	fungi:bacteria ratio	pH	pH_change	~	LUI_change	b	-0.01	0.12	-0.08	0.933	-0.01	0.14	-0.08	0.933
South-West	fungi:bacteria ratio	pH	fungi_bac	~	pH_historic	c	0.21	0.12	1.80	0.073	0.23	0.13	1.84	0.066
South-West	fungi:bacteria ratio	pH	fungi_bac	~	pH_change	d	-0.16	0.15	-1.09	0.278	-0.14	0.13	-1.09	0.274
South-West	fungi:bacteria ratio	pH	fungi_bac	~	LUI_historic	e	-0.39	0.16	-2.46	0.014	-0.32	0.12	-2.58	0.010
South-West	fungi:bacteria ratio	pH	fungi_bac	~	LUI_change	f	0.00	0.12	-0.02	0.984	0.00	0.13	-0.02	0.984
South-West	fungi:bacteria ratio	pH	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	fungi:bacteria ratio	pH	pH_historic	~~	pH_historic		0.06	0.01	5.00	0.000	0.99	0.03	37.71	0.000
South-West	fungi:bacteria ratio	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	1.00	0.00	298.93	0.000
South-West	fungi:bacteria ratio	pH	fungi_bac	~~	fungi_bac		0.04	0.01	5.00	0.000	0.81	0.10	8.24	0.000
South-West	fungi:bacteria ratio	pH	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	fungi:bacteria ratio	pH	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	fungi:bacteria ratio	pH	LUI_hist_in	:=	a*c	LUI_hist_in	-0.03	0.04	-0.62	0.532	-0.02	0.03	-0.63	0.529
South-West	fungi:bacteria ratio	pH	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.02	0.08	0.934	0.00	0.02	0.08	0.934
South-West	fungi:bacteria ratio	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.42	0.16	-2.56	0.010	-0.34	0.13	-2.72	0.007
South-West	fungi:bacteria ratio	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.00	0.13	-0.01	0.994	0.00	0.13	-0.01	0.994
South-West	fungi:bacteria ratio	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.42	0.16	-2.56	0.010	-0.34	0.12	-2.75	0.006
South-West	fungi:bacteria ratio	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.00	0.13	0.01	0.990	0.05	0.14	0.36	0.721

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*p*	est.std	se.std	z.std	*p*.std
South-West	fungi	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	1.04	0.14	7.23	0.000	0.72	0.07	10.44	0.000
South-West	fungi	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	0.06	0.11	0.57	0.570	0.08	0.14	0.57	0.569
South-West	fungi	CWM_leaf_P	fungi	~	CWM_leafP_historic	c	-0.26	0.15	-1.72	0.086	-0.34	0.19	-1.76	0.078
South-West	fungi	CWM_leaf_P	fungi	~	CWM_leafP_change	d	-0.18	0.16	-1.10	0.271	-0.15	0.13	-1.11	0.266
South-West	fungi	CWM_leaf_P	fungi	~	LUI_historic	e	0.18	0.22	0.82	0.411	0.16	0.20	0.83	0.408
South-West	fungi	CWM_leaf_P	fungi	~	LUI_change	f	-0.18	0.13	-1.41	0.158	-0.19	0.13	-1.44	0.151
South-West	fungi	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	fungi	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	4.90	0.000	0.48	0.10	4.80	0.000
South-West	fungi	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.03	0.01	4.90	0.000	0.99	0.02	42.42	0.000
South-West	fungi	CWM_leaf_P	fungi	~~	fungi		0.04	0.01	4.90	0.000	0.88	0.09	10.11	0.000
South-West	fungi	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	fungi	CWM_leaf_P	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	fungi	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	-0.27	0.16	-1.67	0.095	-0.24	0.14	-1.71	0.087
South-West	fungi	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	-0.01	0.02	-0.51	0.614	-0.01	0.02	-0.51	0.612
South-West	fungi	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.09	0.16	-0.58	0.564	-0.08	0.14	-0.58	0.563
South-West	fungi	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.19	0.13	-1.49	0.137	-0.21	0.14	-1.52	0.129
South-West	fungi	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.09	0.16	-0.57	0.568	-0.06	0.14	-0.40	0.688
South-West	fungi	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.19	0.13	-1.49	0.137	-0.20	0.14	-1.45	0.147
South-West	fungi	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.38	0.18	2.09	0.037	0.29	0.13	2.18	0.029
South-West	fungi	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.24	0.11	2.18	0.029	0.30	0.13	2.29	0.022
South-West	fungi	CWM_MycInt	fungi	~	CWM_MycInt_historic	c	0.05	0.12	0.38	0.706	0.05	0.14	0.38	0.706
South-West	fungi	CWM_MycInt	fungi	~	CWM_MycInt_change	d	0.31	0.17	1.88	0.060	0.26	0.14	1.93	0.053
South-West	fungi	CWM_MycInt	fungi	~	LUI_historic	e	-0.13	0.16	-0.78	0.433	-0.11	0.14	-0.79	0.431
South-West	fungi	CWM_MycInt	fungi	~	LUI_change	f	-0.33	0.13	-2.50	0.013	-0.35	0.13	-2.63	0.008
South-West	fungi	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	fungi	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	4.90	0.000	0.92	0.08	12.02	0.000
South-West	fungi	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	4.90	0.000	0.91	0.08	11.52	0.000
South-West	fungi	CWM_MycInt	fungi	~~	fungi		0.04	0.01	4.90	0.000	0.86	0.09	9.19	0.000
South-West	fungi	CWM_MycInt	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	fungi	CWM_MycInt	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	fungi	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.02	0.05	0.37	0.711	0.02	0.04	0.37	0.711
South-West	fungi	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.07	0.05	1.43	0.154	0.08	0.06	1.44	0.151
South-West	fungi	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.11	0.15	-0.70	0.481	-0.10	0.13	-0.71	0.480
South-West	fungi	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.25	0.13	-1.96	0.050	-0.27	0.13	-2.03	0.042
South-West	fungi	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.11	0.15	-0.70	0.486	-0.06	0.14	-0.46	0.649
South-West	fungi	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.25	0.13	-1.95	0.051	-0.26	0.13	-1.95	0.051
South-West	fungi	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.16	1.17	0.244	0.16	0.14	1.18	0.238
South-West	fungi	Plant_biomass	Plant_biomass	~	LUI_change	b	-0.04	0.13	-0.29	0.771	-0.04	0.14	-0.29	0.771
South-West	fungi	Plant_biomass	fungi	~	Plant_biomass	c	-0.04	0.13	-0.31	0.759	-0.04	0.14	-0.31	0.759
South-West	fungi	Plant_biomass	fungi	~	LUI_historic	e	-0.13	0.16	-0.80	0.425	-0.11	0.14	-0.80	0.422
South-West	fungi	Plant_biomass	fungi	~	LUI_change	f	-0.24	0.12	-1.94	0.052	-0.27	0.13	-2.01	0.044
South-West	fungi	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	fungi	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.04	0.01	5.00	0.000	0.97	0.05	20.22	0.000
South-West	fungi	Plant_biomass	fungi	~~	fungi		0.04	0.01	5.00	0.000	0.92	0.07	12.76	0.000
South-West	fungi	Plant_biomass	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	fungi	Plant_biomass	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	fungi	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.03	-0.30	0.767	-0.01	0.02	-0.30	0.767
South-West	fungi	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	0.21	0.833	0.00	0.01	0.21	0.833
South-West	fungi	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.13	0.15	-0.86	0.391	-0.12	0.14	-0.86	0.388
South-West	fungi	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.23	0.12	-1.93	0.054	-0.27	0.13	-2.00	0.046
South-West	fungi	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.13	0.15	-0.85	0.396	-0.08	0.14	-0.56	0.574
South-West	fungi	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.23	0.12	-1.92	0.054	-0.25	0.13	-1.87	0.062
South-West	fungi	Lignin_content	Lignin_content	~	LUI_historic	a	0.03	0.19	0.13	0.895	0.02	0.15	0.13	0.895
South-West	fungi	Lignin_content	Lignin_content	~	LUI_change	b	0.08	0.15	0.54	0.589	0.08	0.15	0.54	0.588
South-West	fungi	Lignin_content	fungi	~	Lignin_content	c	-0.09	0.12	-0.71	0.477	-0.10	0.14	-0.72	0.475
South-West	fungi	Lignin_content	fungi	~	LUI_historic	e	-0.14	0.16	-0.87	0.386	-0.12	0.14	-0.87	0.383
South-West	fungi	Lignin_content	fungi	~	LUI_change	f	-0.23	0.12	-1.84	0.066	-0.26	0.14	-1.90	0.057
South-West	fungi	Lignin_content	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.95	0.342	-0.14	0.14	-0.98	0.329
South-West	fungi	Lignin_content	Lignin_content	~~	Lignin_content		0.06	0.01	4.90	0.000	0.99	0.02	44.29	0.000
South-West	fungi	Lignin_content	fungi	~~	fungi		0.04	0.01	4.90	0.000	0.91	0.08	11.82	0.000
South-West	fungi	Lignin_content	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	fungi	Lignin_content	LUI_change	~~	LUI_change		0.06	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	fungi	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	-0.13	0.897	0.00	0.02	-0.13	0.897
South-West	fungi	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	-0.01	0.02	-0.43	0.667	-0.01	0.02	-0.43	0.666
South-West	fungi	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.14	0.16	-0.88	0.381	-0.12	0.14	-0.88	0.378
South-West	fungi	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.23	0.12	-1.89	0.059	-0.27	0.14	-1.96	0.050
South-West	fungi	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.14	0.16	-0.87	0.385	-0.09	0.14	-0.60	0.548
South-West	fungi	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.23	0.12	-1.89	0.059	-0.25	0.14	-1.83	0.067
South-West	fungi	pH	pH_historic	~	LUI_historic	a	-0.13	0.19	-0.67	0.505	-0.09	0.14	-0.67	0.504
South-West	fungi	pH	pH_change	~	LUI_change	b	-0.01	0.12	-0.08	0.933	-0.01	0.14	-0.08	0.933
South-West	fungi	pH	fungi	~	pH_historic	c	0.11	0.11	0.94	0.348	0.13	0.14	0.95	0.344
South-West	fungi	pH	fungi	~	pH_change	d	0.00	0.14	0.01	0.991	0.00	0.14	0.01	0.991
South-West	fungi	pH	fungi	~	LUI_historic	e	-0.11	0.15	-0.72	0.471	-0.10	0.14	-0.73	0.468
South-West	fungi	pH	fungi	~	LUI_change	f	-0.19	0.12	-1.59	0.111	-0.22	0.14	-1.63	0.103
South-West	fungi	pH	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	fungi	pH	pH_historic	~~	pH_historic		0.06	0.01	5.00	0.000	0.99	0.03	37.71	0.000
South-West	fungi	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	1.00	0.00	298.94	0.000
South-West	fungi	pH	fungi	~~	fungi		0.04	0.01	5.00	0.000	0.93	0.07	13.43	0.000
South-West	fungi	pH	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	fungi	pH	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	fungi	pH	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.03	-0.54	0.587	-0.01	0.02	-0.55	0.586
South-West	fungi	pH	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.00	-0.01	0.991	0.00	0.00	-0.01	0.991
South-West	fungi	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.12	0.15	-0.81	0.421	-0.11	0.14	-0.81	0.418
South-West	fungi	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.19	0.12	-1.60	0.111	-0.22	0.14	-1.63	0.103
South-West	fungi	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.12	0.15	-0.80	0.425	-0.08	0.14	-0.57	0.571
South-West	fungi	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.19	0.12	-1.59	0.112	-0.20	0.13	-1.51	0.131

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*p*	est.std	se.std	z.std	*p*.std
South-West	ergosterol	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	1.04	0.14	7.23	0.000	0.72	0.07	10.44	0.000
South-West	ergosterol	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	0.06	0.11	0.57	0.570	0.08	0.14	0.57	0.569
South-West	ergosterol	CWM_leaf_P	Ergosterol	~	CWM_leafP_historic	c	-0.41	0.16	-2.59	0.010	-0.47	0.17	-2.71	0.007
South-West	ergosterol	CWM_leaf_P	Ergosterol	~	CWM_leafP_change	d	0.00	0.17	0.00	0.997	0.00	0.13	0.00	0.997
South-West	ergosterol	CWM_leaf_P	Ergosterol	~	LUI_historic	e	0.18	0.23	0.78	0.438	0.14	0.18	0.78	0.437
South-West	ergosterol	CWM_leaf_P	Ergosterol	~	LUI_change	f	-0.37	0.13	-2.86	0.004	-0.36	0.12	-3.02	0.003
South-West	ergosterol	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	ergosterol	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	4.90	0.000	0.48	0.10	4.80	0.000
South-West	ergosterol	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.03	0.01	4.90	0.000	0.99	0.02	42.42	0.000
South-West	ergosterol	CWM_leaf_P	Ergosterol	~~	Ergosterol		0.04	0.01	4.90	0.000	0.74	0.11	7.03	0.000
South-West	ergosterol	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	ergosterol	CWM_leaf_P	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	ergosterol	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	-0.43	0.18	-2.44	0.015	-0.34	0.13	-2.54	0.011
South-West	ergosterol	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	0.00	0.997	0.00	0.01	0.00	0.997
South-West	ergosterol	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.25	0.17	-1.47	0.141	-0.20	0.13	-1.49	0.135
South-West	ergosterol	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.37	0.13	-2.87	0.004	-0.36	0.12	-3.03	0.002
South-West	ergosterol	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.25	0.17	-1.46	0.144	-0.16	0.14	-1.10	0.271
South-West	ergosterol	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.37	0.13	-2.86	0.004	-0.34	0.12	-2.78	0.005
South-West	ergosterol	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.38	0.18	2.09	0.037	0.29	0.13	2.18	0.029
South-West	ergosterol	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.24	0.11	2.18	0.029	0.30	0.13	2.29	0.022
South-West	ergosterol	CWM_MycInt	Ergosterol	~	CWM_MycInt_historic	c	-0.08	0.13	-0.63	0.527	-0.08	0.13	-0.63	0.527
South-West	ergosterol	CWM_MycInt	Ergosterol	~	CWM_MycInt_change	d	0.30	0.18	1.72	0.086	0.22	0.13	1.74	0.081
South-West	ergosterol	CWM_MycInt	Ergosterol	~	LUI_historic	e	-0.21	0.17	-1.26	0.209	-0.16	0.13	-1.27	0.205
South-West	ergosterol	CWM_MycInt	Ergosterol	~	LUI_change	f	-0.53	0.14	-3.82	0.000	-0.50	0.12	-4.27	0.000
South-West	ergosterol	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	ergosterol	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	4.90	0.000	0.92	0.08	12.02	0.000
South-West	ergosterol	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	4.90	0.000	0.91	0.08	11.52	0.000
South-West	ergosterol	CWM_MycInt	Ergosterol	~~	Ergosterol		0.04	0.01	4.90	0.000	0.74	0.11	6.88	0.000
South-West	ergosterol	CWM_MycInt	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	ergosterol	CWM_MycInt	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	ergosterol	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	-0.03	0.05	-0.61	0.545	-0.02	0.04	-0.61	0.544
South-West	ergosterol	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.07	0.05	1.35	0.177	0.07	0.05	1.35	0.176
South-West	ergosterol	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.24	0.16	-1.49	0.135	-0.19	0.12	-1.51	0.130
South-West	ergosterol	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.46	0.14	-3.37	0.001	-0.43	0.12	-3.71	0.000
South-West	ergosterol	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.24	0.16	-1.48	0.139	-0.14	0.14	-1.00	0.320
South-West	ergosterol	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.46	0.14	-3.36	0.001	-0.41	0.12	-3.46	0.001
South-West	ergosterol	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.16	1.17	0.244	0.16	0.14	1.18	0.238
South-West	ergosterol	Plant_biomass	Plant_biomass	~	LUI_change	b	-0.04	0.13	-0.29	0.771	-0.04	0.14	-0.29	0.771
South-West	ergosterol	Plant_biomass	Ergosterol	~	Plant_biomass	c	0.09	0.15	0.61	0.545	0.08	0.13	0.61	0.544
South-West	ergosterol	Plant_biomass	Ergosterol	~	LUI_historic	e	-0.30	0.17	-1.75	0.080	-0.23	0.13	-1.79	0.074
South-West	ergosterol	Plant_biomass	Ergosterol	~	LUI_change	f	-0.40	0.13	-3.02	0.003	-0.39	0.12	-3.25	0.001
South-West	ergosterol	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	ergosterol	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.04	0.01	5.00	0.000	0.97	0.05	20.22	0.000
South-West	ergosterol	Plant_biomass	Ergosterol	~~	Ergosterol		0.05	0.01	5.00	0.000	0.82	0.10	8.27	0.000
South-West	ergosterol	Plant_biomass	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	ergosterol	Plant_biomass	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	ergosterol	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.02	0.03	0.54	0.591	0.01	0.02	0.54	0.591
South-West	ergosterol	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	-0.26	0.793	0.00	0.01	-0.26	0.793
South-West	ergosterol	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.28	0.17	-1.67	0.095	-0.22	0.13	-1.70	0.089
South-West	ergosterol	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.41	0.13	-3.03	0.002	-0.39	0.12	-3.28	0.001
South-West	ergosterol	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.28	0.17	-1.66	0.098	-0.16	0.14	-1.15	0.250
South-West	ergosterol	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.40	0.13	-3.02	0.003	-0.36	0.12	-2.94	0.003
South-West	ergosterol	Lignin_content	Lignin_content	~	LUI_historic	a	0.03	0.19	0.13	0.895	0.02	0.15	0.13	0.895
South-West	ergosterol	Lignin_content	Lignin_content	~	LUI_change	b	0.08	0.15	0.54	0.589	0.08	0.15	0.54	0.588
South-West	ergosterol	Lignin_content	Ergosterol	~	Lignin_content	c	-0.20	0.13	-1.57	0.117	-0.20	0.13	-1.60	0.111
South-West	ergosterol	Lignin_content	Ergosterol	~	LUI_historic	e	-0.28	0.17	-1.64	0.100	-0.21	0.13	-1.67	0.095
South-West	ergosterol	Lignin_content	Ergosterol	~	LUI_change	f	-0.39	0.13	-2.91	0.004	-0.38	0.12	-3.11	0.002
South-West	ergosterol	Lignin_content	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.95	0.342	-0.14	0.14	-0.98	0.329
South-West	ergosterol	Lignin_content	Lignin_content	~~	Lignin_content		0.06	0.01	4.90	0.000	0.99	0.02	44.29	0.000
South-West	ergosterol	Lignin_content	Ergosterol	~~	Ergosterol		0.05	0.01	4.90	0.000	0.78	0.11	7.44	0.000
South-West	ergosterol	Lignin_content	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	ergosterol	Lignin_content	LUI_change	~~	LUI_change		0.06	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	ergosterol	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.04	-0.13	0.896	0.00	0.03	-0.13	0.896
South-West	ergosterol	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	-0.02	0.03	-0.51	0.609	-0.02	0.03	-0.52	0.607
South-West	ergosterol	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.29	0.18	-1.63	0.103	-0.22	0.13	-1.66	0.096
South-West	ergosterol	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.41	0.14	-2.97	0.003	-0.39	0.12	-3.20	0.001
South-West	ergosterol	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.28	0.18	-1.62	0.106	-0.16	0.14	-1.15	0.251
South-West	ergosterol	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.40	0.14	-2.96	0.003	-0.36	0.13	-2.89	0.004
South-West	ergosterol	pH	pH_historic	~	LUI_historic	a	-0.13	0.19	-0.67	0.505	-0.09	0.14	-0.67	0.504
South-West	ergosterol	pH	pH_change	~	LUI_change	b	-0.01	0.12	-0.08	0.933	-0.01	0.14	-0.08	0.933
South-West	ergosterol	pH	Ergosterol	~	pH_historic	c	0.16	0.13	1.25	0.211	0.16	0.13	1.26	0.206
South-West	ergosterol	pH	Ergosterol	~	pH_change	d	-0.02	0.16	-0.12	0.901	-0.02	0.13	-0.12	0.901
South-West	ergosterol	pH	Ergosterol	~	LUI_historic	e	-0.26	0.17	-1.52	0.129	-0.20	0.13	-1.54	0.123
South-West	ergosterol	pH	Ergosterol	~	LUI_change	f	-0.34	0.13	-2.62	0.009	-0.34	0.12	-2.77	0.006
South-West	ergosterol	pH	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	ergosterol	pH	pH_historic	~~	pH_historic		0.06	0.01	5.00	0.000	0.99	0.03	37.71	0.000
South-West	ergosterol	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	1.00	0.00	298.93	0.000
South-West	ergosterol	pH	Ergosterol	~~	Ergosterol		0.05	0.01	5.00	0.000	0.83	0.10	8.73	0.000
South-West	ergosterol	pH	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	ergosterol	pH	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	ergosterol	pH	LUI_hist_in	:=	a*c	LUI_hist_in	-0.02	0.03	-0.59	0.557	-0.02	0.03	-0.59	0.555
South-West	ergosterol	pH	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.00	0.07	0.945	0.00	0.00	0.07	0.945
South-West	ergosterol	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.28	0.17	-1.62	0.106	-0.21	0.13	-1.65	0.099
South-West	ergosterol	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.34	0.13	-2.61	0.009	-0.34	0.12	-2.76	0.006
South-West	ergosterol	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.27	0.17	-1.61	0.109	-0.16	0.14	-1.19	0.234
South-West	ergosterol	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.34	0.13	-2.60	0.009	-0.31	0.13	-2.45	0.014

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*p*	est.std	se.std	z.std	*p* .std
Central	Cmic	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.53	0.09	5.84	0.000	0.64	0.08	7.58	0.000
Central	Cmic	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.05	0.11	-0.46	0.647	-0.07	0.14	-0.46	0.646
Central	Cmic	CWM_leaf_P	Cmic	~	CWM_leafP_historic	c	-0.13	0.18	-0.72	0.472	-0.13	0.17	-0.72	0.470
Central	Cmic	CWM_leaf_P	Cmic	~	CWM_leafP_change	d	0.06	0.20	0.27	0.785	0.04	0.14	0.27	0.785
Central	Cmic	CWM_leaf_P	Cmic	~	LUI_historic	e	-0.18	0.15	-1.16	0.248	-0.20	0.17	-1.17	0.242
Central	Cmic	CWM_leaf_P	Cmic	~	LUI_change	f	0.03	0.15	0.21	0.833	0.03	0.14	0.21	0.833
Central	Cmic	CWM_leaf_P	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	Cmic	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	5.00	0.000	0.59	0.11	5.55	0.000
Central	Cmic	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.02	0.00	5.00	0.000	1.00	0.02	54.73	0.000
Central	Cmic	CWM_leaf_P	Cmic	~~	Cmic		0.05	0.01	5.00	0.000	0.91	0.08	11.77	0.000
Central	Cmic	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Cmic	CWM_leaf_P	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Cmic	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	-0.07	0.10	-0.71	0.475	-0.08	0.11	-0.72	0.473
Central	Cmic	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	-0.23	0.815	0.00	0.01	-0.24	0.815
Central	Cmic	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.24	0.12	-2.08	0.038	-0.28	0.13	-2.17	0.030
Central	Cmic	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.03	0.15	0.19	0.846	0.03	0.14	0.19	0.846
Central	Cmic	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.24	0.12	-2.08	0.038	-0.28	0.13	-2.16	0.031
Central	Cmic	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.03	0.15	0.19	0.850	0.01	0.14	0.06	0.954
Central	Cmic	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	-0.11	0.13	-0.88	0.380	-0.12	0.14	-0.88	0.377
Central	Cmic	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.04	0.13	0.30	0.768	0.04	0.14	0.30	0.768
Central	Cmic	CWM_MycInt	Cmic	~	CWM_MycInt_historic	c	0.15	0.13	1.16	0.247	0.15	0.13	1.17	0.242
Central	Cmic	CWM_MycInt	Cmic	~	CWM_MycInt_change	d	0.10	0.16	0.58	0.562	0.08	0.13	0.58	0.561
Central	Cmic	CWM_MycInt	Cmic	~	LUI_historic	e	-0.26	0.12	-2.18	0.029	-0.29	0.13	-2.27	0.023
Central	Cmic	CWM_MycInt	Cmic	~	LUI_change	f	0.01	0.15	0.07	0.947	0.01	0.13	0.07	0.947
Central	Cmic	CWM_MycInt	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	Cmic	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	5.00	0.000	0.99	0.03	28.71	0.000
Central	Cmic	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	1.00	0.01	84.79	0.000
Central	Cmic	CWM_MycInt	Cmic	~~	Cmic		0.04	0.01	5.00	0.000	0.88	0.09	10.03	0.000
Central	Cmic	CWM_MycInt	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Cmic	CWM_MycInt	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Cmic	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	-0.02	0.02	-0.70	0.484	-0.02	0.03	-0.71	0.481
Central	Cmic	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	0.26	0.792	0.00	0.01	0.26	0.792
Central	Cmic	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.27	0.12	-2.31	0.021	-0.31	0.13	-2.43	0.015
Central	Cmic	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.01	0.15	0.09	0.928	0.01	0.13	0.09	0.928
Central	Cmic	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.27	0.12	-2.31	0.021	-0.31	0.13	-2.42	0.015
Central	Cmic	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.01	0.15	0.09	0.933	-0.01	0.14	-0.06	0.956
Central	Cmic	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.03	0.12	0.23	0.821	0.03	0.14	0.23	0.821
Central	Cmic	Plant_biomass	Plant_biomass	~	LUI_change	b	0.13	0.15	0.87	0.385	0.12	0.14	0.88	0.382
Central	Cmic	Plant_biomass	Cmic	~	Plant_biomass	c	0.14	0.14	0.98	0.325	0.13	0.13	0.99	0.321
Central	Cmic	Plant_biomass	Cmic	~	LUI_historic	e	-0.25	0.12	-2.13	0.033	-0.29	0.13	-2.22	0.026
Central	Cmic	Plant_biomass	Cmic	~	LUI_change	f	0.01	0.15	0.05	0.964	0.01	0.14	0.05	0.964
Central	Cmic	Plant_biomass	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	Cmic	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	5.00	0.000	0.98	0.04	27.60	0.000
Central	Cmic	Plant_biomass	Cmic	~~	Cmic		0.05	0.01	5.00	0.000	0.90	0.08	11.35	0.000
Central	Cmic	Plant_biomass	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Cmic	Plant_biomass	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Cmic	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	0.22	0.825	0.00	0.02	0.22	0.825
Central	Cmic	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.02	0.03	0.65	0.515	0.02	0.03	0.65	0.513
Central	Cmic	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.25	0.12	-2.08	0.038	-0.28	0.13	-2.17	0.030
Central	Cmic	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.03	0.15	0.17	0.869	0.02	0.14	0.17	0.869
Central	Cmic	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.25	0.12	-2.08	0.038	-0.28	0.13	-2.16	0.031
Central	Cmic	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.02	0.15	0.16	0.873	0.00	0.14	0.03	0.976
Central	Cmic	Lignin_content	Lignin_content	~	LUI_historic	a	0.07	0.12	0.60	0.548	0.09	0.14	0.60	0.547
Central	Cmic	Lignin_content	Lignin_content	~	LUI_change	b	0.07	0.16	0.47	0.642	0.07	0.14	0.47	0.641
Central	Cmic	Lignin_content	Cmic	~	Lignin_content	c	0.05	0.14	0.38	0.702	0.05	0.14	0.38	0.702
Central	Cmic	Lignin_content	Cmic	~	LUI_historic	e	-0.25	0.12	-2.11	0.035	-0.29	0.13	-2.20	0.028
Central	Cmic	Lignin_content	Cmic	~	LUI_change	f	0.02	0.15	0.14	0.889	0.02	0.14	0.14	0.889
Central	Cmic	Lignin_content	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	Cmic	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	5.00	0.000	0.99	0.03	32.09	0.000
Central	Cmic	Lignin_content	Cmic	~~	Cmic		0.05	0.01	5.00	0.000	0.92	0.07	12.32	0.000
Central	Cmic	Lignin_content	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Cmic	Lignin_content	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Cmic	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	0.32	0.747	0.00	0.01	0.32	0.747
Central	Cmic	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	0.30	0.768	0.00	0.01	0.30	0.768
Central	Cmic	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.25	0.12	-2.08	0.038	-0.28	0.13	-2.17	0.030
Central	Cmic	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.03	0.15	0.17	0.869	0.02	0.14	0.17	0.869
Central	Cmic	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.25	0.12	-2.08	0.038	-0.28	0.13	-2.16	0.031
Central	Cmic	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.02	0.15	0.16	0.873	0.00	0.14	0.03	0.976
Central	Cmic	pH	pH_historic	~	LUI_historic	a	-0.04	0.11	-0.32	0.747	-0.05	0.14	-0.32	0.747
Central	Cmic	pH	pH_change	~	LUI_change	b	-0.16	0.15	-1.07	0.286	-0.15	0.14	-1.08	0.280
Central	Cmic	pH	Cmic	~	pH_historic	c	0.00	0.14	-0.02	0.985	0.00	0.13	-0.02	0.985
Central	Cmic	pH	Cmic	~	pH_change	d	-0.15	0.15	-1.05	0.296	-0.14	0.13	-1.06	0.291
Central	Cmic	pH	Cmic	~	LUI_historic	e	-0.26	0.12	-2.23	0.026	-0.30	0.13	-2.33	0.020
Central	Cmic	pH	Cmic	~	LUI_change	f	0.00	0.15	0.02	0.983	0.00	0.14	0.02	0.983
Central	Cmic	pH	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	Cmic	pH	pH_historic	~~	pH_historic		0.04	0.01	5.00	0.000	1.00	0.01	77.64	0.000
Central	Cmic	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	0.98	0.04	23.68	0.000
Central	Cmic	pH	Cmic	~~	Cmic		0.05	0.01	5.00	0.000	0.89	0.08	10.85	0.000
Central	Cmic	pH	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Cmic	pH	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Cmic	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	0.02	0.985	0.00	0.01	0.02	0.985
Central	Cmic	pH	LUI_change_in	:=	b*d	LUI_change_in	0.02	0.03	0.75	0.455	0.02	0.03	0.75	0.453
Central	Cmic	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.26	0.12	-2.23	0.026	-0.30	0.13	-2.33	0.020
Central	Cmic	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.03	0.15	0.18	0.860	0.02	0.14	0.18	0.860
Central	Cmic	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.26	0.12	-2.23	0.026	-0.30	0.13	-2.32	0.020
Central	Cmic	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.03	0.15	0.17	0.864	0.01	0.14	0.03	0.972

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*p*	est.std	se.std	z.std	*p*.std
Central	Nmic	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.53	0.09	5.84	0.000	0.64	0.08	7.58	0.000
Central	Nmic	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.05	0.11	-0.46	0.647	-0.07	0.14	-0.46	0.646
Central	Nmic	CWM_leaf_P	Nmic	~	CWM_leafP_historic	c	-0.17	0.15	-1.12	0.264	-0.18	0.16	-1.13	0.259
Central	Nmic	CWM_leaf_P	Nmic	~	CWM_leafP_change	d	-0.03	0.17	-0.17	0.862	-0.02	0.13	-0.17	0.862
Central	Nmic	CWM_leaf_P	Nmic	~	LUI_historic	e	-0.25	0.13	-2.00	0.045	-0.32	0.16	-2.06	0.039
Central	Nmic	CWM_leaf_P	Nmic	~	LUI_change	f	-0.08	0.13	-0.64	0.524	-0.08	0.13	-0.64	0.523
Central	Nmic	CWM_leaf_P	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	Nmic	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	5.00	0.000	0.59	0.11	5.55	0.000
Central	Nmic	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.02	0.00	5.00	0.000	1.00	0.02	54.73	0.000
Central	Nmic	CWM_leaf_P	Nmic	~~	Nmic		0.03	0.01	5.00	0.000	0.78	0.10	7.49	0.000
Central	Nmic	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Nmic	CWM_leaf_P	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Nmic	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	-0.09	0.08	-1.10	0.272	-0.12	0.10	-1.11	0.267
Central	Nmic	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	0.16	0.871	0.00	0.01	0.16	0.871
Central	Nmic	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.34	0.10	-3.47	0.001	-0.44	0.11	-3.86	0.000
Central	Nmic	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.08	0.13	-0.63	0.530	-0.08	0.13	-0.63	0.529
Central	Nmic	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.34	0.10	-3.48	0.001	-0.44	0.11	-3.91	0.000
Central	Nmic	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.08	0.13	-0.64	0.524	-0.11	0.14	-0.77	0.442
Central	Nmic	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	-0.11	0.13	-0.88	0.380	-0.12	0.14	-0.88	0.377
Central	Nmic	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.04	0.13	0.30	0.768	0.04	0.14	0.30	0.768
Central	Nmic	CWM_MycInt	Nmic	~	CWM_MycInt_historic	c	0.14	0.11	1.25	0.211	0.16	0.13	1.26	0.207
Central	Nmic	CWM_MycInt	Nmic	~	CWM_MycInt_change	d	-0.09	0.14	-0.67	0.502	-0.08	0.13	-0.67	0.501
Central	Nmic	CWM_MycInt	Nmic	~	LUI_historic	e	-0.30	0.10	-3.09	0.002	-0.39	0.12	-3.33	0.001
Central	Nmic	CWM_MycInt	Nmic	~	LUI_change	f	-0.10	0.12	-0.77	0.444	-0.10	0.13	-0.77	0.442
Central	Nmic	CWM_MycInt	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	Nmic	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	5.00	0.000	0.99	0.03	28.71	0.000
Central	Nmic	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	1.00	0.01	84.79	0.000
Central	Nmic	CWM_MycInt	Nmic	~~	Nmic		0.03	0.01	5.00	0.000	0.79	0.10	7.66	0.000
Central	Nmic	CWM_MycInt	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Nmic	CWM_MycInt	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Nmic	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	-0.02	0.02	-0.72	0.473	-0.02	0.03	-0.73	0.468
Central	Nmic	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	-0.27	0.787	0.00	0.01	-0.27	0.787
Central	Nmic	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.31	0.10	-3.21	0.001	-0.41	0.12	-3.52	0.000
Central	Nmic	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.10	0.13	-0.79	0.429	-0.10	0.13	-0.79	0.428
Central	Nmic	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.31	0.10	-3.22	0.001	-0.42	0.12	-3.57	0.000
Central	Nmic	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.10	0.13	-0.80	0.425	-0.13	0.14	-0.92	0.360
Central	Nmic	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.03	0.12	0.23	0.821	0.03	0.14	0.23	0.821
Central	Nmic	Plant_biomass	Plant_biomass	~	LUI_change	b	0.13	0.15	0.87	0.385	0.12	0.14	0.88	0.382
Central	Nmic	Plant_biomass	Nmic	~	Plant_biomass	c	0.10	0.12	0.81	0.417	0.10	0.13	0.82	0.415
Central	Nmic	Plant_biomass	Nmic	~	LUI_historic	e	-0.34	0.10	-3.52	0.000	-0.44	0.11	-3.91	0.000
Central	Nmic	Plant_biomass	Nmic	~	LUI_change	f	-0.10	0.13	-0.76	0.445	-0.10	0.13	-0.77	0.444
Central	Nmic	Plant_biomass	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	Nmic	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	5.00	0.000	0.98	0.04	27.60	0.000
Central	Nmic	Plant_biomass	Nmic	~~	Nmic		0.03	0.01	5.00	0.000	0.79	0.10	7.64	0.000
Central	Nmic	Plant_biomass	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Nmic	Plant_biomass	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Nmic	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	0.22	0.827	0.00	0.02	0.22	0.827
Central	Nmic	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.01	0.02	0.59	0.553	0.01	0.02	0.59	0.553
Central	Nmic	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.34	0.10	-3.47	0.001	-0.44	0.11	-3.85	0.000
Central	Nmic	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.08	0.13	-0.67	0.506	-0.08	0.13	-0.67	0.505
Central	Nmic	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.34	0.10	-3.47	0.001	-0.44	0.11	-3.91	0.000
Central	Nmic	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.09	0.13	-0.67	0.501	-0.11	0.14	-0.80	0.422
Central	Nmic	Lignin_content	Lignin_content	~	LUI_historic	a	0.07	0.12	0.60	0.548	0.09	0.14	0.60	0.547
Central	Nmic	Lignin_content	Lignin_content	~	LUI_change	b	0.07	0.16	0.47	0.642	0.07	0.14	0.47	0.641
Central	Nmic	Lignin_content	Nmic	~	Lignin_content	c	0.12	0.11	1.07	0.283	0.14	0.13	1.08	0.280
Central	Nmic	Lignin_content	Nmic	~	LUI_historic	e	-0.35	0.10	-3.59	0.000	-0.45	0.11	-3.99	0.000
Central	Nmic	Lignin_content	Nmic	~	LUI_change	f	-0.09	0.13	-0.74	0.459	-0.09	0.13	-0.74	0.457
Central	Nmic	Lignin_content	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	Nmic	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	5.00	0.000	0.99	0.03	32.09	0.000
Central	Nmic	Lignin_content	Nmic	~~	Nmic		0.03	0.01	5.00	0.000	0.78	0.10	7.50	0.000
Central	Nmic	Lignin_content	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Nmic	Lignin_content	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Nmic	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.02	0.52	0.600	0.01	0.02	0.52	0.601
Central	Nmic	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.01	0.02	0.43	0.670	0.01	0.02	0.43	0.670
Central	Nmic	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.34	0.10	-3.47	0.001	-0.44	0.11	-3.85	0.000
Central	Nmic	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.08	0.13	-0.67	0.506	-0.08	0.13	-0.67	0.505
Central	Nmic	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.34	0.10	-3.47	0.001	-0.44	0.11	-3.91	0.000
Central	Nmic	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.09	0.13	-0.67	0.501	-0.11	0.14	-0.80	0.422
Central	Nmic	pH	pH_historic	~	LUI_historic	a	-0.04	0.11	-0.32	0.747	-0.05	0.14	-0.32	0.747
Central	Nmic	pH	pH_change	~	LUI_change	b	-0.16	0.15	-1.07	0.286	-0.15	0.14	-1.08	0.280
Central	Nmic	pH	Nmic	~	pH_historic	c	0.07	0.12	0.58	0.562	0.07	0.13	0.58	0.561
Central	Nmic	pH	Nmic	~	pH_change	d	0.06	0.12	0.48	0.633	0.06	0.13	0.48	0.633
Central	Nmic	pH	Nmic	~	LUI_historic	e	-0.33	0.10	-3.38	0.001	-0.43	0.11	-3.73	0.000
Central	Nmic	pH	Nmic	~	LUI_change	f	-0.09	0.13	-0.72	0.474	-0.09	0.13	-0.72	0.472
Central	Nmic	pH	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	Nmic	pH	pH_historic	~~	pH_historic		0.04	0.01	5.00	0.000	1.00	0.01	77.64	0.000
Central	Nmic	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	0.98	0.04	23.68	0.000
Central	Nmic	pH	Nmic	~~	Nmic		0.03	0.01	5.00	0.000	0.79	0.10	7.74	0.000
Central	Nmic	pH	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Nmic	pH	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Nmic	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	-0.28	0.778	0.00	0.01	-0.28	0.778
Central	Nmic	pH	LUI_change_in	:=	b*d	LUI_change_in	-0.01	0.02	-0.44	0.663	-0.01	0.02	-0.44	0.663
Central	Nmic	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.33	0.10	-3.40	0.001	-0.43	0.11	-3.76	0.000
Central	Nmic	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.10	0.13	-0.80	0.427	-0.10	0.13	-0.80	0.425
Central	Nmic	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.33	0.10	-3.41	0.001	-0.44	0.11	-3.82	0.000
Central	Nmic	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.10	0.13	-0.80	0.422	-0.13	0.14	-0.92	0.357

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*p*	est.std	se.std	z.std	*p*.std
Central	Cmic:Nmic ratio	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.53	0.09	5.84	0.000	0.64	0.08	7.58	0.000
Central	Cmic:Nmic ratio	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.05	0.11	-0.46	0.647	-0.07	0.14	-0.46	0.646
Central	Cmic:Nmic ratio	CWM_leaf_P	RatioCmic_Nmic	~	CWM_leafP_historic	c	0.02	0.18	0.11	0.915	0.02	0.17	0.11	0.915
Central	Cmic:Nmic ratio	CWM_leaf_P	RatioCmic_Nmic	~	CWM_leafP_change	d	0.07	0.21	0.36	0.722	0.05	0.13	0.36	0.721
Central	Cmic:Nmic ratio	CWM_leaf_P	RatioCmic_Nmic	~	LUI_historic	e	0.27	0.15	1.78	0.076	0.31	0.17	1.83	0.067
Central	Cmic:Nmic ratio	CWM_leaf_P	RatioCmic_Nmic	~	LUI_change	f	-0.07	0.15	-0.48	0.633	-0.06	0.13	-0.48	0.633
Central	Cmic:Nmic ratio	CWM_leaf_P	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	Cmic:Nmic ratio	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	5.00	0.000	0.59	0.11	5.55	0.000
Central	Cmic:Nmic ratio	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.02	0.00	5.00	0.000	1.00	0.02	54.73	0.000
Central	Cmic:Nmic ratio	CWM_leaf_P	RatioCmic_Nmic	~~	RatioCmic_Nmic		0.05	0.01	5.00	0.000	0.89	0.08	10.83	0.000
Central	Cmic:Nmic ratio	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Cmic:Nmic ratio	CWM_leaf_P	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Cmic:Nmic ratio	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.10	0.11	0.915	0.01	0.11	0.11	0.915
Central	Cmic:Nmic ratio	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	-0.28	0.779	0.00	0.01	-0.28	0.778
Central	Cmic:Nmic ratio	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.28	0.12	2.39	0.017	0.32	0.13	2.52	0.012
Central	Cmic:Nmic ratio	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.08	0.15	-0.50	0.617	-0.07	0.13	-0.50	0.616
Central	Cmic:Nmic ratio	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.28	0.12	2.39	0.017	0.32	0.13	2.49	0.013
Central	Cmic:Nmic ratio	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.08	0.15	-0.49	0.621	-0.05	0.14	-0.33	0.741
Central	Cmic:Nmic ratio	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	-0.11	0.13	-0.88	0.380	-0.12	0.14	-0.88	0.377
Central	Cmic:Nmic ratio	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.04	0.13	0.30	0.768	0.04	0.14	0.30	0.768
Central	Cmic:Nmic ratio	CWM_MycInt	RatioCmic_Nmic	~	CWM_MycInt_historic	c	0.01	0.13	0.10	0.921	0.01	0.14	0.10	0.921
Central	Cmic:Nmic ratio	CWM_MycInt	RatioCmic_Nmic	~	CWM_MycInt_change	d	0.22	0.17	1.32	0.187	0.18	0.13	1.34	0.180
Central	Cmic:Nmic ratio	CWM_MycInt	RatioCmic_Nmic	~	LUI_historic	e	0.22	0.12	1.89	0.059	0.26	0.13	1.95	0.052
Central	Cmic:Nmic ratio	CWM_MycInt	RatioCmic_Nmic	~	LUI_change	f	-0.08	0.15	-0.53	0.595	-0.07	0.13	-0.53	0.594
Central	Cmic:Nmic ratio	CWM_MycInt	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	Cmic:Nmic ratio	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	5.00	0.000	0.99	0.03	28.71	0.000
Central	Cmic:Nmic ratio	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	1.00	0.01	84.79	0.000
Central	Cmic:Nmic ratio	CWM_MycInt	RatioCmic_Nmic	~~	RatioCmic_Nmic		0.05	0.01	5.00	0.000	0.90	0.08	11.40	0.000
Central	Cmic:Nmic ratio	CWM_MycInt	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Cmic:Nmic ratio	CWM_MycInt	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Cmic:Nmic ratio	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	-0.10	0.922	0.00	0.02	-0.10	0.922
Central	Cmic:Nmic ratio	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.01	0.03	0.29	0.773	0.01	0.03	0.29	0.773
Central	Cmic:Nmic ratio	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.22	0.12	1.89	0.059	0.25	0.13	1.95	0.051
Central	Cmic:Nmic ratio	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.07	0.15	-0.47	0.639	-0.06	0.14	-0.47	0.638
Central	Cmic:Nmic ratio	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.22	0.12	1.89	0.059	0.25	0.13	1.92	0.056
Central	Cmic:Nmic ratio	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.07	0.15	-0.46	0.642	-0.05	0.14	-0.34	0.734
Central	Cmic:Nmic ratio	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.03	0.12	0.23	0.821	0.03	0.14	0.23	0.821
Central	Cmic:Nmic ratio	Plant_biomass	Plant_biomass	~	LUI_change	b	0.13	0.15	0.87	0.385	0.12	0.14	0.88	0.382
Central	Cmic:Nmic ratio	Plant_biomass	RatioCmic_Nmic	~	Plant_biomass	c	-0.16	0.14	-1.14	0.254	-0.15	0.13	-1.15	0.249
Central	Cmic:Nmic ratio	Plant_biomass	RatioCmic_Nmic	~	LUI_historic	e	0.29	0.12	2.45	0.014	0.32	0.13	2.58	0.010
Central	Cmic:Nmic ratio	Plant_biomass	RatioCmic_Nmic	~	LUI_change	f	-0.06	0.15	-0.36	0.719	-0.05	0.13	-0.36	0.719
Central	Cmic:Nmic ratio	Plant_biomass	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	Cmic:Nmic ratio	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	5.00	0.000	0.98	0.04	27.60	0.000
Central	Cmic:Nmic ratio	Plant_biomass	RatioCmic_Nmic	~~	RatioCmic_Nmic		0.05	0.01	5.00	0.000	0.87	0.09	9.94	0.000
Central	Cmic:Nmic ratio	Plant_biomass	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Cmic:Nmic ratio	Plant_biomass	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Cmic:Nmic ratio	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	-0.22	0.824	-0.01	0.02	-0.22	0.824
Central	Cmic:Nmic ratio	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	-0.02	0.03	-0.69	0.489	-0.02	0.03	-0.69	0.488
Central	Cmic:Nmic ratio	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.28	0.12	2.38	0.017	0.32	0.13	2.51	0.012
Central	Cmic:Nmic ratio	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.08	0.15	-0.50	0.620	-0.07	0.13	-0.50	0.619
Central	Cmic:Nmic ratio	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.28	0.12	2.38	0.017	0.32	0.13	2.47	0.013
Central	Cmic:Nmic ratio	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.08	0.15	-0.49	0.624	-0.05	0.14	-0.33	0.744
Central	Cmic:Nmic ratio	Lignin_content	Lignin_content	~	LUI_historic	a	0.07	0.12	0.60	0.548	0.09	0.14	0.60	0.547
Central	Cmic:Nmic ratio	Lignin_content	Lignin_content	~	LUI_change	b	0.07	0.16	0.47	0.642	0.07	0.14	0.47	0.641
Central	Cmic:Nmic ratio	Lignin_content	RatioCmic_Nmic	~	Lignin_content	c	-0.08	0.14	-0.57	0.570	-0.08	0.13	-0.57	0.569
Central	Cmic:Nmic ratio	Lignin_content	RatioCmic_Nmic	~	LUI_historic	e	0.29	0.12	2.43	0.015	0.33	0.13	2.56	0.010
Central	Cmic:Nmic ratio	Lignin_content	RatioCmic_Nmic	~	LUI_change	f	-0.07	0.15	-0.46	0.646	-0.06	0.13	-0.46	0.646
Central	Cmic:Nmic ratio	Lignin_content	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	Cmic:Nmic ratio	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	5.00	0.000	0.99	0.03	32.09	0.000
Central	Cmic:Nmic ratio	Lignin_content	RatioCmic_Nmic	~~	RatioCmic_Nmic		0.05	0.01	5.00	0.000	0.89	0.08	10.69	0.000
Central	Cmic:Nmic ratio	Lignin_content	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Cmic:Nmic ratio	Lignin_content	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Cmic:Nmic ratio	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.01	-0.41	0.680	-0.01	0.02	-0.41	0.680
Central	Cmic:Nmic ratio	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	-0.01	0.02	-0.36	0.719	-0.01	0.01	-0.36	0.719
Central	Cmic:Nmic ratio	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.28	0.12	2.38	0.017	0.32	0.13	2.51	0.012
Central	Cmic:Nmic ratio	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.08	0.15	-0.50	0.620	-0.07	0.13	-0.50	0.619
Central	Cmic:Nmic ratio	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.28	0.12	2.38	0.017	0.32	0.13	2.47	0.013
Central	Cmic:Nmic ratio	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.08	0.15	-0.49	0.624	-0.05	0.14	-0.33	0.744
Central	Cmic:Nmic ratio	pH	pH_historic	~	LUI_historic	a	-0.04	0.11	-0.32	0.747	-0.05	0.14	-0.32	0.747
Central	Cmic:Nmic ratio	pH	pH_change	~	LUI_change	b	-0.16	0.15	-1.07	0.286	-0.15	0.14	-1.08	0.280
Central	Cmic:Nmic ratio	pH	RatioCmic_Nmic	~	pH_historic	c	-0.50	0.14	-3.68	0.000	-0.42	0.11	-3.97	0.000
Central	Cmic:Nmic ratio	pH	RatioCmic_Nmic	~	pH_change	d	-0.37	0.14	-2.74	0.006	-0.32	0.11	-2.83	0.005
Central	Cmic:Nmic ratio	pH	RatioCmic_Nmic	~	LUI_historic	e	0.22	0.11	2.05	0.041	0.24	0.11	2.08	0.037
Central	Cmic:Nmic ratio	pH	RatioCmic_Nmic	~	LUI_change	f	-0.02	0.14	-0.13	0.897	-0.02	0.12	-0.13	0.897
Central	Cmic:Nmic ratio	pH	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	Cmic:Nmic ratio	pH	pH_historic	~~	pH_historic		0.04	0.01	5.00	0.000	1.00	0.01	77.64	0.000
Central	Cmic:Nmic ratio	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	0.98	0.04	23.68	0.000
Central	Cmic:Nmic ratio	pH	RatioCmic_Nmic	~~	RatioCmic_Nmic		0.04	0.01	5.00	0.000	0.66	0.11	6.26	0.000
Central	Cmic:Nmic ratio	pH	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Cmic:Nmic ratio	pH	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Cmic:Nmic ratio	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.02	0.06	0.32	0.748	0.02	0.06	0.32	0.747
Central	Cmic:Nmic ratio	pH	LUI_change_in	:=	b*d	LUI_change_in	0.06	0.06	1.00	0.320	0.05	0.05	1.00	0.317
Central	Cmic:Nmic ratio	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.24	0.12	1.97	0.049	0.26	0.13	2.03	0.043
Central	Cmic:Nmic ratio	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.04	0.15	0.26	0.793	0.03	0.12	0.26	0.793
Central	Cmic:Nmic ratio	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.24	0.12	1.97	0.049	0.26	0.13	2.05	0.041
Central	Cmic:Nmic ratio	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.04	0.15	0.27	0.789	0.05	0.13	0.38	0.704

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*p*	est.std	se.std	z.std	*p*.std
Central	Pmic	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.54	0.09	5.79	0.000	0.65	0.09	7.65	0.000
Central	Pmic	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.07	0.11	-0.59	0.557	-0.09	0.15	-0.59	0.555
Central	Pmic	CWM_leaf_P	Pmic	~	CWM_leafP_historic	c	0.34	0.19	1.78	0.075	0.33	0.18	1.84	0.066
Central	Pmic	CWM_leaf_P	Pmic	~	CWM_leafP_change	d	0.21	0.21	0.98	0.326	0.14	0.14	0.99	0.322
Central	Pmic	CWM_leaf_P	Pmic	~	LUI_historic	e	-0.10	0.16	-0.62	0.536	-0.12	0.19	-0.62	0.534
Central	Pmic	CWM_leaf_P	Pmic	~	LUI_change	f	0.08	0.16	0.52	0.605	0.07	0.14	0.52	0.604
Central	Pmic	CWM_leaf_P	LUI_historic	~~	LUI_change	g	0.00	0.01	0.48	0.629	0.07	0.15	0.49	0.626
Central	Pmic	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	4.74	0.000	0.57	0.11	5.13	0.000
Central	Pmic	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.02	0.01	4.74	0.000	0.99	0.03	38.44	0.000
Central	Pmic	CWM_leaf_P	Pmic	~~	Pmic		0.05	0.01	4.74	0.000	0.90	0.08	10.81	0.000
Central	Pmic	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.07	0.02	4.74	0.000	1.00	0.00	NA	NA
Central	Pmic	CWM_leaf_P	LUI_change	~~	LUI_change		0.04	0.01	4.74	0.000	1.00	0.00	NA	NA
Central	Pmic	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.18	0.11	1.70	0.089	0.22	0.12	1.75	0.080
Central	Pmic	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	-0.01	0.03	-0.50	0.614	-0.01	0.02	-0.51	0.614
Central	Pmic	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.09	0.12	0.69	0.489	0.10	0.15	0.70	0.487
Central	Pmic	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.07	0.16	0.43	0.668	0.06	0.14	0.43	0.668
Central	Pmic	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.09	0.12	0.69	0.487	0.11	0.15	0.73	0.467
Central	Pmic	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.07	0.16	0.43	0.667	0.07	0.14	0.48	0.632
Central	Pmic	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	-0.12	0.14	-0.92	0.359	-0.14	0.15	-0.93	0.354
Central	Pmic	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.02	0.14	0.17	0.868	0.03	0.15	0.17	0.868
Central	Pmic	CWM_MycInt	Pmic	~	CWM_MycInt_historic	c	0.01	0.14	0.05	0.957	0.01	0.15	0.05	0.957
Central	Pmic	CWM_MycInt	Pmic	~	CWM_MycInt_change	d	0.10	0.17	0.58	0.564	0.09	0.15	0.58	0.563
Central	Pmic	CWM_MycInt	Pmic	~	LUI_historic	e	0.05	0.12	0.44	0.661	0.07	0.15	0.44	0.660
Central	Pmic	CWM_MycInt	Pmic	~	LUI_change	f	0.06	0.16	0.37	0.711	0.06	0.15	0.37	0.711
Central	Pmic	CWM_MycInt	LUI_historic	~~	LUI_change	g	0.00	0.01	0.48	0.629	0.07	0.15	0.49	0.626
Central	Pmic	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.06	0.01	4.74	0.000	0.98	0.04	24.75	0.000
Central	Pmic	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.04	0.01	4.74	0.000	1.00	0.01	135.81	0.000
Central	Pmic	CWM_MycInt	Pmic	~~	Pmic		0.05	0.01	4.74	0.000	0.99	0.04	27.13	0.000
Central	Pmic	CWM_MycInt	LUI_historic	~~	LUI_historic		0.07	0.02	4.74	0.000	1.00	0.00	NA	NA
Central	Pmic	CWM_MycInt	LUI_change	~~	LUI_change		0.04	0.01	4.74	0.000	1.00	0.00	NA	NA
Central	Pmic	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	-0.05	0.957	0.00	0.02	-0.05	0.957
Central	Pmic	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	0.16	0.873	0.00	0.01	0.16	0.873
Central	Pmic	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.05	0.12	0.44	0.663	0.07	0.15	0.44	0.663
Central	Pmic	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.06	0.16	0.38	0.701	0.06	0.15	0.38	0.701
Central	Pmic	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.05	0.12	0.44	0.662	0.07	0.15	0.47	0.642
Central	Pmic	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.06	0.16	0.39	0.700	0.06	0.15	0.42	0.677
Central	Pmic	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.03	0.13	0.21	0.836	0.03	0.15	0.21	0.836
Central	Pmic	Plant_biomass	Plant_biomass	~	LUI_change	b	0.14	0.16	0.85	0.393	0.13	0.15	0.86	0.390
Central	Pmic	Plant_biomass	Pmic	~	Plant_biomass	c	-0.16	0.15	-1.07	0.284	-0.16	0.15	-1.09	0.278
Central	Pmic	Plant_biomass	Pmic	~	LUI_historic	e	0.09	0.12	0.72	0.472	0.11	0.15	0.72	0.469
Central	Pmic	Plant_biomass	Pmic	~	LUI_change	f	0.08	0.16	0.51	0.611	0.08	0.15	0.51	0.611
Central	Pmic	Plant_biomass	LUI_historic	~~	LUI_change	g	0.00	0.01	0.48	0.629	0.07	0.15	0.49	0.626
Central	Pmic	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	4.74	0.000	0.98	0.04	25.37	0.000
Central	Pmic	Plant_biomass	Pmic	~~	Pmic		0.05	0.01	4.74	0.000	0.96	0.06	17.09	0.000
Central	Pmic	Plant_biomass	LUI_historic	~~	LUI_historic		0.07	0.02	4.74	0.000	1.00	0.00	NA	NA
Central	Pmic	Plant_biomass	LUI_change	~~	LUI_change		0.04	0.01	4.74	0.000	1.00	0.00	NA	NA
Central	Pmic	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	-0.20	0.839	-0.01	0.02	-0.20	0.839
Central	Pmic	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	-0.02	0.03	-0.67	0.504	-0.02	0.03	-0.67	0.503
Central	Pmic	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.08	0.12	0.68	0.497	0.10	0.15	0.68	0.495
Central	Pmic	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.06	0.16	0.37	0.711	0.06	0.15	0.37	0.710
Central	Pmic	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.08	0.12	0.68	0.496	0.11	0.15	0.71	0.478
Central	Pmic	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.06	0.16	0.37	0.709	0.06	0.15	0.42	0.675
Central	Pmic	Lignin_content	Lignin_content	~	LUI_historic	a	0.10	0.13	0.75	0.455	0.11	0.15	0.75	0.452
Central	Pmic	Lignin_content	Lignin_content	~	LUI_change	b	0.07	0.17	0.38	0.703	0.06	0.15	0.38	0.703
Central	Pmic	Lignin_content	Pmic	~	Lignin_content	c	0.00	0.14	0.02	0.984	0.00	0.15	0.02	0.984
Central	Pmic	Lignin_content	Pmic	~	LUI_historic	e	0.08	0.12	0.67	0.501	0.10	0.15	0.68	0.499
Central	Pmic	Lignin_content	Pmic	~	LUI_change	f	0.06	0.16	0.37	0.712	0.06	0.15	0.37	0.711
Central	Pmic	Lignin_content	LUI_historic	~~	LUI_change	g	0.00	0.01	0.48	0.629	0.07	0.15	0.49	0.626
Central	Pmic	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	4.74	0.000	0.98	0.04	26.22	0.000
Central	Pmic	Lignin_content	Pmic	~~	Pmic		0.05	0.01	4.74	0.000	0.99	0.04	28.36	0.000
Central	Pmic	Lignin_content	LUI_historic	~~	LUI_historic		0.07	0.02	4.74	0.000	1.00	0.00	NA	NA
Central	Pmic	Lignin_content	LUI_change	~~	LUI_change		0.04	0.01	4.74	0.000	1.00	0.00	NA	NA
Central	Pmic	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	0.02	0.984	0.00	0.02	0.02	0.984
Central	Pmic	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	0.02	0.984	0.00	0.01	0.02	0.984
Central	Pmic	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.08	0.12	0.68	0.497	0.10	0.15	0.68	0.495
Central	Pmic	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.06	0.16	0.37	0.711	0.06	0.15	0.37	0.710
Central	Pmic	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.08	0.12	0.68	0.496	0.11	0.15	0.71	0.478
Central	Pmic	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.06	0.16	0.37	0.709	0.06	0.15	0.42	0.675
Central	Pmic	pH	pH_historic	~	LUI_historic	a	-0.02	0.12	-0.16	0.875	-0.02	0.15	-0.16	0.875
Central	Pmic	pH	pH_change	~	LUI_change	b	-0.16	0.16	-1.01	0.314	-0.15	0.15	-1.02	0.309
Central	Pmic	pH	Pmic	~	pH_historic	c	0.22	0.15	1.46	0.143	0.21	0.14	1.50	0.135
Central	Pmic	pH	Pmic	~	pH_change	d	0.16	0.15	1.04	0.297	0.15	0.14	1.05	0.292
Central	Pmic	pH	Pmic	~	LUI_historic	e	0.11	0.12	0.92	0.357	0.13	0.14	0.93	0.353
Central	Pmic	pH	Pmic	~	LUI_change	f	0.04	0.16	0.23	0.820	0.03	0.15	0.23	0.820
Central	Pmic	pH	LUI_historic	~~	LUI_change	g	0.00	0.01	0.48	0.629	0.07	0.15	0.49	0.626
Central	Pmic	pH	pH_historic	~~	pH_historic		0.05	0.01	4.74	0.000	1.00	0.01	143.35	0.000
Central	Pmic	pH	pH_change	~~	pH_change		0.04	0.01	4.74	0.000	0.98	0.04	22.61	0.000
Central	Pmic	pH	Pmic	~~	Pmic		0.05	0.01	4.74	0.000	0.92	0.08	11.79	0.000
Central	Pmic	pH	LUI_historic	~~	LUI_historic		0.07	0.02	4.74	0.000	1.00	0.00	NA	NA
Central	Pmic	pH	LUI_change	~~	LUI_change		0.04	0.01	4.74	0.000	1.00	0.00	NA	NA
Central	Pmic	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.03	-0.16	0.876	-0.01	0.03	-0.16	0.876
Central	Pmic	pH	LUI_change_in	:=	b*d	LUI_change_in	-0.03	0.03	-0.72	0.469	-0.02	0.03	-0.73	0.467
Central	Pmic	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.11	0.12	0.87	0.386	0.13	0.15	0.87	0.382
Central	Pmic	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.01	0.16	0.07	0.941	0.01	0.15	0.07	0.941
Central	Pmic	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.11	0.12	0.87	0.385	0.13	0.15	0.88	0.378
Central	Pmic	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.01	0.16	0.08	0.939	0.02	0.15	0.14	0.892

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*p*	est.std	se.std	z.std	*p*.std
Central	beta-glucosidase	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.53	0.09	5.84	0.000	0.64	0.08	7.58	0.000
Central	beta-glucosidase	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.05	0.11	-0.46	0.647	-0.07	0.14	-0.46	0.646
Central	beta-glucosidase	CWM_leaf_P	Glucosidase	~	CWM_leafP_historic	c	-0.16	0.11	-1.47	0.141	-0.21	0.14	-1.48	0.139
Central	beta-glucosidase	CWM_leaf_P	Glucosidase	~	CWM_leafP_change	d	-0.59	0.12	-4.76	0.000	-0.53	0.10	-5.45	0.000
Central	beta-glucosidase	CWM_leaf_P	Glucosidase	~	LUI_historic	e	-0.08	0.09	-0.84	0.401	-0.12	0.14	-0.84	0.400
Central	beta-glucosidase	CWM_leaf_P	Glucosidase	~	LUI_change	f	0.13	0.09	1.43	0.153	0.16	0.11	1.44	0.151
Central	beta-glucosidase	CWM_leaf_P	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	beta-glucosidase	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	5.00	0.000	0.59	0.11	5.55	0.000
Central	beta-glucosidase	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.02	0.00	5.00	0.000	1.00	0.02	54.73	0.000
Central	beta-glucosidase	CWM_leaf_P	Glucosidase	~~	Glucosidase		0.02	0.00	5.00	0.000	0.61	0.10	5.82	0.000
Central	beta-glucosidase	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	beta-glucosidase	CWM_leaf_P	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	beta-glucosidase	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	-0.09	0.06	-1.43	0.154	-0.13	0.09	-1.44	0.150
Central	beta-glucosidase	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.03	0.06	0.46	0.649	0.03	0.07	0.46	0.647
Central	beta-glucosidase	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.16	0.07	-2.25	0.024	-0.25	0.11	-2.29	0.022
Central	beta-glucosidase	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.16	0.11	1.44	0.149	0.19	0.13	1.47	0.143
Central	beta-glucosidase	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.16	0.07	-2.25	0.025	-0.24	0.11	-2.12	0.034
Central	beta-glucosidase	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.16	0.11	1.44	0.150	0.18	0.14	1.30	0.195
Central	beta-glucosidase	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	-0.11	0.13	-0.88	0.380	-0.12	0.14	-0.88	0.377
Central	beta-glucosidase	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.04	0.13	0.30	0.768	0.04	0.14	0.30	0.768
Central	beta-glucosidase	CWM_MycInt	Glucosidase	~	CWM_MycInt_historic	c	-0.17	0.09	-1.84	0.065	-0.24	0.13	-1.89	0.059
Central	beta-glucosidase	CWM_MycInt	Glucosidase	~	CWM_MycInt_change	d	-0.08	0.12	-0.67	0.503	-0.09	0.13	-0.67	0.502
Central	beta-glucosidase	CWM_MycInt	Glucosidase	~	LUI_historic	e	-0.15	0.08	-1.86	0.063	-0.25	0.13	-1.91	0.056
Central	beta-glucosidase	CWM_MycInt	Glucosidase	~	LUI_change	f	0.17	0.11	1.61	0.108	0.21	0.13	1.64	0.102
Central	beta-glucosidase	CWM_MycInt	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	beta-glucosidase	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	5.00	0.000	0.99	0.03	28.71	0.000
Central	beta-glucosidase	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	1.00	0.01	84.79	0.000
Central	beta-glucosidase	CWM_MycInt	Glucosidase	~~	Glucosidase		0.02	0.00	5.00	0.000	0.85	0.09	9.27	0.000
Central	beta-glucosidase	CWM_MycInt	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	beta-glucosidase	CWM_MycInt	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	beta-glucosidase	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.02	0.02	0.79	0.428	0.03	0.04	0.79	0.428
Central	beta-glucosidase	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	-0.27	0.787	0.00	0.01	-0.27	0.787
Central	beta-glucosidase	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.14	0.09	-1.59	0.111	-0.22	0.13	-1.63	0.103
Central	beta-glucosidase	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.17	0.11	1.57	0.116	0.21	0.13	1.60	0.109
Central	beta-glucosidase	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.14	0.09	-1.59	0.113	-0.20	0.14	-1.50	0.135
Central	beta-glucosidase	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.17	0.11	1.57	0.117	0.19	0.13	1.46	0.145
Central	beta-glucosidase	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.03	0.12	0.23	0.821	0.03	0.14	0.23	0.821
Central	beta-glucosidase	Plant_biomass	Plant_biomass	~	LUI_change	b	0.13	0.15	0.87	0.385	0.12	0.14	0.88	0.382
Central	beta-glucosidase	Plant_biomass	Glucosidase	~	Plant_biomass	c	0.21	0.10	2.09	0.037	0.27	0.13	2.16	0.031
Central	beta-glucosidase	Plant_biomass	Glucosidase	~	LUI_historic	e	-0.16	0.08	-1.98	0.047	-0.26	0.13	-2.04	0.041
Central	beta-glucosidase	Plant_biomass	Glucosidase	~	LUI_change	f	0.13	0.11	1.20	0.232	0.16	0.13	1.21	0.227
Central	beta-glucosidase	Plant_biomass	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	beta-glucosidase	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	5.00	0.000	0.98	0.04	27.60	0.000
Central	beta-glucosidase	Plant_biomass	Glucosidase	~~	Glucosidase		0.02	0.00	5.00	0.000	0.84	0.10	8.72	0.000
Central	beta-glucosidase	Plant_biomass	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	beta-glucosidase	Plant_biomass	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	beta-glucosidase	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.02	0.23	0.822	0.01	0.04	0.23	0.822
Central	beta-glucosidase	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.03	0.03	0.80	0.423	0.03	0.04	0.81	0.418
Central	beta-glucosidase	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.16	0.09	-1.84	0.066	-0.25	0.13	-1.90	0.058
Central	beta-glucosidase	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.15	0.11	1.40	0.161	0.19	0.13	1.43	0.154
Central	beta-glucosidase	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.16	0.09	-1.83	0.067	-0.24	0.13	-1.77	0.077
Central	beta-glucosidase	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.15	0.11	1.40	0.162	0.17	0.14	1.27	0.206
Central	beta-glucosidase	Lignin_content	Lignin_content	~	LUI_historic	a	0.07	0.12	0.60	0.548	0.09	0.14	0.60	0.547
Central	beta-glucosidase	Lignin_content	Lignin_content	~	LUI_change	b	0.07	0.16	0.47	0.642	0.07	0.14	0.47	0.641
Central	beta-glucosidase	Lignin_content	Glucosidase	~	Lignin_content	c	0.10	0.10	1.04	0.300	0.14	0.13	1.05	0.296
Central	beta-glucosidase	Lignin_content	Glucosidase	~	LUI_historic	e	-0.16	0.09	-1.94	0.052	-0.26	0.13	-2.00	0.045
Central	beta-glucosidase	Lignin_content	Glucosidase	~	LUI_change	f	0.15	0.11	1.35	0.178	0.18	0.13	1.37	0.172
Central	beta-glucosidase	Lignin_content	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	beta-glucosidase	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	5.00	0.000	0.99	0.03	32.09	0.000
Central	beta-glucosidase	Lignin_content	Glucosidase	~~	Glucosidase		0.02	0.01	5.00	0.000	0.89	0.08	10.63	0.000
Central	beta-glucosidase	Lignin_content	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	beta-glucosidase	Lignin_content	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	beta-glucosidase	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.01	0.52	0.603	0.01	0.02	0.52	0.603
Central	beta-glucosidase	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.01	0.02	0.42	0.672	0.01	0.02	0.43	0.671
Central	beta-glucosidase	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.16	0.09	-1.84	0.066	-0.25	0.13	-1.90	0.058
Central	beta-glucosidase	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.15	0.11	1.40	0.161	0.19	0.13	1.43	0.154
Central	beta-glucosidase	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.16	0.09	-1.83	0.067	-0.24	0.13	-1.77	0.077
Central	beta-glucosidase	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.15	0.11	1.40	0.162	0.17	0.14	1.27	0.206
Central	beta-glucosidase	pH	pH_historic	~	LUI_historic	a	-0.04	0.11	-0.32	0.747	-0.05	0.14	-0.32	0.747
Central	beta-glucosidase	pH	pH_change	~	LUI_change	b	-0.16	0.15	-1.07	0.286	-0.15	0.14	-1.08	0.280
Central	beta-glucosidase	pH	Glucosidase	~	pH_historic	c	0.09	0.10	0.83	0.409	0.11	0.13	0.83	0.406
Central	beta-glucosidase	pH	Glucosidase	~	pH_change	d	-0.04	0.11	-0.41	0.680	-0.06	0.14	-0.41	0.679
Central	beta-glucosidase	pH	Glucosidase	~	LUI_historic	e	-0.16	0.08	-1.86	0.063	-0.25	0.13	-1.92	0.055
Central	beta-glucosidase	pH	Glucosidase	~	LUI_change	f	0.13	0.11	1.17	0.244	0.16	0.13	1.18	0.238
Central	beta-glucosidase	pH	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	beta-glucosidase	pH	pH_historic	~~	pH_historic		0.04	0.01	5.00	0.000	1.00	0.01	77.64	0.000
Central	beta-glucosidase	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	0.98	0.04	23.68	0.000
Central	beta-glucosidase	pH	Glucosidase	~~	Glucosidase		0.02	0.01	5.00	0.000	0.90	0.08	11.07	0.000
Central	beta-glucosidase	pH	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	beta-glucosidase	pH	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	beta-glucosidase	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	-0.30	0.764	-0.01	0.02	-0.30	0.764
Central	beta-glucosidase	pH	LUI_change_in	:=	b*d	LUI_change_in	0.01	0.02	0.39	0.700	0.01	0.02	0.39	0.700
Central	beta-glucosidase	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.16	0.09	-1.89	0.059	-0.26	0.13	-1.95	0.051
Central	beta-glucosidase	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.14	0.11	1.24	0.215	0.17	0.13	1.26	0.209
Central	beta-glucosidase	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.16	0.09	-1.88	0.060	-0.24	0.13	-1.84	0.066
Central	beta-glucosidase	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.14	0.11	1.24	0.217	0.15	0.14	1.10	0.274

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*p*	est.std	se.std	z.std	*p*.std
Central	beta-xylosidase	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.47	0.09	5.05	0.000	0.59	0.09	6.24	0.000
Central	beta-xylosidase	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.04	0.11	-0.35	0.724	-0.05	0.14	-0.35	0.724
Central	beta-xylosidase	CWM_leaf_P	Xylosidase	~	CWM_leafP_historic	c	0.04	0.13	0.29	0.773	0.05	0.16	0.29	0.773
Central	beta-xylosidase	CWM_leaf_P	Xylosidase	~	CWM_leafP_change	d	-0.41	0.13	-3.08	0.002	-0.39	0.12	-3.31	0.001
Central	beta-xylosidase	CWM_leaf_P	Xylosidase	~	LUI_historic	e	-0.15	0.10	-1.45	0.147	-0.23	0.15	-1.47	0.142
Central	beta-xylosidase	CWM_leaf_P	Xylosidase	~	LUI_change	f	0.16	0.10	1.56	0.119	0.20	0.12	1.58	0.113
Central	beta-xylosidase	CWM_leaf_P	LUI_historic	~~	LUI_change	g	0.00	0.01	0.06	0.949	0.01	0.14	0.06	0.949
Central	beta-xylosidase	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	4.90	0.000	0.65	0.11	5.89	0.000
Central	beta-xylosidase	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.02	0.01	4.90	0.000	1.00	0.02	68.09	0.000
Central	beta-xylosidase	CWM_leaf_P	Xylosidase	~~	Xylosidase		0.02	0.00	4.90	0.000	0.76	0.11	7.20	0.000
Central	beta-xylosidase	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.06	0.01	4.90	0.000	1.00	0.00	NA	NA
Central	beta-xylosidase	CWM_leaf_P	LUI_change	~~	LUI_change		0.04	0.01	4.90	0.000	1.00	0.00	NA	NA
Central	beta-xylosidase	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.02	0.06	0.29	0.774	0.03	0.09	0.29	0.774
Central	beta-xylosidase	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.02	0.05	0.35	0.726	0.02	0.06	0.35	0.725
Central	beta-xylosidase	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.13	0.08	-1.58	0.114	-0.20	0.12	-1.61	0.108
Central	beta-xylosidase	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.17	0.11	1.57	0.116	0.22	0.14	1.61	0.108
Central	beta-xylosidase	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.13	0.08	-1.58	0.114	-0.20	0.13	-1.55	0.122
Central	beta-xylosidase	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.17	0.11	1.57	0.116	0.22	0.14	1.56	0.118
Central	beta-xylosidase	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	-0.07	0.13	-0.53	0.596	-0.08	0.14	-0.53	0.595
Central	beta-xylosidase	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.01	0.13	0.08	0.935	0.01	0.14	0.08	0.935
Central	beta-xylosidase	CWM_MycInt	Xylosidase	~	CWM_MycInt_historic	c	-0.12	0.10	-1.23	0.218	-0.17	0.13	-1.25	0.213
Central	beta-xylosidase	CWM_MycInt	Xylosidase	~	CWM_MycInt_change	d	0.08	0.12	0.62	0.533	0.08	0.13	0.63	0.532
Central	beta-xylosidase	CWM_MycInt	Xylosidase	~	LUI_historic	e	-0.16	0.09	-1.78	0.076	-0.24	0.13	-1.82	0.068
Central	beta-xylosidase	CWM_MycInt	Xylosidase	~	LUI_change	f	0.19	0.11	1.72	0.085	0.23	0.13	1.76	0.078
Central	beta-xylosidase	CWM_MycInt	LUI_historic	~~	LUI_change	g	0.00	0.01	0.06	0.949	0.01	0.14	0.06	0.949
Central	beta-xylosidase	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	4.90	0.000	0.99	0.02	45.45	0.000
Central	beta-xylosidase	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	4.90	0.000	1.00	0.00	295.85	0.000
Central	beta-xylosidase	CWM_MycInt	Xylosidase	~~	Xylosidase		0.02	0.01	4.90	0.000	0.86	0.09	9.40	0.000
Central	beta-xylosidase	CWM_MycInt	LUI_historic	~~	LUI_historic		0.06	0.01	4.90	0.000	1.00	0.00	NA	NA
Central	beta-xylosidase	CWM_MycInt	LUI_change	~~	LUI_change		0.04	0.01	4.90	0.000	1.00	0.00	NA	NA
Central	beta-xylosidase	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.02	0.49	0.627	0.01	0.03	0.49	0.627
Central	beta-xylosidase	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	0.08	0.936	0.00	0.01	0.08	0.936
Central	beta-xylosidase	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.15	0.09	-1.66	0.097	-0.23	0.13	-1.70	0.089
Central	beta-xylosidase	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.19	0.11	1.72	0.085	0.23	0.13	1.77	0.078
Central	beta-xylosidase	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.15	0.09	-1.66	0.097	-0.22	0.14	-1.64	0.101
Central	beta-xylosidase	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.19	0.11	1.72	0.085	0.23	0.14	1.70	0.089
Central	beta-xylosidase	Plant_biomass	Plant_biomass	~	LUI_historic	a	-0.01	0.12	-0.09	0.925	-0.01	0.14	-0.09	0.925
Central	beta-xylosidase	Plant_biomass	Plant_biomass	~	LUI_change	b	0.10	0.16	0.65	0.518	0.09	0.14	0.65	0.516
Central	beta-xylosidase	Plant_biomass	Xylosidase	~	Plant_biomass	c	0.25	0.10	2.53	0.011	0.33	0.12	2.67	0.008
Central	beta-xylosidase	Plant_biomass	Xylosidase	~	LUI_historic	e	-0.13	0.08	-1.49	0.137	-0.19	0.13	-1.51	0.131
Central	beta-xylosidase	Plant_biomass	Xylosidase	~	LUI_change	f	0.15	0.11	1.42	0.156	0.19	0.13	1.44	0.150
Central	beta-xylosidase	Plant_biomass	LUI_historic	~~	LUI_change	g	0.00	0.01	0.06	0.949	0.01	0.14	0.06	0.949
Central	beta-xylosidase	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	4.90	0.000	0.99	0.03	36.93	0.000
Central	beta-xylosidase	Plant_biomass	Xylosidase	~~	Xylosidase		0.02	0.00	4.90	0.000	0.81	0.10	7.90	0.000
Central	beta-xylosidase	Plant_biomass	LUI_historic	~~	LUI_historic		0.06	0.01	4.90	0.000	1.00	0.00	NA	NA
Central	beta-xylosidase	Plant_biomass	LUI_change	~~	LUI_change		0.04	0.01	4.90	0.000	1.00	0.00	NA	NA
Central	beta-xylosidase	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.03	-0.09	0.925	0.00	0.05	-0.09	0.925
Central	beta-xylosidase	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.03	0.04	0.63	0.531	0.03	0.05	0.63	0.527
Central	beta-xylosidase	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.13	0.09	-1.43	0.153	-0.20	0.14	-1.46	0.145
Central	beta-xylosidase	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.17	0.11	1.56	0.119	0.22	0.14	1.60	0.110
Central	beta-xylosidase	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.13	0.09	-1.43	0.153	-0.20	0.14	-1.41	0.159
Central	beta-xylosidase	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.17	0.11	1.56	0.119	0.21	0.14	1.55	0.121
Central	beta-xylosidase	Lignin_content	Lignin_content	~	LUI_historic	a	0.07	0.13	0.53	0.595	0.08	0.14	0.53	0.594
Central	beta-xylosidase	Lignin_content	Lignin_content	~	LUI_change	b	0.07	0.16	0.45	0.656	0.06	0.14	0.45	0.655
Central	beta-xylosidase	Lignin_content	Xylosidase	~	Lignin_content	c	0.23	0.09	2.55	0.011	0.33	0.12	2.68	0.007
Central	beta-xylosidase	Lignin_content	Xylosidase	~	LUI_historic	e	-0.14	0.08	-1.72	0.086	-0.22	0.13	-1.75	0.080
Central	beta-xylosidase	Lignin_content	Xylosidase	~	LUI_change	f	0.16	0.11	1.50	0.135	0.19	0.13	1.52	0.129
Central	beta-xylosidase	Lignin_content	LUI_historic	~~	LUI_change	g	0.00	0.01	0.06	0.949	0.01	0.14	0.06	0.949
Central	beta-xylosidase	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	4.90	0.000	0.99	0.03	34.64	0.000
Central	beta-xylosidase	Lignin_content	Xylosidase	~~	Xylosidase		0.02	0.00	4.90	0.000	0.81	0.10	7.87	0.000
Central	beta-xylosidase	Lignin_content	LUI_historic	~~	LUI_historic		0.06	0.01	4.90	0.000	1.00	0.00	NA	NA
Central	beta-xylosidase	Lignin_content	LUI_change	~~	LUI_change		0.04	0.01	4.90	0.000	1.00	0.00	NA	NA
Central	beta-xylosidase	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.02	0.03	0.52	0.603	0.03	0.05	0.52	0.604
Central	beta-xylosidase	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.02	0.04	0.44	0.661	0.02	0.05	0.44	0.659
Central	beta-xylosidase	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.13	0.09	-1.43	0.153	-0.20	0.14	-1.46	0.145
Central	beta-xylosidase	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.17	0.11	1.56	0.119	0.22	0.14	1.60	0.110
Central	beta-xylosidase	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.13	0.09	-1.43	0.153	-0.20	0.14	-1.41	0.159
Central	beta-xylosidase	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.17	0.11	1.56	0.119	0.21	0.14	1.55	0.121
Central	beta-xylosidase	pH	pH_historic	~	LUI_historic	a	-0.01	0.12	-0.11	0.911	-0.02	0.14	-0.11	0.911
Central	beta-xylosidase	pH	pH_change	~	LUI_change	b	-0.15	0.15	-0.99	0.321	-0.14	0.14	-1.00	0.316
Central	beta-xylosidase	pH	Xylosidase	~	pH_historic	c	-0.03	0.10	-0.33	0.742	-0.04	0.13	-0.33	0.742
Central	beta-xylosidase	pH	Xylosidase	~	pH_change	d	-0.22	0.10	-2.12	0.034	-0.28	0.13	-2.20	0.028
Central	beta-xylosidase	pH	Xylosidase	~	LUI_historic	e	-0.15	0.09	-1.75	0.080	-0.23	0.13	-1.79	0.074
Central	beta-xylosidase	pH	Xylosidase	~	LUI_change	f	0.15	0.11	1.38	0.167	0.18	0.13	1.40	0.161
Central	beta-xylosidase	pH	LUI_historic	~~	LUI_change	g	0.00	0.01	0.06	0.949	0.01	0.14	0.06	0.949
Central	beta-xylosidase	pH	pH_historic	~~	pH_historic		0.05	0.01	4.90	0.000	1.00	0.01	215.93	0.000
Central	beta-xylosidase	pH	pH_change	~~	pH_change		0.04	0.01	4.90	0.000	0.98	0.04	24.43	0.000
Central	beta-xylosidase	pH	Xylosidase	~~	Xylosidase		0.02	0.00	4.90	0.000	0.82	0.10	8.28	0.000
Central	beta-xylosidase	pH	LUI_historic	~~	LUI_historic		0.06	0.01	4.90	0.000	1.00	0.00	NA	NA
Central	beta-xylosidase	pH	LUI_change	~~	LUI_change		0.04	0.01	4.90	0.000	1.00	0.00	NA	NA
Central	beta-xylosidase	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.00	0.11	0.916	0.00	0.01	0.11	0.916
Central	beta-xylosidase	pH	LUI_change_in	:=	b*d	LUI_change_in	0.03	0.04	0.90	0.369	0.04	0.04	0.91	0.362
Central	beta-xylosidase	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.15	0.09	-1.74	0.082	-0.23	0.13	-1.78	0.075
Central	beta-xylosidase	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.18	0.11	1.63	0.104	0.22	0.13	1.67	0.096
Central	beta-xylosidase	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.15	0.09	-1.74	0.082	-0.23	0.13	-1.72	0.086
Central	beta-xylosidase	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.18	0.11	1.63	0.104	0.22	0.14	1.61	0.108

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*p*	est.std	se.std	z.std	*p*.std
Central	chitinase	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.53	0.09	5.84	0.000	0.64	0.08	7.58	0.000
Central	chitinase	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.05	0.11	-0.46	0.647	-0.07	0.14	-0.46	0.646
Central	chitinase	CWM_leaf_P	Chitinase	~	CWM_leafP_historic	c	-0.09	0.12	-0.76	0.449	-0.12	0.16	-0.76	0.447
Central	chitinase	CWM_leaf_P	Chitinase	~	CWM_leafP_change	d	-0.42	0.14	-3.00	0.003	-0.36	0.11	-3.18	0.001
Central	chitinase	CWM_leaf_P	Chitinase	~	LUI_historic	e	-0.19	0.10	-1.83	0.067	-0.29	0.15	-1.87	0.062
Central	chitinase	CWM_leaf_P	Chitinase	~	LUI_change	f	0.02	0.10	0.14	0.886	0.02	0.12	0.14	0.886
Central	chitinase	CWM_leaf_P	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	chitinase	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	5.00	0.000	0.59	0.11	5.55	0.000
Central	chitinase	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.02	0.00	5.00	0.000	1.00	0.02	54.73	0.000
Central	chitinase	CWM_leaf_P	Chitinase	~~	Chitinase		0.02	0.00	5.00	0.000	0.73	0.10	7.04	0.000
Central	chitinase	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	chitinase	CWM_leaf_P	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	chitinase	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	-0.05	0.07	-0.75	0.453	-0.08	0.10	-0.75	0.451
Central	chitinase	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.02	0.04	0.45	0.651	0.02	0.05	0.45	0.650
Central	chitinase	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.24	0.08	-2.98	0.003	-0.36	0.12	-3.16	0.002
Central	chitinase	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.04	0.11	0.31	0.756	0.04	0.13	0.31	0.756
Central	chitinase	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.24	0.08	-2.98	0.003	-0.36	0.12	-3.13	0.002
Central	chitinase	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.03	0.11	0.30	0.761	0.02	0.14	0.13	0.900
Central	chitinase	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	-0.11	0.13	-0.88	0.380	-0.12	0.14	-0.88	0.377
Central	chitinase	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.04	0.13	0.30	0.768	0.04	0.14	0.30	0.768
Central	chitinase	CWM_MycInt	Chitinase	~	CWM_MycInt_historic	c	-0.02	0.10	-0.23	0.815	-0.03	0.13	-0.23	0.815
Central	chitinase	CWM_MycInt	Chitinase	~	CWM_MycInt_change	d	-0.01	0.12	-0.06	0.953	-0.01	0.13	-0.06	0.953
Central	chitinase	CWM_MycInt	Chitinase	~	LUI_historic	e	-0.24	0.09	-2.70	0.007	-0.36	0.13	-2.89	0.004
Central	chitinase	CWM_MycInt	Chitinase	~	LUI_change	f	0.03	0.11	0.30	0.764	0.04	0.13	0.30	0.764
Central	chitinase	CWM_MycInt	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	chitinase	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	5.00	0.000	0.99	0.03	28.71	0.000
Central	chitinase	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	1.00	0.01	84.79	0.000
Central	chitinase	CWM_MycInt	Chitinase	~~	Chitinase		0.03	0.01	5.00	0.000	0.87	0.09	9.90	0.000
Central	chitinase	CWM_MycInt	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	chitinase	CWM_MycInt	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	chitinase	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	0.23	0.821	0.00	0.02	0.23	0.821
Central	chitinase	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	-0.06	0.954	0.00	0.01	-0.06	0.954
Central	chitinase	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.23	0.09	-2.69	0.007	-0.36	0.12	-2.88	0.004
Central	chitinase	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.03	0.11	0.30	0.766	0.04	0.13	0.30	0.766
Central	chitinase	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.23	0.09	-2.69	0.007	-0.35	0.12	-2.86	0.004
Central	chitinase	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.03	0.11	0.29	0.771	0.02	0.14	0.12	0.906
Central	chitinase	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.03	0.12	0.23	0.821	0.03	0.14	0.23	0.821
Central	chitinase	Plant_biomass	Plant_biomass	~	LUI_change	b	0.13	0.15	0.87	0.385	0.12	0.14	0.88	0.382
Central	chitinase	Plant_biomass	Chitinase	~	Plant_biomass	c	0.14	0.10	1.37	0.171	0.18	0.13	1.39	0.166
Central	chitinase	Plant_biomass	Chitinase	~	LUI_historic	e	-0.24	0.09	-2.80	0.005	-0.36	0.12	-3.00	0.003
Central	chitinase	Plant_biomass	Chitinase	~	LUI_change	f	0.01	0.11	0.12	0.907	0.02	0.13	0.12	0.907
Central	chitinase	Plant_biomass	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	chitinase	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	5.00	0.000	0.98	0.04	27.60	0.000
Central	chitinase	Plant_biomass	Chitinase	~~	Chitinase		0.02	0.01	5.00	0.000	0.84	0.10	8.85	0.000
Central	chitinase	Plant_biomass	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	chitinase	Plant_biomass	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	chitinase	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	0.22	0.823	0.01	0.03	0.22	0.823
Central	chitinase	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.02	0.03	0.73	0.463	0.02	0.03	0.74	0.462
Central	chitinase	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.24	0.09	-2.71	0.007	-0.36	0.12	-2.90	0.004
Central	chitinase	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.03	0.11	0.28	0.779	0.04	0.13	0.28	0.779
Central	chitinase	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.24	0.09	-2.71	0.007	-0.36	0.12	-2.88	0.004
Central	chitinase	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.03	0.11	0.27	0.784	0.01	0.14	0.10	0.920
Central	chitinase	Lignin_content	Lignin_content	~	LUI_historic	a	0.07	0.12	0.60	0.548	0.09	0.14	0.60	0.547
Central	chitinase	Lignin_content	Lignin_content	~	LUI_change	b	0.07	0.16	0.47	0.642	0.07	0.14	0.47	0.641
Central	chitinase	Lignin_content	Chitinase	~	Lignin_content	c	0.20	0.10	2.07	0.039	0.26	0.12	2.13	0.033
Central	chitinase	Lignin_content	Chitinase	~	LUI_historic	e	-0.25	0.08	-2.99	0.003	-0.38	0.12	-3.21	0.001
Central	chitinase	Lignin_content	Chitinase	~	LUI_change	f	0.02	0.11	0.16	0.876	0.02	0.13	0.16	0.876
Central	chitinase	Lignin_content	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	chitinase	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	5.00	0.000	0.99	0.03	32.09	0.000
Central	chitinase	Lignin_content	Chitinase	~~	Chitinase		0.02	0.01	5.00	0.000	0.80	0.10	7.97	0.000
Central	chitinase	Lignin_content	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	chitinase	Lignin_content	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	chitinase	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.02	0.03	0.58	0.564	0.02	0.04	0.57	0.566
Central	chitinase	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.02	0.03	0.45	0.650	0.02	0.04	0.45	0.650
Central	chitinase	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.24	0.09	-2.71	0.007	-0.36	0.12	-2.90	0.004
Central	chitinase	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.03	0.11	0.28	0.779	0.04	0.13	0.28	0.779
Central	chitinase	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.24	0.09	-2.71	0.007	-0.36	0.12	-2.88	0.004
Central	chitinase	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.03	0.11	0.27	0.784	0.01	0.14	0.10	0.920
Central	chitinase	pH	pH_historic	~	LUI_historic	a	-0.04	0.11	-0.32	0.747	-0.05	0.14	-0.32	0.747
Central	chitinase	pH	pH_change	~	LUI_change	b	-0.16	0.15	-1.07	0.286	-0.15	0.14	-1.08	0.280
Central	chitinase	pH	Chitinase	~	pH_historic	c	0.04	0.11	0.37	0.711	0.05	0.13	0.37	0.711
Central	chitinase	pH	Chitinase	~	pH_change	d	0.10	0.11	0.92	0.358	0.12	0.13	0.92	0.355
Central	chitinase	pH	Chitinase	~	LUI_historic	e	-0.22	0.09	-2.59	0.010	-0.34	0.12	-2.75	0.006
Central	chitinase	pH	Chitinase	~	LUI_change	f	0.04	0.11	0.33	0.742	0.04	0.13	0.33	0.742
Central	chitinase	pH	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	chitinase	pH	pH_historic	~~	pH_historic		0.04	0.01	5.00	0.000	1.00	0.01	77.64	0.000
Central	chitinase	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	0.98	0.04	23.68	0.000
Central	chitinase	pH	Chitinase	~~	Chitinase		0.02	0.01	5.00	0.000	0.87	0.09	9.69	0.000
Central	chitinase	pH	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	chitinase	pH	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	chitinase	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	-0.24	0.808	0.00	0.01	-0.24	0.808
Central	chitinase	pH	LUI_change_in	:=	b*d	LUI_change_in	-0.02	0.02	-0.70	0.486	-0.02	0.03	-0.70	0.485
Central	chitinase	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.23	0.09	-2.61	0.009	-0.34	0.12	-2.77	0.006
Central	chitinase	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.02	0.11	0.19	0.847	0.03	0.13	0.19	0.847
Central	chitinase	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.23	0.09	-2.61	0.009	-0.34	0.12	-2.76	0.006
Central	chitinase	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.02	0.11	0.19	0.852	0.00	0.14	0.03	0.979

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*p*	est.std	se.std	z.std	*p*.std
Central	urease	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.56	0.10	5.76	0.000	0.65	0.09	7.58	0.000
Central	urease	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.02	0.11	-0.14	0.888	-0.02	0.15	-0.14	0.888
Central	urease	CWM_leaf_P	Urease	~	CWM_leafP_historic	c	-0.50	0.18	-2.76	0.006	-0.47	0.16	-2.95	0.003
Central	urease	CWM_leaf_P	Urease	~	CWM_leafP_change	d	-0.29	0.20	-1.43	0.153	-0.18	0.13	-1.45	0.148
Central	urease	CWM_leaf_P	Urease	~	LUI_historic	e	-0.01	0.15	-0.09	0.929	-0.02	0.17	-0.09	0.929
Central	urease	CWM_leaf_P	Urease	~	LUI_change	f	-0.04	0.15	-0.25	0.802	-0.03	0.13	-0.25	0.802
Central	urease	CWM_leaf_P	LUI_historic	~~	LUI_change	g	0.00	0.01	0.30	0.768	0.04	0.15	0.30	0.767
Central	urease	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	4.74	0.000	0.58	0.11	5.15	0.000
Central	urease	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.02	0.01	4.74	0.000	1.00	0.01	159.30	0.000
Central	urease	CWM_leaf_P	Urease	~~	Urease		0.04	0.01	4.74	0.000	0.74	0.11	6.66	0.000
Central	urease	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.07	0.02	4.74	0.000	1.00	0.00	NA	NA
Central	urease	CWM_leaf_P	LUI_change	~~	LUI_change		0.04	0.01	4.74	0.000	1.00	0.00	NA	NA
Central	urease	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	-0.28	0.11	-2.49	0.013	-0.30	0.12	-2.65	0.008
Central	urease	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.01	0.03	0.14	0.888	0.00	0.03	0.14	0.888
Central	urease	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.29	0.13	-2.30	0.022	-0.32	0.13	-2.42	0.016
Central	urease	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.03	0.16	-0.22	0.829	-0.03	0.13	-0.22	0.829
Central	urease	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.29	0.13	-2.30	0.022	-0.32	0.13	-2.43	0.015
Central	urease	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.04	0.16	-0.22	0.825	-0.04	0.14	-0.30	0.761
Central	urease	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	-0.13	0.13	-0.98	0.326	-0.15	0.15	-0.99	0.321
Central	urease	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.09	0.14	0.64	0.525	0.09	0.15	0.64	0.524
Central	urease	CWM_MycInt	Urease	~	CWM_MycInt_historic	c	-0.01	0.14	-0.03	0.974	-0.01	0.14	-0.03	0.974
Central	urease	CWM_MycInt	Urease	~	CWM_MycInt_change	d	0.16	0.18	0.88	0.377	0.12	0.14	0.89	0.374
Central	urease	CWM_MycInt	Urease	~	LUI_historic	e	-0.34	0.13	-2.67	0.008	-0.37	0.13	-2.87	0.004
Central	urease	CWM_MycInt	Urease	~	LUI_change	f	-0.08	0.17	-0.47	0.642	-0.06	0.14	-0.47	0.642
Central	urease	CWM_MycInt	LUI_historic	~~	LUI_change	g	0.00	0.01	0.30	0.768	0.04	0.15	0.30	0.767
Central	urease	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	4.74	0.000	0.98	0.04	23.15	0.000
Central	urease	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	4.74	0.000	0.99	0.03	35.60	0.000
Central	urease	CWM_MycInt	Urease	~~	Urease		0.05	0.01	4.74	0.000	0.84	0.10	8.55	0.000
Central	urease	CWM_MycInt	LUI_historic	~~	LUI_historic		0.07	0.02	4.74	0.000	1.00	0.00	NA	NA
Central	urease	CWM_MycInt	LUI_change	~~	LUI_change		0.04	0.01	4.74	0.000	1.00	0.00	NA	NA
Central	urease	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	0.03	0.974	0.00	0.02	0.03	0.974
Central	urease	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.01	0.03	0.52	0.606	0.01	0.02	0.52	0.606
Central	urease	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.34	0.13	-2.70	0.007	-0.37	0.13	-2.90	0.004
Central	urease	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.06	0.17	-0.38	0.704	-0.05	0.14	-0.38	0.704
Central	urease	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.34	0.13	-2.70	0.007	-0.37	0.13	-2.92	0.004
Central	urease	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.06	0.17	-0.39	0.700	-0.07	0.15	-0.46	0.643
Central	urease	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.03	0.12	0.22	0.826	0.03	0.15	0.22	0.826
Central	urease	Plant_biomass	Plant_biomass	~	LUI_change	b	0.03	0.16	0.19	0.853	0.03	0.15	0.19	0.853
Central	urease	Plant_biomass	Urease	~	Plant_biomass	c	0.03	0.16	0.18	0.860	0.03	0.14	0.18	0.860
Central	urease	Plant_biomass	Urease	~	LUI_historic	e	-0.29	0.13	-2.28	0.023	-0.32	0.13	-2.40	0.016
Central	urease	Plant_biomass	Urease	~	LUI_change	f	-0.07	0.17	-0.41	0.684	-0.06	0.14	-0.41	0.683
Central	urease	Plant_biomass	LUI_historic	~~	LUI_change	g	0.00	0.01	0.30	0.768	0.04	0.15	0.30	0.767
Central	urease	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.04	0.01	4.74	0.000	1.00	0.01	76.48	0.000
Central	urease	Plant_biomass	Urease	~~	Urease		0.05	0.01	4.74	0.000	0.89	0.09	10.21	0.000
Central	urease	Plant_biomass	LUI_historic	~~	LUI_historic		0.07	0.02	4.74	0.000	1.00	0.00	NA	NA
Central	urease	Plant_biomass	LUI_change	~~	LUI_change		0.04	0.01	4.74	0.000	1.00	0.00	NA	NA
Central	urease	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	0.14	0.891	0.00	0.01	0.14	0.891
Central	urease	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	0.13	0.898	0.00	0.01	0.13	0.898
Central	urease	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.29	0.13	-2.27	0.023	-0.32	0.13	-2.40	0.017
Central	urease	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.07	0.17	-0.40	0.687	-0.06	0.14	-0.40	0.687
Central	urease	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.29	0.13	-2.27	0.023	-0.32	0.13	-2.42	0.016
Central	urease	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.07	0.17	-0.41	0.684	-0.07	0.15	-0.48	0.633
Central	urease	Lignin_content	Lignin_content	~	LUI_historic	a	0.11	0.13	0.84	0.401	0.12	0.15	0.85	0.397
Central	urease	Lignin_content	Lignin_content	~	LUI_change	b	0.05	0.17	0.29	0.775	0.04	0.15	0.29	0.774
Central	urease	Lignin_content	Urease	~	Lignin_content	c	0.40	0.14	2.91	0.004	0.38	0.12	3.09	0.002
Central	urease	Lignin_content	Urease	~	LUI_historic	e	-0.33	0.12	-2.82	0.005	-0.37	0.12	-2.98	0.003
Central	urease	Lignin_content	Urease	~	LUI_change	f	-0.09	0.15	-0.56	0.574	-0.07	0.13	-0.56	0.573
Central	urease	Lignin_content	LUI_historic	~~	LUI_change	g	0.00	0.01	0.30	0.768	0.04	0.15	0.30	0.767
Central	urease	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	4.74	0.000	0.98	0.04	25.21	0.000
Central	urease	Lignin_content	Urease	~~	Urease		0.04	0.01	4.74	0.000	0.75	0.11	6.73	0.000
Central	urease	Lignin_content	LUI_historic	~~	LUI_historic		0.07	0.02	4.74	0.000	1.00	0.00	NA	NA
Central	urease	Lignin_content	LUI_change	~~	LUI_change		0.04	0.01	4.74	0.000	1.00	0.00	NA	NA
Central	urease	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.04	0.05	0.81	0.419	0.05	0.06	0.80	0.424
Central	urease	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.02	0.07	0.29	0.776	0.02	0.06	0.29	0.776
Central	urease	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.29	0.13	-2.27	0.023	-0.32	0.13	-2.40	0.017
Central	urease	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.07	0.17	-0.40	0.687	-0.06	0.14	-0.40	0.687
Central	urease	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.29	0.13	-2.27	0.023	-0.32	0.13	-2.42	0.016
Central	urease	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.07	0.17	-0.41	0.684	-0.07	0.15	-0.48	0.633
Central	urease	pH	pH_historic	~	LUI_historic	a	-0.06	0.12	-0.51	0.612	-0.08	0.15	-0.51	0.611
Central	urease	pH	pH_change	~	LUI_change	b	-0.13	0.15	-0.91	0.365	-0.13	0.15	-0.91	0.361
Central	urease	pH	Urease	~	pH_historic	c	0.10	0.15	0.66	0.510	0.09	0.14	0.66	0.508
Central	urease	pH	Urease	~	pH_change	d	0.11	0.17	0.66	0.507	0.09	0.14	0.67	0.505
Central	urease	pH	Urease	~	LUI_historic	e	-0.28	0.13	-2.18	0.030	-0.31	0.13	-2.28	0.022
Central	urease	pH	Urease	~	LUI_change	f	-0.07	0.17	-0.45	0.657	-0.06	0.14	-0.45	0.656
Central	urease	pH	LUI_historic	~~	LUI_change	g	0.00	0.01	0.30	0.768	0.04	0.15	0.30	0.767
Central	urease	pH	pH_historic	~~	pH_historic		0.05	0.01	4.74	0.000	0.99	0.02	44.47	0.000
Central	urease	pH	pH_change	~~	pH_change		0.04	0.01	4.74	0.000	0.98	0.04	25.07	0.000
Central	urease	pH	Urease	~~	Urease		0.05	0.01	4.74	0.000	0.88	0.09	9.63	0.000
Central	urease	pH	LUI_historic	~~	LUI_historic		0.07	0.02	4.74	0.000	1.00	0.00	NA	NA
Central	urease	pH	LUI_change	~~	LUI_change		0.04	0.01	4.74	0.000	1.00	0.00	NA	NA
Central	urease	pH	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.02	-0.40	0.688	-0.01	0.02	-0.40	0.687
Central	urease	pH	LUI_change_in	:=	b*d	LUI_change_in	-0.02	0.03	-0.54	0.592	-0.01	0.02	-0.54	0.591
Central	urease	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.28	0.13	-2.22	0.026	-0.31	0.13	-2.34	0.019
Central	urease	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.09	0.17	-0.54	0.592	-0.08	0.14	-0.54	0.591
Central	urease	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.28	0.13	-2.22	0.026	-0.32	0.13	-2.36	0.018
Central	urease	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.09	0.17	-0.54	0.589	-0.09	0.15	-0.60	0.546

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*p*	est.std	se.std	z.std	*p*.std
Central	DEA	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.53	0.09	5.84	0.000	0.64	0.08	7.58	0.000
Central	DEA	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.05	0.11	-0.46	0.647	-0.07	0.14	-0.46	0.646
Central	DEA	CWM_leaf_P	DEA	~	CWM_leafP_historic	c	0.14	0.13	1.13	0.257	0.20	0.17	1.15	0.252
Central	DEA	CWM_leaf_P	DEA	~	CWM_leafP_change	d	0.03	0.14	0.25	0.807	0.03	0.13	0.25	0.807
Central	DEA	CWM_leaf_P	DEA	~	LUI_historic	e	-0.21	0.11	-1.98	0.047	-0.35	0.17	-2.05	0.040
Central	DEA	CWM_leaf_P	DEA	~	LUI_change	f	0.15	0.11	1.39	0.163	0.19	0.13	1.42	0.156
Central	DEA	CWM_leaf_P	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	DEA	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	5.00	0.000	0.59	0.11	5.55	0.000
Central	DEA	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.02	0.00	5.00	0.000	1.00	0.02	54.73	0.000
Central	DEA	CWM_leaf_P	DEA	~~	DEA		0.02	0.00	5.00	0.000	0.90	0.08	11.14	0.000
Central	DEA	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	DEA	CWM_leaf_P	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	DEA	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.08	0.07	1.11	0.266	0.13	0.11	1.12	0.262
Central	DEA	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	-0.22	0.829	0.00	0.01	-0.22	0.829
Central	DEA	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.13	0.08	-1.61	0.106	-0.22	0.13	-1.65	0.098
Central	DEA	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.15	0.11	1.38	0.167	0.19	0.13	1.40	0.161
Central	DEA	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.13	0.08	-1.61	0.108	-0.21	0.14	-1.54	0.125
Central	DEA	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.15	0.11	1.38	0.169	0.17	0.14	1.26	0.206
Central	DEA	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	-0.11	0.13	-0.88	0.380	-0.12	0.14	-0.88	0.377
Central	DEA	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.04	0.13	0.30	0.768	0.04	0.14	0.30	0.768
Central	DEA	CWM_MycInt	DEA	~	CWM_MycInt_historic	c	-0.02	0.09	-0.26	0.798	-0.04	0.14	-0.26	0.798
Central	DEA	CWM_MycInt	DEA	~	CWM_MycInt_change	d	-0.01	0.12	-0.12	0.901	-0.02	0.14	-0.12	0.901
Central	DEA	CWM_MycInt	DEA	~	LUI_historic	e	-0.13	0.08	-1.60	0.111	-0.22	0.13	-1.63	0.102
Central	DEA	CWM_MycInt	DEA	~	LUI_change	f	0.15	0.11	1.43	0.152	0.20	0.13	1.46	0.145
Central	DEA	CWM_MycInt	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	DEA	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	5.00	0.000	0.99	0.03	28.71	0.000
Central	DEA	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	1.00	0.01	84.79	0.000
Central	DEA	CWM_MycInt	DEA	~~	DEA		0.02	0.00	5.00	0.000	0.92	0.07	12.52	0.000
Central	DEA	CWM_MycInt	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	DEA	CWM_MycInt	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	DEA	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	0.25	0.806	0.00	0.02	0.25	0.806
Central	DEA	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	-0.11	0.909	0.00	0.01	-0.11	0.909
Central	DEA	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.13	0.08	-1.58	0.115	-0.21	0.13	-1.61	0.107
Central	DEA	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.15	0.11	1.43	0.153	0.19	0.13	1.45	0.146
Central	DEA	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.13	0.08	-1.57	0.116	-0.20	0.14	-1.49	0.137
Central	DEA	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.15	0.11	1.42	0.155	0.18	0.14	1.32	0.187
Central	DEA	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.03	0.12	0.23	0.821	0.03	0.14	0.23	0.821
Central	DEA	Plant_biomass	Plant_biomass	~	LUI_change	b	0.13	0.15	0.87	0.385	0.12	0.14	0.88	0.382
Central	DEA	Plant_biomass	DEA	~	Plant_biomass	c	0.34	0.09	3.88	0.000	0.47	0.11	4.32	0.000
Central	DEA	Plant_biomass	DEA	~	LUI_historic	e	-0.14	0.07	-1.98	0.048	-0.24	0.12	-2.01	0.044
Central	DEA	Plant_biomass	DEA	~	LUI_change	f	0.11	0.09	1.12	0.262	0.14	0.12	1.13	0.259
Central	DEA	Plant_biomass	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	DEA	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	5.00	0.000	0.98	0.04	27.60	0.000
Central	DEA	Plant_biomass	DEA	~~	DEA		0.02	0.00	5.00	0.000	0.71	0.11	6.53	0.000
Central	DEA	Plant_biomass	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	DEA	Plant_biomass	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	DEA	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.04	0.23	0.821	0.02	0.07	0.23	0.821
Central	DEA	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.04	0.05	0.85	0.397	0.06	0.07	0.86	0.390
Central	DEA	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.13	0.08	-1.62	0.104	-0.22	0.13	-1.66	0.096
Central	DEA	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.15	0.11	1.41	0.159	0.19	0.13	1.44	0.151
Central	DEA	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.13	0.08	-1.62	0.106	-0.21	0.14	-1.54	0.123
Central	DEA	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.15	0.11	1.41	0.160	0.18	0.14	1.30	0.195
Central	DEA	Lignin_content	Lignin_content	~	LUI_historic	a	0.07	0.12	0.60	0.548	0.09	0.14	0.60	0.547
Central	DEA	Lignin_content	Lignin_content	~	LUI_change	b	0.07	0.16	0.47	0.642	0.07	0.14	0.47	0.641
Central	DEA	Lignin_content	DEA	~	Lignin_content	c	0.05	0.09	0.55	0.581	0.08	0.14	0.55	0.580
Central	DEA	Lignin_content	DEA	~	LUI_historic	e	-0.14	0.08	-1.67	0.095	-0.23	0.13	-1.71	0.087
Central	DEA	Lignin_content	DEA	~	LUI_change	f	0.15	0.11	1.38	0.169	0.19	0.13	1.40	0.162
Central	DEA	Lignin_content	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	DEA	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	5.00	0.000	0.99	0.03	32.09	0.000
Central	DEA	Lignin_content	DEA	~~	DEA		0.02	0.00	5.00	0.000	0.91	0.08	12.09	0.000
Central	DEA	Lignin_content	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	DEA	Lignin_content	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	DEA	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	0.41	0.685	0.01	0.02	0.41	0.684
Central	DEA	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	0.36	0.722	0.01	0.01	0.36	0.722
Central	DEA	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.13	0.08	-1.62	0.104	-0.22	0.13	-1.66	0.096
Central	DEA	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.15	0.11	1.41	0.159	0.19	0.13	1.44	0.151
Central	DEA	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.13	0.08	-1.62	0.106	-0.21	0.14	-1.54	0.123
Central	DEA	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.15	0.11	1.41	0.160	0.18	0.14	1.30	0.195
Central	DEA	pH	pH_historic	~	LUI_historic	a	-0.04	0.11	-0.32	0.747	-0.05	0.14	-0.32	0.747
Central	DEA	pH	pH_change	~	LUI_change	b	-0.16	0.15	-1.07	0.286	-0.15	0.14	-1.08	0.280
Central	DEA	pH	DEA	~	pH_historic	c	-0.06	0.10	-0.60	0.548	-0.08	0.13	-0.60	0.547
Central	DEA	pH	DEA	~	pH_change	d	-0.04	0.10	-0.37	0.712	-0.05	0.14	-0.37	0.712
Central	DEA	pH	DEA	~	LUI_historic	e	-0.14	0.08	-1.71	0.088	-0.23	0.13	-1.75	0.080
Central	DEA	pH	DEA	~	LUI_change	f	0.16	0.11	1.47	0.140	0.20	0.13	1.50	0.133
Central	DEA	pH	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	DEA	pH	pH_historic	~~	pH_historic		0.04	0.01	5.00	0.000	1.00	0.01	77.64	0.000
Central	DEA	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	0.98	0.04	23.68	0.000
Central	DEA	pH	DEA	~~	DEA		0.02	0.00	5.00	0.000	0.90	0.08	11.35	0.000
Central	DEA	pH	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	DEA	pH	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	DEA	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	0.28	0.776	0.00	0.01	0.28	0.776
Central	DEA	pH	LUI_change_in	:=	b*d	LUI_change_in	0.01	0.02	0.35	0.727	0.01	0.02	0.35	0.727
Central	DEA	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.14	0.08	-1.67	0.094	-0.23	0.13	-1.72	0.086
Central	DEA	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.16	0.11	1.54	0.123	0.21	0.13	1.58	0.115
Central	DEA	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.14	0.08	-1.67	0.095	-0.21	0.14	-1.58	0.114
Central	DEA	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.16	0.11	1.54	0.123	0.19	0.14	1.43	0.153

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*p*	est.std	se.std	z.std	*p*.std
Central	phosphatase	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.53	0.09	5.84	0.000	0.64	0.08	7.58	0.000
Central	phosphatase	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.05	0.11	-0.46	0.647	-0.07	0.14	-0.46	0.646
Central	phosphatase	CWM_leaf_P	Phosphatase	~	CWM_leafP_historic	c	-0.08	0.13	-0.58	0.563	-0.10	0.17	-0.58	0.562
Central	phosphatase	CWM_leaf_P	Phosphatase	~	CWM_leafP_change	d	-0.25	0.15	-1.73	0.084	-0.23	0.13	-1.77	0.077
Central	phosphatase	CWM_leaf_P	Phosphatase	~	LUI_historic	e	-0.17	0.11	-1.50	0.133	-0.25	0.17	-1.53	0.126
Central	phosphatase	CWM_leaf_P	Phosphatase	~	LUI_change	f	0.07	0.11	0.60	0.548	0.08	0.13	0.60	0.547
Central	phosphatase	CWM_leaf_P	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	phosphatase	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	5.00	0.000	0.59	0.11	5.55	0.000
Central	phosphatase	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.02	0.00	5.00	0.000	1.00	0.02	54.73	0.000
Central	phosphatase	CWM_leaf_P	Phosphatase	~~	Phosphatase		0.02	0.01	5.00	0.000	0.84	0.09	8.99	0.000
Central	phosphatase	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	phosphatase	CWM_leaf_P	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	phosphatase	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	-0.04	0.07	-0.58	0.565	-0.06	0.11	-0.58	0.564
Central	phosphatase	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.01	0.03	0.44	0.658	0.02	0.03	0.44	0.657
Central	phosphatase	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.21	0.09	-2.42	0.016	-0.32	0.12	-2.54	0.011
Central	phosphatase	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.08	0.11	0.69	0.488	0.09	0.13	0.70	0.487
Central	phosphatase	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.21	0.09	-2.41	0.016	-0.31	0.13	-2.48	0.013
Central	phosphatase	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.08	0.11	0.69	0.492	0.07	0.14	0.52	0.605
Central	phosphatase	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	-0.11	0.13	-0.88	0.380	-0.12	0.14	-0.88	0.377
Central	phosphatase	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.04	0.13	0.30	0.768	0.04	0.14	0.30	0.768
Central	phosphatase	CWM_MycInt	Phosphatase	~	CWM_MycInt_historic	c	-0.06	0.10	-0.57	0.570	-0.08	0.13	-0.57	0.569
Central	phosphatase	CWM_MycInt	Phosphatase	~	CWM_MycInt_change	d	-0.01	0.12	-0.07	0.945	-0.01	0.13	-0.07	0.945
Central	phosphatase	CWM_MycInt	Phosphatase	~	LUI_historic	e	-0.21	0.09	-2.36	0.018	-0.32	0.13	-2.48	0.013
Central	phosphatase	CWM_MycInt	Phosphatase	~	LUI_change	f	0.08	0.11	0.72	0.473	0.10	0.13	0.72	0.472
Central	phosphatase	CWM_MycInt	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	phosphatase	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	5.00	0.000	0.99	0.03	28.71	0.000
Central	phosphatase	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	1.00	0.01	84.79	0.000
Central	phosphatase	CWM_MycInt	Phosphatase	~~	Phosphatase		0.03	0.01	5.00	0.000	0.89	0.08	10.84	0.000
Central	phosphatase	CWM_MycInt	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	phosphatase	CWM_MycInt	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	phosphatase	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.01	0.48	0.633	0.01	0.02	0.48	0.633
Central	phosphatase	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	-0.07	0.946	0.00	0.01	-0.07	0.946
Central	phosphatase	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.20	0.09	-2.30	0.022	-0.31	0.13	-2.41	0.016
Central	phosphatase	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.08	0.11	0.72	0.475	0.10	0.13	0.72	0.473
Central	phosphatase	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.20	0.09	-2.29	0.022	-0.30	0.13	-2.36	0.019
Central	phosphatase	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.08	0.11	0.71	0.478	0.08	0.14	0.54	0.588
Central	phosphatase	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.03	0.12	0.23	0.821	0.03	0.14	0.23	0.821
Central	phosphatase	Plant_biomass	Plant_biomass	~	LUI_change	b	0.13	0.15	0.87	0.385	0.12	0.14	0.88	0.382
Central	phosphatase	Plant_biomass	Phosphatase	~	Plant_biomass	c	0.18	0.10	1.71	0.087	0.23	0.13	1.75	0.080
Central	phosphatase	Plant_biomass	Phosphatase	~	LUI_historic	e	-0.21	0.09	-2.44	0.015	-0.32	0.12	-2.57	0.010
Central	phosphatase	Plant_biomass	Phosphatase	~	LUI_change	f	0.05	0.11	0.48	0.635	0.06	0.13	0.48	0.634
Central	phosphatase	Plant_biomass	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	phosphatase	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	5.00	0.000	0.98	0.04	27.60	0.000
Central	phosphatase	Plant_biomass	Phosphatase	~~	Phosphatase		0.02	0.01	5.00	0.000	0.85	0.09	9.08	0.000
Central	phosphatase	Plant_biomass	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	phosphatase	Plant_biomass	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	phosphatase	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.02	0.23	0.822	0.01	0.03	0.22	0.822
Central	phosphatase	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.02	0.03	0.78	0.439	0.03	0.04	0.78	0.436
Central	phosphatase	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.20	0.09	-2.32	0.020	-0.31	0.13	-2.44	0.015
Central	phosphatase	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.08	0.11	0.67	0.503	0.09	0.13	0.67	0.502
Central	phosphatase	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.20	0.09	-2.32	0.020	-0.31	0.13	-2.39	0.017
Central	phosphatase	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.08	0.11	0.66	0.507	0.07	0.14	0.50	0.619
Central	phosphatase	Lignin_content	Lignin_content	~	LUI_historic	a	0.07	0.12	0.60	0.548	0.09	0.14	0.60	0.547
Central	phosphatase	Lignin_content	Lignin_content	~	LUI_change	b	0.07	0.16	0.47	0.642	0.07	0.14	0.47	0.641
Central	phosphatase	Lignin_content	Phosphatase	~	Lignin_content	c	0.12	0.10	1.21	0.225	0.16	0.13	1.23	0.220
Central	phosphatase	Lignin_content	Phosphatase	~	LUI_historic	e	-0.21	0.09	-2.45	0.014	-0.33	0.13	-2.58	0.010
Central	phosphatase	Lignin_content	Phosphatase	~	LUI_change	f	0.07	0.11	0.60	0.550	0.08	0.13	0.60	0.549
Central	phosphatase	Lignin_content	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	phosphatase	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	5.00	0.000	0.99	0.03	32.09	0.000
Central	phosphatase	Lignin_content	Phosphatase	~~	Phosphatase		0.02	0.01	5.00	0.000	0.87	0.09	9.91	0.000
Central	phosphatase	Lignin_content	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	phosphatase	Lignin_content	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	phosphatase	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.02	0.54	0.591	0.01	0.03	0.54	0.591
Central	phosphatase	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.01	0.02	0.43	0.664	0.01	0.02	0.44	0.664
Central	phosphatase	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.20	0.09	-2.32	0.020	-0.31	0.13	-2.44	0.015
Central	phosphatase	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.08	0.11	0.67	0.503	0.09	0.13	0.67	0.502
Central	phosphatase	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.20	0.09	-2.32	0.020	-0.31	0.13	-2.39	0.017
Central	phosphatase	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.08	0.11	0.66	0.507	0.07	0.14	0.50	0.619
Central	phosphatase	pH	pH_historic	~	LUI_historic	a	-0.04	0.11	-0.32	0.747	-0.05	0.14	-0.32	0.747
Central	phosphatase	pH	pH_change	~	LUI_change	b	-0.16	0.15	-1.07	0.286	-0.15	0.14	-1.08	0.280
Central	phosphatase	pH	Phosphatase	~	pH_historic	c	0.16	0.10	1.52	0.130	0.20	0.13	1.54	0.123
Central	phosphatase	pH	Phosphatase	~	pH_change	d	-0.07	0.10	-0.68	0.497	-0.09	0.13	-0.68	0.496
Central	phosphatase	pH	Phosphatase	~	LUI_historic	e	-0.20	0.08	-2.40	0.017	-0.31	0.13	-2.51	0.012
Central	phosphatase	pH	Phosphatase	~	LUI_change	f	0.03	0.11	0.26	0.792	0.04	0.13	0.26	0.792
Central	phosphatase	pH	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	phosphatase	pH	pH_historic	~~	pH_historic		0.04	0.01	5.00	0.000	1.00	0.01	77.64	0.000
Central	phosphatase	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	0.98	0.04	23.68	0.000
Central	phosphatase	pH	Phosphatase	~~	Phosphatase		0.02	0.01	5.00	0.000	0.85	0.09	9.14	0.000
Central	phosphatase	pH	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	phosphatase	pH	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	phosphatase	pH	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.02	-0.32	0.753	-0.01	0.03	-0.32	0.752
Central	phosphatase	pH	LUI_change_in	:=	b*d	LUI_change_in	0.01	0.02	0.57	0.567	0.01	0.02	0.57	0.566
Central	phosphatase	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.21	0.09	-2.41	0.016	-0.32	0.13	-2.55	0.011
Central	phosphatase	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.04	0.11	0.37	0.713	0.05	0.13	0.37	0.713
Central	phosphatase	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.21	0.09	-2.41	0.016	-0.32	0.13	-2.52	0.012
Central	phosphatase	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.04	0.11	0.36	0.718	0.03	0.14	0.20	0.842

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*p*	est.std	se.std	z.std	*p*.std
Central	bacteria	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.53	0.09	5.84	0.000	0.64	0.08	7.58	0.000
Central	bacteria	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.05	0.11	-0.46	0.647	-0.07	0.14	-0.46	0.646
Central	bacteria	CWM_leaf_P	bactotal	~	CWM_leafP_historic	c	0.05	0.18	0.30	0.764	0.05	0.18	0.30	0.764
Central	bacteria	CWM_leaf_P	bactotal	~	CWM_leafP_change	d	0.04	0.20	0.23	0.819	0.03	0.14	0.23	0.819
Central	bacteria	CWM_leaf_P	bactotal	~	LUI_historic	e	-0.05	0.15	-0.36	0.717	-0.07	0.18	-0.36	0.716
Central	bacteria	CWM_leaf_P	bactotal	~	LUI_change	f	0.22	0.15	1.51	0.131	0.21	0.14	1.54	0.123
Central	bacteria	CWM_leaf_P	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	bacteria	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	5.00	0.000	0.59	0.11	5.55	0.000
Central	bacteria	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.02	0.00	5.00	0.000	1.00	0.02	54.73	0.000
Central	bacteria	CWM_leaf_P	bactotal	~~	bactotal		0.04	0.01	5.00	0.000	0.95	0.06	16.53	0.000
Central	bacteria	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	bacteria	CWM_leaf_P	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	bacteria	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.03	0.09	0.30	0.765	0.03	0.11	0.30	0.764
Central	bacteria	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	-0.20	0.838	0.00	0.01	-0.20	0.838
Central	bacteria	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.03	0.11	-0.22	0.824	-0.03	0.14	-0.22	0.824
Central	bacteria	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.22	0.15	1.50	0.135	0.21	0.14	1.53	0.126
Central	bacteria	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.02	0.11	-0.22	0.829	-0.02	0.14	-0.13	0.901
Central	bacteria	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.22	0.15	1.50	0.135	0.21	0.14	1.52	0.129
Central	bacteria	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	-0.11	0.13	-0.88	0.380	-0.12	0.14	-0.88	0.377
Central	bacteria	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.04	0.13	0.30	0.768	0.04	0.14	0.30	0.768
Central	bacteria	CWM_MycInt	bactotal	~	CWM_MycInt_historic	c	-0.26	0.12	-2.20	0.028	-0.27	0.12	-2.26	0.024
Central	bacteria	CWM_MycInt	bactotal	~	CWM_MycInt_change	d	0.35	0.15	2.37	0.018	0.29	0.12	2.46	0.014
Central	bacteria	CWM_MycInt	bactotal	~	LUI_historic	e	-0.15	0.10	-1.47	0.142	-0.18	0.12	-1.49	0.137
Central	bacteria	CWM_MycInt	bactotal	~	LUI_change	f	0.24	0.13	1.79	0.074	0.22	0.12	1.82	0.068
Central	bacteria	CWM_MycInt	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	bacteria	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	5.00	0.000	0.99	0.03	28.71	0.000
Central	bacteria	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	1.00	0.01	84.79	0.000
Central	bacteria	CWM_MycInt	bactotal	~~	bactotal		0.04	0.01	5.00	0.000	0.77	0.10	7.52	0.000
Central	bacteria	CWM_MycInt	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	bacteria	CWM_MycInt	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	bacteria	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.03	0.03	0.82	0.415	0.03	0.04	0.82	0.415
Central	bacteria	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.01	0.05	0.29	0.770	0.01	0.04	0.29	0.769
Central	bacteria	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.12	0.11	-1.16	0.248	-0.15	0.13	-1.17	0.244
Central	bacteria	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.25	0.14	1.79	0.073	0.23	0.13	1.84	0.066
Central	bacteria	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.12	0.11	-1.15	0.251	-0.14	0.13	-1.02	0.309
Central	bacteria	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.25	0.14	1.79	0.074	0.23	0.13	1.74	0.082
Central	bacteria	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.03	0.12	0.23	0.821	0.03	0.14	0.23	0.821
Central	bacteria	Plant_biomass	Plant_biomass	~	LUI_change	b	0.13	0.15	0.87	0.385	0.12	0.14	0.88	0.382
Central	bacteria	Plant_biomass	bactotal	~	Plant_biomass	c	0.40	0.12	3.26	0.001	0.41	0.12	3.56	0.000
Central	bacteria	Plant_biomass	bactotal	~	LUI_historic	e	-0.04	0.10	-0.36	0.722	-0.05	0.13	-0.36	0.722
Central	bacteria	Plant_biomass	bactotal	~	LUI_change	f	0.17	0.13	1.25	0.211	0.16	0.13	1.26	0.207
Central	bacteria	Plant_biomass	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	bacteria	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	5.00	0.000	0.98	0.04	27.60	0.000
Central	bacteria	Plant_biomass	bactotal	~~	bactotal		0.04	0.01	5.00	0.000	0.79	0.10	7.69	0.000
Central	bacteria	Plant_biomass	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	bacteria	Plant_biomass	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	bacteria	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.05	0.23	0.821	0.01	0.06	0.23	0.821
Central	bacteria	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.05	0.06	0.84	0.401	0.05	0.06	0.85	0.395
Central	bacteria	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.03	0.11	-0.23	0.819	-0.03	0.14	-0.23	0.819
Central	bacteria	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.22	0.15	1.51	0.132	0.21	0.14	1.54	0.123
Central	bacteria	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.03	0.11	-0.22	0.824	-0.02	0.14	-0.13	0.897
Central	bacteria	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.22	0.15	1.51	0.132	0.21	0.14	1.53	0.126
Central	bacteria	Lignin_content	Lignin_content	~	LUI_historic	a	0.07	0.12	0.60	0.548	0.09	0.14	0.60	0.547
Central	bacteria	Lignin_content	Lignin_content	~	LUI_change	b	0.07	0.16	0.47	0.642	0.07	0.14	0.47	0.641
Central	bacteria	Lignin_content	bactotal	~	Lignin_content	c	0.12	0.13	0.94	0.349	0.13	0.14	0.95	0.345
Central	bacteria	Lignin_content	bactotal	~	LUI_historic	e	-0.04	0.11	-0.31	0.757	-0.04	0.14	-0.31	0.757
Central	bacteria	Lignin_content	bactotal	~	LUI_change	f	0.21	0.15	1.46	0.145	0.20	0.14	1.49	0.137
Central	bacteria	Lignin_content	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	bacteria	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	5.00	0.000	0.99	0.03	32.09	0.000
Central	bacteria	Lignin_content	bactotal	~~	bactotal		0.04	0.01	5.00	0.000	0.94	0.07	14.40	0.000
Central	bacteria	Lignin_content	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	bacteria	Lignin_content	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	bacteria	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.02	0.51	0.613	0.01	0.02	0.51	0.612
Central	bacteria	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.01	0.02	0.42	0.677	0.01	0.02	0.42	0.676
Central	bacteria	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.03	0.11	-0.23	0.819	-0.03	0.14	-0.23	0.819
Central	bacteria	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.22	0.15	1.51	0.132	0.21	0.14	1.54	0.123
Central	bacteria	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.03	0.11	-0.22	0.824	-0.02	0.14	-0.13	0.897
Central	bacteria	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.22	0.15	1.51	0.132	0.21	0.14	1.53	0.126
Central	bacteria	pH	pH_historic	~	LUI_historic	a	-0.04	0.11	-0.32	0.747	-0.05	0.14	-0.32	0.747
Central	bacteria	pH	pH_change	~	LUI_change	b	-0.16	0.15	-1.07	0.286	-0.15	0.14	-1.08	0.280
Central	bacteria	pH	bactotal	~	pH_historic	c	0.27	0.14	1.97	0.049	0.26	0.13	2.03	0.042
Central	bacteria	pH	bactotal	~	pH_change	d	0.12	0.14	0.89	0.376	0.12	0.13	0.89	0.373
Central	bacteria	pH	bactotal	~	LUI_historic	e	0.00	0.11	-0.01	0.991	0.00	0.13	-0.01	0.991
Central	bacteria	pH	bactotal	~	LUI_change	f	0.18	0.14	1.23	0.218	0.17	0.13	1.25	0.213
Central	bacteria	pH	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	bacteria	pH	pH_historic	~~	pH_historic		0.04	0.01	5.00	0.000	1.00	0.01	77.64	0.000
Central	bacteria	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	0.98	0.04	23.68	0.000
Central	bacteria	pH	bactotal	~~	bactotal		0.04	0.01	5.00	0.000	0.90	0.08	11.03	0.000
Central	bacteria	pH	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	bacteria	pH	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	bacteria	pH	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.03	-0.32	0.750	-0.01	0.04	-0.32	0.750
Central	bacteria	pH	LUI_change_in	:=	b*d	LUI_change_in	-0.02	0.03	-0.68	0.495	-0.02	0.03	-0.68	0.494
Central	bacteria	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.01	0.11	-0.10	0.922	-0.01	0.14	-0.10	0.922
Central	bacteria	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.16	0.14	1.10	0.270	0.15	0.13	1.11	0.265
Central	bacteria	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.01	0.11	-0.09	0.926	0.00	0.14	-0.03	0.977
Central	bacteria	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.16	0.14	1.10	0.270	0.15	0.13	1.11	0.267

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*p*	est.std	se.std	z.std	*p*.std
Central	fungi:bacteria ratio	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.53	0.09	5.84	0.000	0.64	0.08	7.58	0.000
Central	fungi:bacteria ratio	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.05	0.11	-0.46	0.647	-0.07	0.14	-0.46	0.646
Central	fungi:bacteria ratio	CWM_leaf_P	fungi_bac	~	CWM_leafP_historic	c	-0.11	0.16	-0.69	0.491	-0.11	0.15	-0.69	0.490
Central	fungi:bacteria ratio	CWM_leaf_P	fungi_bac	~	CWM_leafP_change	d	-0.09	0.18	-0.50	0.616	-0.06	0.12	-0.50	0.615
Central	fungi:bacteria ratio	CWM_leaf_P	fungi_bac	~	LUI_historic	e	-0.14	0.14	-1.02	0.310	-0.16	0.15	-1.02	0.308
Central	fungi:bacteria ratio	CWM_leaf_P	fungi_bac	~	LUI_change	f	-0.55	0.14	-3.97	0.000	-0.47	0.11	-4.45	0.000
Central	fungi:bacteria ratio	CWM_leaf_P	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	fungi:bacteria ratio	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	5.00	0.000	0.59	0.11	5.55	0.000
Central	fungi:bacteria ratio	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.02	0.00	5.00	0.000	1.00	0.02	54.73	0.000
Central	fungi:bacteria ratio	CWM_leaf_P	fungi_bac	~~	fungi_bac		0.04	0.01	5.00	0.000	0.71	0.11	6.54	0.000
Central	fungi:bacteria ratio	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	fungi:bacteria ratio	CWM_leaf_P	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	fungi:bacteria ratio	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	-0.06	0.09	-0.68	0.494	-0.07	0.10	-0.69	0.493
Central	fungi:bacteria ratio	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	0.34	0.735	0.00	0.01	0.34	0.735
Central	fungi:bacteria ratio	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.20	0.11	-1.87	0.061	-0.22	0.12	-1.91	0.056
Central	fungi:bacteria ratio	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.54	0.14	-3.93	0.000	-0.47	0.11	-4.40	0.000
Central	fungi:bacteria ratio	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.20	0.11	-1.89	0.059	-0.25	0.13	-1.93	0.054
Central	fungi:bacteria ratio	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.54	0.14	-3.94	0.000	-0.48	0.11	-4.48	0.000
Central	fungi:bacteria ratio	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	-0.11	0.13	-0.88	0.380	-0.12	0.14	-0.88	0.377
Central	fungi:bacteria ratio	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.04	0.13	0.30	0.768	0.04	0.14	0.30	0.768
Central	fungi:bacteria ratio	CWM_MycInt	fungi_bac	~	CWM_MycInt_historic	c	0.14	0.12	1.23	0.221	0.15	0.12	1.23	0.218
Central	fungi:bacteria ratio	CWM_MycInt	fungi_bac	~	CWM_MycInt_change	d	-0.09	0.15	-0.63	0.529	-0.07	0.12	-0.63	0.528
Central	fungi:bacteria ratio	CWM_MycInt	fungi_bac	~	LUI_historic	e	-0.16	0.11	-1.48	0.140	-0.18	0.12	-1.49	0.137
Central	fungi:bacteria ratio	CWM_MycInt	fungi_bac	~	LUI_change	f	-0.56	0.14	-4.11	0.000	-0.48	0.10	-4.63	0.000
Central	fungi:bacteria ratio	CWM_MycInt	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	fungi:bacteria ratio	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	5.00	0.000	0.99	0.03	28.71	0.000
Central	fungi:bacteria ratio	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	1.00	0.01	84.79	0.000
Central	fungi:bacteria ratio	CWM_MycInt	fungi_bac	~~	fungi_bac		0.04	0.01	5.00	0.000	0.69	0.11	6.39	0.000
Central	fungi:bacteria ratio	CWM_MycInt	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	fungi:bacteria ratio	CWM_MycInt	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	fungi:bacteria ratio	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	-0.02	0.02	-0.71	0.476	-0.02	0.03	-0.72	0.473
Central	fungi:bacteria ratio	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	-0.27	0.789	0.00	0.01	-0.27	0.789
Central	fungi:bacteria ratio	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.17	0.11	-1.61	0.107	-0.19	0.12	-1.63	0.102
Central	fungi:bacteria ratio	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.56	0.14	-4.12	0.000	-0.49	0.10	-4.66	0.000
Central	fungi:bacteria ratio	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.17	0.11	-1.63	0.103	-0.22	0.13	-1.67	0.095
Central	fungi:bacteria ratio	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.56	0.14	-4.13	0.000	-0.50	0.11	-4.74	0.000
Central	fungi:bacteria ratio	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.03	0.12	0.23	0.821	0.03	0.14	0.23	0.821
Central	fungi:bacteria ratio	Plant_biomass	Plant_biomass	~	LUI_change	b	0.13	0.15	0.87	0.385	0.12	0.14	0.88	0.382
Central	fungi:bacteria ratio	Plant_biomass	fungi_bac	~	Plant_biomass	c	-0.17	0.13	-1.34	0.180	-0.16	0.12	-1.35	0.177
Central	fungi:bacteria ratio	Plant_biomass	fungi_bac	~	LUI_historic	e	-0.19	0.11	-1.85	0.064	-0.22	0.12	-1.88	0.060
Central	fungi:bacteria ratio	Plant_biomass	fungi_bac	~	LUI_change	f	-0.52	0.14	-3.83	0.000	-0.45	0.11	-4.23	0.000
Central	fungi:bacteria ratio	Plant_biomass	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	fungi:bacteria ratio	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	5.00	0.000	0.98	0.04	27.60	0.000
Central	fungi:bacteria ratio	Plant_biomass	fungi_bac	~~	fungi_bac		0.04	0.01	5.00	0.000	0.69	0.11	6.34	0.000
Central	fungi:bacteria ratio	Plant_biomass	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	fungi:bacteria ratio	Plant_biomass	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	fungi:bacteria ratio	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.02	-0.22	0.823	-0.01	0.02	-0.22	0.823
Central	fungi:bacteria ratio	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	-0.02	0.03	-0.73	0.466	-0.02	0.03	-0.74	0.462
Central	fungi:bacteria ratio	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.20	0.11	-1.86	0.063	-0.22	0.12	-1.89	0.058
Central	fungi:bacteria ratio	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.55	0.14	-3.95	0.000	-0.47	0.11	-4.44	0.000
Central	fungi:bacteria ratio	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.20	0.11	-1.88	0.061	-0.25	0.13	-1.91	0.056
Central	fungi:bacteria ratio	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.55	0.14	-3.95	0.000	-0.49	0.11	-4.51	0.000
Central	fungi:bacteria ratio	Lignin_content	Lignin_content	~	LUI_historic	a	0.07	0.12	0.60	0.548	0.09	0.14	0.60	0.547
Central	fungi:bacteria ratio	Lignin_content	Lignin_content	~	LUI_change	b	0.07	0.16	0.47	0.642	0.07	0.14	0.47	0.641
Central	fungi:bacteria ratio	Lignin_content	fungi_bac	~	Lignin_content	c	0.15	0.12	1.23	0.220	0.15	0.12	1.23	0.217
Central	fungi:bacteria ratio	Lignin_content	fungi_bac	~	LUI_historic	e	-0.21	0.11	-1.99	0.047	-0.24	0.12	-2.02	0.043
Central	fungi:bacteria ratio	Lignin_content	fungi_bac	~	LUI_change	f	-0.56	0.14	-4.08	0.000	-0.48	0.11	-4.58	0.000
Central	fungi:bacteria ratio	Lignin_content	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	fungi:bacteria ratio	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	5.00	0.000	0.99	0.03	32.09	0.000
Central	fungi:bacteria ratio	Lignin_content	fungi_bac	~~	fungi_bac		0.04	0.01	5.00	0.000	0.69	0.11	6.38	0.000
Central	fungi:bacteria ratio	Lignin_content	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	fungi:bacteria ratio	Lignin_content	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	fungi:bacteria ratio	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.02	0.54	0.590	0.01	0.02	0.54	0.590
Central	fungi:bacteria ratio	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.01	0.03	0.44	0.664	0.01	0.02	0.43	0.665
Central	fungi:bacteria ratio	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.20	0.11	-1.86	0.063	-0.22	0.12	-1.89	0.058
Central	fungi:bacteria ratio	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.55	0.14	-3.95	0.000	-0.47	0.11	-4.44	0.000
Central	fungi:bacteria ratio	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.20	0.11	-1.88	0.061	-0.25	0.13	-1.91	0.056
Central	fungi:bacteria ratio	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.55	0.14	-3.95	0.000	-0.49	0.11	-4.51	0.000
Central	fungi:bacteria ratio	pH	pH_historic	~	LUI_historic	a	-0.04	0.11	-0.32	0.747	-0.05	0.14	-0.32	0.747
Central	fungi:bacteria ratio	pH	pH_change	~	LUI_change	b	-0.16	0.15	-1.07	0.286	-0.15	0.14	-1.08	0.280
Central	fungi:bacteria ratio	pH	fungi_bac	~	pH_historic	c	0.10	0.13	0.78	0.434	0.09	0.12	0.79	0.433
Central	fungi:bacteria ratio	pH	fungi_bac	~	pH_change	d	-0.02	0.13	-0.12	0.908	-0.01	0.12	-0.12	0.908
Central	fungi:bacteria ratio	pH	fungi_bac	~	LUI_historic	e	-0.20	0.11	-1.84	0.066	-0.22	0.12	-1.87	0.062
Central	fungi:bacteria ratio	pH	fungi_bac	~	LUI_change	f	-0.57	0.14	-4.12	0.000	-0.49	0.11	-4.65	0.000
Central	fungi:bacteria ratio	pH	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	fungi:bacteria ratio	pH	pH_historic	~~	pH_historic		0.04	0.01	5.00	0.000	1.00	0.01	77.64	0.000
Central	fungi:bacteria ratio	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	0.98	0.04	23.68	0.000
Central	fungi:bacteria ratio	pH	fungi_bac	~~	fungi_bac		0.04	0.01	5.00	0.000	0.69	0.11	6.38	0.000
Central	fungi:bacteria ratio	pH	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	fungi:bacteria ratio	pH	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	fungi:bacteria ratio	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	-0.30	0.766	0.00	0.01	-0.30	0.765
Central	fungi:bacteria ratio	pH	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.02	0.12	0.909	0.00	0.02	0.12	0.909
Central	fungi:bacteria ratio	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.20	0.11	-1.87	0.062	-0.22	0.12	-1.90	0.058
Central	fungi:bacteria ratio	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.57	0.14	-4.15	0.000	-0.49	0.10	-4.69	0.000
Central	fungi:bacteria ratio	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.20	0.11	-1.88	0.060	-0.25	0.13	-1.90	0.057
Central	fungi:bacteria ratio	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.57	0.14	-4.15	0.000	-0.50	0.11	-4.77	0.000

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*p*	est.std	se.std	z.std	*p*.std
Central	fungi	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.53	0.09	5.84	0.000	0.64	0.08	7.58	0.000
Central	fungi	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.05	0.11	-0.46	0.647	-0.07	0.14	-0.46	0.646
Central	fungi	CWM_leaf_P	fungi	~	CWM_leafP_historic	c	-0.03	0.17	-0.16	0.876	-0.03	0.17	-0.16	0.876
Central	fungi	CWM_leaf_P	fungi	~	CWM_leafP_change	d	0.03	0.19	0.18	0.855	0.02	0.13	0.18	0.855
Central	fungi	CWM_leaf_P	fungi	~	LUI_historic	e	-0.18	0.14	-1.25	0.212	-0.21	0.17	-1.26	0.207
Central	fungi	CWM_leaf_P	fungi	~	LUI_change	f	-0.29	0.14	-2.10	0.036	-0.28	0.13	-2.17	0.030
Central	fungi	CWM_leaf_P	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	fungi	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	5.00	0.000	0.59	0.11	5.55	0.000
Central	fungi	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.02	0.00	5.00	0.000	1.00	0.02	54.73	0.000
Central	fungi	CWM_leaf_P	fungi	~~	fungi		0.04	0.01	5.00	0.000	0.86	0.09	9.49	0.000
Central	fungi	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	fungi	CWM_leaf_P	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	fungi	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.09	-0.16	0.876	-0.02	0.11	-0.16	0.876
Central	fungi	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	-0.17	0.866	0.00	0.01	-0.17	0.866
Central	fungi	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.19	0.11	-1.75	0.081	-0.23	0.13	-1.79	0.074
Central	fungi	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.30	0.14	-2.11	0.035	-0.28	0.13	-2.19	0.028
Central	fungi	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.19	0.11	-1.75	0.079	-0.25	0.13	-1.86	0.063
Central	fungi	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.30	0.14	-2.12	0.034	-0.29	0.13	-2.26	0.024
Central	fungi	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	-0.11	0.13	-0.88	0.380	-0.12	0.14	-0.88	0.377
Central	fungi	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.04	0.13	0.30	0.768	0.04	0.14	0.30	0.768
Central	fungi	CWM_MycInt	fungi	~	CWM_MycInt_historic	c	-0.16	0.12	-1.35	0.176	-0.17	0.12	-1.37	0.172
Central	fungi	CWM_MycInt	fungi	~	CWM_MycInt_change	d	0.21	0.15	1.39	0.165	0.17	0.12	1.41	0.160
Central	fungi	CWM_MycInt	fungi	~	LUI_historic	e	-0.27	0.11	-2.52	0.012	-0.32	0.12	-2.63	0.008
Central	fungi	CWM_MycInt	fungi	~	LUI_change	f	-0.28	0.14	-2.11	0.035	-0.26	0.12	-2.17	0.030
Central	fungi	CWM_MycInt	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	fungi	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	5.00	0.000	0.99	0.03	28.71	0.000
Central	fungi	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	1.00	0.01	84.79	0.000
Central	fungi	CWM_MycInt	fungi	~~	fungi		0.04	0.01	5.00	0.000	0.78	0.10	7.60	0.000
Central	fungi	CWM_MycInt	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	fungi	CWM_MycInt	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	fungi	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.02	0.02	0.74	0.462	0.02	0.03	0.74	0.462
Central	fungi	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.01	0.03	0.29	0.773	0.01	0.03	0.29	0.773
Central	fungi	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.25	0.11	-2.33	0.020	-0.30	0.12	-2.43	0.015
Central	fungi	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.28	0.14	-2.01	0.044	-0.26	0.12	-2.07	0.038
Central	fungi	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.25	0.11	-2.34	0.019	-0.31	0.13	-2.49	0.013
Central	fungi	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.28	0.14	-2.02	0.044	-0.28	0.13	-2.14	0.033
Central	fungi	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.03	0.12	0.23	0.821	0.03	0.14	0.23	0.821
Central	fungi	Plant_biomass	Plant_biomass	~	LUI_change	b	0.13	0.15	0.87	0.385	0.12	0.14	0.88	0.382
Central	fungi	Plant_biomass	fungi	~	Plant_biomass	c	0.23	0.13	1.82	0.069	0.23	0.13	1.86	0.063
Central	fungi	Plant_biomass	fungi	~	LUI_historic	e	-0.20	0.11	-1.86	0.063	-0.24	0.12	-1.91	0.057
Central	fungi	Plant_biomass	fungi	~	LUI_change	f	-0.33	0.14	-2.39	0.017	-0.31	0.12	-2.49	0.013
Central	fungi	Plant_biomass	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	fungi	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	5.00	0.000	0.98	0.04	27.60	0.000
Central	fungi	Plant_biomass	fungi	~~	fungi		0.04	0.01	5.00	0.000	0.81	0.10	8.07	0.000
Central	fungi	Plant_biomass	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	fungi	Plant_biomass	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	fungi	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.03	0.23	0.822	0.01	0.03	0.23	0.822
Central	fungi	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.03	0.04	0.78	0.433	0.03	0.04	0.78	0.434
Central	fungi	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.19	0.11	-1.75	0.081	-0.23	0.13	-1.79	0.073
Central	fungi	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.30	0.14	-2.12	0.034	-0.28	0.13	-2.20	0.028
Central	fungi	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.19	0.11	-1.76	0.079	-0.25	0.13	-1.87	0.062
Central	fungi	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.30	0.14	-2.12	0.034	-0.29	0.13	-2.27	0.023
Central	fungi	Lignin_content	Lignin_content	~	LUI_historic	a	0.07	0.12	0.60	0.548	0.09	0.14	0.60	0.547
Central	fungi	Lignin_content	Lignin_content	~	LUI_change	b	0.07	0.16	0.47	0.642	0.07	0.14	0.47	0.641
Central	fungi	Lignin_content	fungi	~	Lignin_content	c	0.09	0.12	0.74	0.458	0.10	0.13	0.75	0.456
Central	fungi	Lignin_content	fungi	~	LUI_historic	e	-0.20	0.11	-1.81	0.070	-0.24	0.13	-1.86	0.063
Central	fungi	Lignin_content	fungi	~	LUI_change	f	-0.30	0.14	-2.17	0.030	-0.29	0.13	-2.26	0.024
Central	fungi	Lignin_content	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	fungi	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	5.00	0.000	0.99	0.03	32.09	0.000
Central	fungi	Lignin_content	fungi	~~	fungi		0.04	0.01	5.00	0.000	0.85	0.09	9.19	0.000
Central	fungi	Lignin_content	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	fungi	Lignin_content	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	fungi	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.02	0.47	0.641	0.01	0.02	0.47	0.640
Central	fungi	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.01	0.02	0.39	0.694	0.01	0.02	0.39	0.694
Central	fungi	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.19	0.11	-1.75	0.081	-0.23	0.13	-1.79	0.073
Central	fungi	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.30	0.14	-2.12	0.034	-0.28	0.13	-2.20	0.028
Central	fungi	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.19	0.11	-1.76	0.079	-0.25	0.13	-1.87	0.062
Central	fungi	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.30	0.14	-2.12	0.034	-0.29	0.13	-2.27	0.023
Central	fungi	pH	pH_historic	~	LUI_historic	a	-0.04	0.11	-0.32	0.747	-0.05	0.14	-0.32	0.747
Central	fungi	pH	pH_change	~	LUI_change	b	-0.16	0.15	-1.07	0.286	-0.15	0.14	-1.08	0.280
Central	fungi	pH	fungi	~	pH_historic	c	0.25	0.13	1.89	0.059	0.24	0.12	1.93	0.054
Central	fungi	pH	fungi	~	pH_change	d	0.06	0.13	0.43	0.670	0.05	0.13	0.43	0.670
Central	fungi	pH	fungi	~	LUI_historic	e	-0.17	0.11	-1.63	0.103	-0.20	0.12	-1.66	0.098
Central	fungi	pH	fungi	~	LUI_change	f	-0.34	0.14	-2.49	0.013	-0.32	0.12	-2.61	0.009
Central	fungi	pH	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	fungi	pH	pH_historic	~~	pH_historic		0.04	0.01	5.00	0.000	1.00	0.01	77.64	0.000
Central	fungi	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	0.98	0.04	23.68	0.000
Central	fungi	pH	fungi	~~	fungi		0.04	0.01	5.00	0.000	0.78	0.10	7.67	0.000
Central	fungi	pH	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	fungi	pH	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	fungi	pH	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.03	-0.32	0.751	-0.01	0.03	-0.32	0.750
Central	fungi	pH	LUI_change_in	:=	b*d	LUI_change_in	-0.01	0.02	-0.40	0.692	-0.01	0.02	-0.40	0.692
Central	fungi	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.18	0.11	-1.66	0.097	-0.22	0.13	-1.69	0.090
Central	fungi	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.35	0.14	-2.58	0.010	-0.32	0.12	-2.71	0.007
Central	fungi	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.18	0.11	-1.67	0.095	-0.24	0.13	-1.77	0.077
Central	fungi	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.35	0.14	-2.59	0.010	-0.34	0.12	-2.78	0.006

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*p*	est.std	se.std	z.std	*p*.std
Central	ergosterol	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.54	0.10	5.66	0.000	0.64	0.09	7.34	0.000
Central	ergosterol	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.05	0.11	-0.48	0.633	-0.07	0.15	-0.48	0.632
Central	ergosterol	CWM_leaf_P	Ergosterol	~	CWM_leafP_historic	c	-0.21	0.18	-1.14	0.255	-0.21	0.18	-1.15	0.249
Central	ergosterol	CWM_leaf_P	Ergosterol	~	CWM_leafP_change	d	-0.08	0.20	-0.39	0.700	-0.05	0.14	-0.39	0.700
Central	ergosterol	CWM_leaf_P	Ergosterol	~	LUI_historic	e	-0.07	0.15	-0.45	0.651	-0.08	0.18	-0.45	0.651
Central	ergosterol	CWM_leaf_P	Ergosterol	~	LUI_change	f	0.08	0.16	0.49	0.628	0.07	0.14	0.49	0.627
Central	ergosterol	CWM_leaf_P	LUI_historic	~~	LUI_change	g	0.00	0.01	0.56	0.576	0.08	0.15	0.57	0.572
Central	ergosterol	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	4.85	0.000	0.60	0.11	5.39	0.000
Central	ergosterol	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.02	0.01	4.85	0.000	1.00	0.02	49.28	0.000
Central	ergosterol	CWM_leaf_P	Ergosterol	~~	Ergosterol		0.05	0.01	4.85	0.000	0.92	0.08	12.39	0.000
Central	ergosterol	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.07	0.01	4.85	0.000	1.00	0.00	NA	NA
Central	ergosterol	CWM_leaf_P	LUI_change	~~	LUI_change		0.04	0.01	4.85	0.000	1.00	0.00	NA	NA
Central	ergosterol	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	-0.11	0.10	-1.12	0.264	-0.13	0.12	-1.13	0.258
Central	ergosterol	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	0.30	0.764	0.00	0.01	0.30	0.764
Central	ergosterol	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.18	0.12	-1.50	0.133	-0.21	0.14	-1.54	0.124
Central	ergosterol	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.08	0.15	0.51	0.608	0.07	0.14	0.51	0.608
Central	ergosterol	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.18	0.12	-1.50	0.134	-0.21	0.14	-1.49	0.135
Central	ergosterol	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.08	0.15	0.51	0.612	0.06	0.14	0.38	0.704
Central	ergosterol	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	-0.13	0.13	-1.01	0.311	-0.15	0.14	-1.02	0.306
Central	ergosterol	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.04	0.14	0.27	0.790	0.04	0.15	0.27	0.790
Central	ergosterol	CWM_MycInt	Ergosterol	~	CWM_MycInt_historic	c	0.00	0.13	-0.03	0.977	0.00	0.14	-0.03	0.977
Central	ergosterol	CWM_MycInt	Ergosterol	~	CWM_MycInt_change	d	0.30	0.16	1.80	0.071	0.24	0.13	1.85	0.064
Central	ergosterol	CWM_MycInt	Ergosterol	~	LUI_historic	e	-0.27	0.12	-2.28	0.023	-0.31	0.13	-2.39	0.017
Central	ergosterol	CWM_MycInt	Ergosterol	~	LUI_change	f	0.07	0.15	0.47	0.640	0.06	0.13	0.47	0.640
Central	ergosterol	CWM_MycInt	LUI_historic	~~	LUI_change	g	0.00	0.01	0.56	0.576	0.08	0.15	0.57	0.572
Central	ergosterol	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	4.85	0.000	0.98	0.04	23.44	0.000
Central	ergosterol	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.04	0.01	4.85	0.000	1.00	0.01	88.40	0.000
Central	ergosterol	CWM_MycInt	Ergosterol	~~	Ergosterol		0.04	0.01	4.85	0.000	0.84	0.10	8.84	0.000
Central	ergosterol	CWM_MycInt	LUI_historic	~~	LUI_historic		0.07	0.01	4.85	0.000	1.00	0.00	NA	NA
Central	ergosterol	CWM_MycInt	LUI_change	~~	LUI_change		0.04	0.01	4.85	0.000	1.00	0.00	NA	NA
Central	ergosterol	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	0.03	0.977	0.00	0.02	0.03	0.977
Central	ergosterol	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.01	0.04	0.26	0.792	0.01	0.04	0.26	0.792
Central	ergosterol	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.27	0.12	-2.30	0.021	-0.31	0.13	-2.41	0.016
Central	ergosterol	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.08	0.16	0.52	0.603	0.07	0.14	0.52	0.602
Central	ergosterol	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.27	0.12	-2.30	0.021	-0.30	0.13	-2.36	0.018
Central	ergosterol	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.08	0.16	0.51	0.608	0.05	0.15	0.32	0.747
Central	ergosterol	Plant_biomass	Plant_biomass	~	LUI_historic	a	-0.01	0.12	-0.07	0.944	-0.01	0.15	-0.07	0.944
Central	ergosterol	Plant_biomass	Plant_biomass	~	LUI_change	b	0.13	0.15	0.87	0.383	0.13	0.14	0.88	0.379
Central	ergosterol	Plant_biomass	Ergosterol	~	Plant_biomass	c	0.14	0.15	0.95	0.344	0.14	0.14	0.96	0.340
Central	ergosterol	Plant_biomass	Ergosterol	~	LUI_historic	e	-0.18	0.12	-1.50	0.132	-0.21	0.14	-1.54	0.124
Central	ergosterol	Plant_biomass	Ergosterol	~	LUI_change	f	0.05	0.16	0.34	0.734	0.05	0.14	0.34	0.733
Central	ergosterol	Plant_biomass	LUI_historic	~~	LUI_change	g	0.00	0.01	0.56	0.576	0.08	0.15	0.57	0.572
Central	ergosterol	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.04	0.01	4.85	0.000	0.98	0.04	27.15	0.000
Central	ergosterol	Plant_biomass	Ergosterol	~~	Ergosterol		0.05	0.01	4.85	0.000	0.93	0.07	13.37	0.000
Central	ergosterol	Plant_biomass	LUI_historic	~~	LUI_historic		0.07	0.01	4.85	0.000	1.00	0.00	NA	NA
Central	ergosterol	Plant_biomass	LUI_change	~~	LUI_change		0.04	0.01	4.85	0.000	1.00	0.00	NA	NA
Central	ergosterol	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	-0.07	0.944	0.00	0.02	-0.07	0.944
Central	ergosterol	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.02	0.03	0.64	0.521	0.02	0.03	0.64	0.519
Central	ergosterol	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.18	0.12	-1.50	0.134	-0.21	0.14	-1.54	0.125
Central	ergosterol	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.07	0.16	0.46	0.646	0.07	0.14	0.46	0.646
Central	ergosterol	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.18	0.12	-1.50	0.134	-0.21	0.14	-1.50	0.134
Central	ergosterol	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.07	0.16	0.45	0.650	0.05	0.15	0.33	0.741
Central	ergosterol	Lignin_content	Lignin_content	~	LUI_historic	a	0.06	0.13	0.49	0.622	0.07	0.15	0.49	0.622
Central	ergosterol	Lignin_content	Lignin_content	~	LUI_change	b	0.11	0.17	0.65	0.515	0.09	0.15	0.65	0.514
Central	ergosterol	Lignin_content	Ergosterol	~	Lignin_content	c	0.30	0.13	2.27	0.023	0.31	0.13	2.37	0.018
Central	ergosterol	Lignin_content	Ergosterol	~	LUI_historic	e	-0.20	0.11	-1.74	0.082	-0.24	0.13	-1.78	0.075
Central	ergosterol	Lignin_content	Ergosterol	~	LUI_change	f	0.04	0.15	0.27	0.789	0.04	0.14	0.27	0.789
Central	ergosterol	Lignin_content	LUI_historic	~~	LUI_change	g	0.00	0.01	0.56	0.576	0.08	0.15	0.57	0.572
Central	ergosterol	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	4.85	0.000	0.99	0.04	27.85	0.000
Central	ergosterol	Lignin_content	Ergosterol	~~	Ergosterol		0.04	0.01	4.85	0.000	0.86	0.09	9.11	0.000
Central	ergosterol	Lignin_content	LUI_historic	~~	LUI_historic		0.07	0.01	4.85	0.000	1.00	0.00	NA	NA
Central	ergosterol	Lignin_content	LUI_change	~~	LUI_change		0.04	0.01	4.85	0.000	1.00	0.00	NA	NA
Central	ergosterol	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.02	0.04	0.48	0.630	0.02	0.05	0.48	0.631
Central	ergosterol	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.03	0.05	0.63	0.532	0.03	0.05	0.63	0.530
Central	ergosterol	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.18	0.12	-1.50	0.134	-0.21	0.14	-1.54	0.125
Central	ergosterol	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.07	0.16	0.46	0.646	0.07	0.14	0.46	0.646
Central	ergosterol	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.18	0.12	-1.50	0.134	-0.21	0.14	-1.50	0.134
Central	ergosterol	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.07	0.16	0.45	0.650	0.05	0.15	0.33	0.741
Central	ergosterol	pH	pH_historic	~	LUI_historic	a	-0.02	0.12	-0.15	0.883	-0.02	0.15	-0.15	0.883
Central	ergosterol	pH	pH_change	~	LUI_change	b	-0.20	0.15	-1.35	0.178	-0.19	0.14	-1.37	0.170
Central	ergosterol	pH	Ergosterol	~	pH_historic	c	0.29	0.15	1.97	0.048	0.27	0.13	2.04	0.041
Central	ergosterol	pH	Ergosterol	~	pH_change	d	0.15	0.15	1.02	0.307	0.14	0.14	1.03	0.303
Central	ergosterol	pH	Ergosterol	~	LUI_historic	e	-0.16	0.12	-1.36	0.174	-0.19	0.14	-1.38	0.167
Central	ergosterol	pH	Ergosterol	~	LUI_change	f	0.05	0.16	0.32	0.751	0.04	0.14	0.32	0.751
Central	ergosterol	pH	LUI_historic	~~	LUI_change	g	0.00	0.01	0.56	0.576	0.08	0.15	0.57	0.572
Central	ergosterol	pH	pH_historic	~~	pH_historic		0.04	0.01	4.85	0.000	1.00	0.01	159.91	0.000
Central	ergosterol	pH	pH_change	~~	pH_change		0.04	0.01	4.85	0.000	0.96	0.05	17.77	0.000
Central	ergosterol	pH	Ergosterol	~~	Ergosterol		0.04	0.01	4.85	0.000	0.87	0.09	9.66	0.000
Central	ergosterol	pH	LUI_historic	~~	LUI_historic		0.07	0.01	4.85	0.000	1.00	0.00	NA	NA
Central	ergosterol	pH	LUI_change	~~	LUI_change		0.04	0.01	4.85	0.000	1.00	0.00	NA	NA
Central	ergosterol	pH	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.03	-0.15	0.883	-0.01	0.04	-0.15	0.883
Central	ergosterol	pH	LUI_change_in	:=	b*d	LUI_change_in	-0.03	0.04	-0.81	0.416	-0.03	0.03	-0.82	0.413
Central	ergosterol	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.16	0.12	-1.35	0.177	-0.19	0.14	-1.37	0.170
Central	ergosterol	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.02	0.15	0.12	0.903	0.02	0.14	0.12	0.903
Central	ergosterol	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.16	0.12	-1.35	0.177	-0.19	0.14	-1.37	0.171
Central	ergosterol	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.02	0.15	0.12	0.907	0.00	0.14	0.01	0.994

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*p*	est.std	se.std	z.std	*p*.std
North-East	Cmic	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.03	0.11	0.32	0.747	0.05	0.14	0.32	0.747
North-East	Cmic	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.30	0.17	-1.77	0.077	-0.24	0.13	-1.82	0.068
North-East	Cmic	CWM_leaf_P	Cmic	~	CWM_leafP_historic	c	-0.09	0.13	-0.64	0.520	-0.09	0.14	-0.65	0.518
North-East	Cmic	CWM_leaf_P	Cmic	~	CWM_leafP_change	d	0.05	0.14	0.35	0.726	0.05	0.15	0.35	0.726
North-East	Cmic	CWM_leaf_P	Cmic	~	LUI_historic	e	0.03	0.11	0.31	0.754	0.05	0.16	0.31	0.753
North-East	Cmic	CWM_leaf_P	Cmic	~	LUI_change	f	0.02	0.19	0.11	0.915	0.02	0.16	0.11	0.915
North-East	Cmic	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	Cmic	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.05	0.01	5.00	0.000	1.00	0.01	77.51	0.000
North-East	Cmic	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.04	0.01	5.00	0.000	0.94	0.07	14.57	0.000
North-East	Cmic	CWM_leaf_P	Cmic	~~	Cmic		0.04	0.01	5.00	0.000	0.99	0.03	31.73	0.000
North-East	Cmic	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	Cmic	CWM_leaf_P	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	Cmic	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	-0.29	0.773	0.00	0.01	-0.29	0.773
North-East	Cmic	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	-0.01	0.04	-0.34	0.731	-0.01	0.04	-0.34	0.731
North-East	Cmic	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.03	0.11	0.29	0.774	0.05	0.16	0.29	0.774
North-East	Cmic	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.01	0.18	0.03	0.976	0.01	0.16	0.03	0.976
North-East	Cmic	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.03	0.11	0.29	0.772	0.04	0.14	0.30	0.762
North-East	Cmic	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.01	0.18	0.03	0.978	-0.02	0.14	-0.10	0.918
North-East	Cmic	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.16	0.09	1.72	0.086	0.24	0.13	1.77	0.077
North-East	Cmic	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	-0.15	0.15	-1.01	0.311	-0.14	0.14	-1.02	0.306
North-East	Cmic	CWM_MycInt	Cmic	~	CWM_MycInt_historic	c	0.37	0.14	2.56	0.010	0.33	0.12	2.68	0.007
North-East	Cmic	CWM_MycInt	Cmic	~	CWM_MycInt_change	d	0.39	0.15	2.64	0.008	0.33	0.12	2.77	0.006
North-East	Cmic	CWM_MycInt	Cmic	~	LUI_historic	e	0.01	0.11	0.12	0.908	0.02	0.14	0.12	0.908
North-East	Cmic	CWM_MycInt	Cmic	~	LUI_change	f	-0.03	0.18	-0.19	0.852	-0.03	0.14	-0.19	0.852
North-East	Cmic	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	Cmic	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.04	0.01	5.00	0.000	0.94	0.06	14.99	0.000
North-East	Cmic	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	0.98	0.04	24.93	0.000
North-East	Cmic	CWM_MycInt	Cmic	~~	Cmic		0.04	0.01	5.00	0.000	0.77	0.10	7.60	0.000
North-East	Cmic	CWM_MycInt	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	Cmic	CWM_MycInt	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	Cmic	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.06	0.04	1.43	0.154	0.08	0.05	1.45	0.146
North-East	Cmic	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	-0.06	0.06	-0.95	0.344	-0.05	0.05	-0.96	0.340
North-East	Cmic	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.07	0.11	0.65	0.519	0.09	0.14	0.65	0.517
North-East	Cmic	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.09	0.19	-0.50	0.617	-0.07	0.15	-0.50	0.616
North-East	Cmic	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.07	0.11	0.67	0.501	0.13	0.13	0.94	0.348
North-East	Cmic	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.09	0.18	-0.51	0.609	-0.11	0.13	-0.85	0.398
North-East	Cmic	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.12	1.61	0.109	0.25	0.15	1.65	0.100
North-East	Cmic	Plant_biomass	Plant_biomass	~	LUI_change	b	0.04	0.20	0.19	0.850	0.03	0.15	0.19	0.850
North-East	Cmic	Plant_biomass	Cmic	~	Plant_biomass	c	0.40	0.12	3.37	0.001	0.45	0.12	3.73	0.000
North-East	Cmic	Plant_biomass	Cmic	~	LUI_historic	e	-0.05	0.10	-0.52	0.601	-0.08	0.15	-0.52	0.600
North-East	Cmic	Plant_biomass	Cmic	~	LUI_change	f	-0.04	0.17	-0.23	0.820	-0.03	0.14	-0.23	0.820
North-East	Cmic	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	Cmic	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	4.95	0.000	0.94	0.06	14.84	0.000
North-East	Cmic	Plant_biomass	Cmic	~~	Cmic		0.03	0.01	4.95	0.000	0.81	0.10	8.04	0.000
North-East	Cmic	Plant_biomass	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	Cmic	Plant_biomass	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	Cmic	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.08	0.05	1.45	0.147	0.11	0.08	1.47	0.141
North-East	Cmic	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.02	0.08	0.19	0.851	0.01	0.07	0.19	0.851
North-East	Cmic	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.02	0.11	0.21	0.833	0.03	0.16	0.21	0.833
North-East	Cmic	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.02	0.19	-0.12	0.902	-0.02	0.16	-0.12	0.902
North-East	Cmic	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.02	0.11	0.22	0.827	0.04	0.14	0.29	0.769
North-East	Cmic	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.02	0.19	-0.13	0.899	-0.03	0.14	-0.24	0.812
North-East	Cmic	Lignin_content	Lignin_content	~	LUI_historic	a	0.22	0.12	1.87	0.062	0.29	0.15	1.93	0.054
North-East	Cmic	Lignin_content	Lignin_content	~	LUI_change	b	0.22	0.20	1.11	0.265	0.17	0.15	1.13	0.260
North-East	Cmic	Lignin_content	Cmic	~	Lignin_content	c	-0.10	0.13	-0.72	0.472	-0.11	0.15	-0.72	0.470
North-East	Cmic	Lignin_content	Cmic	~	LUI_historic	e	0.04	0.11	0.39	0.696	0.06	0.16	0.39	0.696
North-East	Cmic	Lignin_content	Cmic	~	LUI_change	f	0.00	0.19	-0.01	0.992	0.00	0.16	-0.01	0.992
North-East	Cmic	Lignin_content	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	Cmic	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	4.95	0.000	0.93	0.07	13.39	0.000
North-East	Cmic	Lignin_content	Cmic	~~	Cmic		0.04	0.01	4.95	0.000	0.99	0.03	31.36	0.000
North-East	Cmic	Lignin_content	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	Cmic	Lignin_content	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	Cmic	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	-0.02	0.03	-0.67	0.503	-0.03	0.05	-0.67	0.501
North-East	Cmic	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	-0.02	0.04	-0.60	0.546	-0.02	0.03	-0.61	0.544
North-East	Cmic	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.02	0.11	0.21	0.833	0.03	0.16	0.21	0.833
North-East	Cmic	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.02	0.19	-0.12	0.902	-0.02	0.16	-0.12	0.902
North-East	Cmic	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.02	0.11	0.22	0.827	0.04	0.14	0.29	0.769
North-East	Cmic	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.02	0.19	-0.13	0.899	-0.03	0.14	-0.24	0.812
North-East	Cmic	pH	pH_historic	~	LUI_historic	a	-0.02	0.16	-0.13	0.897	-0.02	0.14	-0.13	0.897
North-East	Cmic	pH	pH_change	~	LUI_change	b	0.04	0.10	0.40	0.686	0.06	0.14	0.40	0.686
North-East	Cmic	pH	Cmic	~	pH_historic	c	-0.13	0.09	-1.50	0.134	-0.21	0.13	-1.53	0.126
North-East	Cmic	pH	Cmic	~	pH_change	d	0.17	0.23	0.74	0.459	0.10	0.14	0.74	0.457
North-East	Cmic	pH	Cmic	~	LUI_historic	e	0.02	0.11	0.18	0.860	0.03	0.15	0.18	0.860
North-East	Cmic	pH	Cmic	~	LUI_change	f	-0.07	0.18	-0.36	0.717	-0.06	0.15	-0.36	0.717
North-East	Cmic	pH	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	Cmic	pH	pH_historic	~~	pH_historic		0.10	0.02	5.00	0.000	1.00	0.01	193.05	0.000
North-East	Cmic	pH	pH_change	~~	pH_change		0.01	0.00	5.00	0.000	1.00	0.02	62.03	0.000
North-East	Cmic	pH	Cmic	~~	Cmic		0.04	0.01	5.00	0.000	0.94	0.06	14.83	0.000
North-East	Cmic	pH	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	Cmic	pH	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	Cmic	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	0.13	0.897	0.00	0.03	0.13	0.897
North-East	Cmic	pH	LUI_change_in	:=	b*d	LUI_change_in	0.01	0.02	0.35	0.723	0.01	0.02	0.36	0.723
North-East	Cmic	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.02	0.11	0.20	0.844	0.03	0.16	0.20	0.844
North-East	Cmic	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.06	0.18	-0.32	0.746	-0.05	0.15	-0.32	0.746
North-East	Cmic	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.02	0.11	0.21	0.833	0.05	0.14	0.37	0.712
North-East	Cmic	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.06	0.18	-0.33	0.743	-0.06	0.14	-0.45	0.651

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*p*	est.std	se.std	z.std	*p*.std
North-East	Nmic	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.03	0.11	0.32	0.747	0.05	0.14	0.32	0.747
North-East	Nmic	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.30	0.17	-1.77	0.077	-0.24	0.13	-1.82	0.068
North-East	Nmic	CWM_leaf_P	Nmic	~	CWM_leafP_historic	c	0.03	0.13	0.24	0.807	0.03	0.14	0.24	0.807
North-East	Nmic	CWM_leaf_P	Nmic	~	CWM_leafP_change	d	0.12	0.13	0.86	0.388	0.13	0.14	0.87	0.384
North-East	Nmic	CWM_leaf_P	Nmic	~	LUI_historic	e	0.04	0.11	0.36	0.718	0.06	0.16	0.36	0.718
North-East	Nmic	CWM_leaf_P	Nmic	~	LUI_change	f	0.03	0.18	0.16	0.876	0.03	0.16	0.16	0.876
North-East	Nmic	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	Nmic	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.05	0.01	5.00	0.000	1.00	0.01	77.51	0.000
North-East	Nmic	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.04	0.01	5.00	0.000	0.94	0.07	14.57	0.000
North-East	Nmic	CWM_leaf_P	Nmic	~~	Nmic		0.04	0.01	5.00	0.000	0.98	0.04	25.41	0.000
North-East	Nmic	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	Nmic	CWM_leaf_P	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	Nmic	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	0.20	0.846	0.00	0.01	0.20	0.846
North-East	Nmic	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	-0.04	0.05	-0.78	0.438	-0.03	0.04	-0.78	0.435
North-East	Nmic	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.04	0.11	0.37	0.711	0.06	0.16	0.37	0.710
North-East	Nmic	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.01	0.18	-0.04	0.972	-0.01	0.16	-0.04	0.972
North-East	Nmic	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.04	0.10	0.38	0.706	0.06	0.14	0.43	0.669
North-East	Nmic	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.01	0.18	-0.04	0.968	-0.03	0.14	-0.22	0.830
North-East	Nmic	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.16	0.09	1.72	0.086	0.24	0.13	1.77	0.077
North-East	Nmic	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	-0.15	0.15	-1.01	0.311	-0.14	0.14	-1.02	0.306
North-East	Nmic	CWM_MycInt	Nmic	~	CWM_MycInt_historic	c	0.15	0.15	1.03	0.303	0.15	0.14	1.04	0.298
North-East	Nmic	CWM_MycInt	Nmic	~	CWM_MycInt_change	d	0.09	0.15	0.58	0.559	0.08	0.14	0.59	0.558
North-East	Nmic	CWM_MycInt	Nmic	~	LUI_historic	e	0.02	0.11	0.17	0.864	0.03	0.16	0.17	0.864
North-East	Nmic	CWM_MycInt	Nmic	~	LUI_change	f	-0.03	0.18	-0.15	0.878	-0.02	0.16	-0.15	0.878
North-East	Nmic	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	Nmic	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.04	0.01	5.00	0.000	0.94	0.06	14.99	0.000
North-East	Nmic	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	0.98	0.04	24.93	0.000
North-East	Nmic	CWM_MycInt	Nmic	~~	Nmic		0.04	0.01	5.00	0.000	0.97	0.05	19.21	0.000
North-East	Nmic	CWM_MycInt	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	Nmic	CWM_MycInt	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	Nmic	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.02	0.03	0.88	0.377	0.04	0.04	0.89	0.373
North-East	Nmic	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	-0.01	0.03	-0.51	0.613	-0.01	0.02	-0.51	0.612
North-East	Nmic	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.04	0.11	0.40	0.691	0.06	0.16	0.40	0.690
North-East	Nmic	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.04	0.18	-0.23	0.819	-0.04	0.15	-0.23	0.819
North-East	Nmic	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.04	0.11	0.41	0.680	0.08	0.14	0.55	0.583
North-East	Nmic	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.04	0.18	-0.24	0.814	-0.06	0.14	-0.44	0.657
North-East	Nmic	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.12	1.61	0.109	0.25	0.15	1.65	0.100
North-East	Nmic	Plant_biomass	Plant_biomass	~	LUI_change	b	0.04	0.20	0.19	0.850	0.03	0.15	0.19	0.850
North-East	Nmic	Plant_biomass	Nmic	~	Plant_biomass	c	0.32	0.12	2.69	0.007	0.37	0.13	2.88	0.004
North-East	Nmic	Plant_biomass	Nmic	~	LUI_historic	e	-0.02	0.10	-0.23	0.817	-0.04	0.15	-0.23	0.817
North-East	Nmic	Plant_biomass	Nmic	~	LUI_change	f	-0.01	0.17	-0.08	0.939	-0.01	0.15	-0.08	0.939
North-East	Nmic	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	Nmic	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	4.95	0.000	0.94	0.06	14.84	0.000
North-East	Nmic	Plant_biomass	Nmic	~~	Nmic		0.03	0.01	4.95	0.000	0.87	0.09	9.66	0.000
North-East	Nmic	Plant_biomass	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	Nmic	Plant_biomass	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	Nmic	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.06	0.05	1.38	0.168	0.09	0.07	1.40	0.161
North-East	Nmic	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.01	0.07	0.19	0.851	0.01	0.06	0.19	0.851
North-East	Nmic	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.04	0.11	0.35	0.724	0.06	0.16	0.35	0.723
North-East	Nmic	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.00	0.18	0.00	0.997	0.00	0.16	0.00	0.997
North-East	Nmic	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.04	0.11	0.36	0.719	0.06	0.14	0.39	0.694
North-East	Nmic	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.00	0.18	-0.01	0.994	-0.03	0.14	-0.17	0.863
North-East	Nmic	Lignin_content	Lignin_content	~	LUI_historic	a	0.22	0.12	1.87	0.062	0.29	0.15	1.93	0.054
North-East	Nmic	Lignin_content	Lignin_content	~	LUI_change	b	0.22	0.20	1.11	0.265	0.17	0.15	1.13	0.260
North-East	Nmic	Lignin_content	Nmic	~	Lignin_content	c	0.05	0.13	0.42	0.676	0.06	0.15	0.42	0.676
North-East	Nmic	Lignin_content	Nmic	~	LUI_historic	e	0.03	0.11	0.24	0.814	0.04	0.16	0.24	0.814
North-East	Nmic	Lignin_content	Nmic	~	LUI_change	f	-0.01	0.18	-0.07	0.945	-0.01	0.16	-0.07	0.945
North-East	Nmic	Lignin_content	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	Nmic	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	4.95	0.000	0.93	0.07	13.39	0.000
North-East	Nmic	Lignin_content	Nmic	~~	Nmic		0.04	0.01	4.95	0.000	0.99	0.02	42.81	0.000
North-East	Nmic	Lignin_content	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	Nmic	Lignin_content	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	Nmic	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.03	0.41	0.684	0.02	0.04	0.41	0.683
North-East	Nmic	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.01	0.03	0.39	0.696	0.01	0.03	0.39	0.695
North-East	Nmic	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.04	0.11	0.35	0.724	0.06	0.16	0.35	0.723
North-East	Nmic	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.00	0.18	0.00	0.997	0.00	0.16	0.00	0.997
North-East	Nmic	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.04	0.11	0.36	0.719	0.06	0.14	0.39	0.694
North-East	Nmic	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.00	0.18	-0.01	0.994	-0.03	0.14	-0.17	0.863
North-East	Nmic	pH	pH_historic	~	LUI_historic	a	-0.02	0.16	-0.13	0.897	-0.02	0.14	-0.13	0.897
North-East	Nmic	pH	pH_change	~	LUI_change	b	0.04	0.10	0.40	0.686	0.06	0.14	0.40	0.686
North-East	Nmic	pH	Nmic	~	pH_historic	c	0.00	0.08	-0.05	0.962	-0.01	0.14	-0.05	0.962
North-East	Nmic	pH	Nmic	~	pH_change	d	0.45	0.22	2.01	0.044	0.27	0.13	2.09	0.037
North-East	Nmic	pH	Nmic	~	LUI_historic	e	0.06	0.10	0.60	0.549	0.09	0.15	0.60	0.548
North-East	Nmic	pH	Nmic	~	LUI_change	f	0.00	0.17	-0.01	0.990	0.00	0.15	-0.01	0.990
North-East	Nmic	pH	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	Nmic	pH	pH_historic	~~	pH_historic		0.10	0.02	5.00	0.000	1.00	0.01	193.05	0.000
North-East	Nmic	pH	pH_change	~~	pH_change		0.01	0.00	5.00	0.000	1.00	0.02	62.03	0.000
North-East	Nmic	pH	Nmic	~~	Nmic		0.04	0.01	5.00	0.000	0.92	0.07	12.41	0.000
North-East	Nmic	pH	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	Nmic	pH	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	Nmic	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.00	0.05	0.964	0.00	0.00	0.05	0.964
North-East	Nmic	pH	LUI_change_in	:=	b*d	LUI_change_in	0.02	0.05	0.40	0.692	0.02	0.04	0.40	0.692
North-East	Nmic	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.06	0.10	0.60	0.548	0.09	0.15	0.60	0.547
North-East	Nmic	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.02	0.18	0.09	0.930	0.01	0.16	0.09	0.930
North-East	Nmic	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.06	0.10	0.61	0.545	0.08	0.14	0.62	0.536
North-East	Nmic	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.01	0.18	0.08	0.935	-0.03	0.14	-0.18	0.859

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*p*	est.std	se.std	z.std	*p*.std
North-East	Cmic:Nmic ratio	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.03	0.11	0.32	0.747	0.05	0.14	0.32	0.747
North-East	Cmic:Nmic ratio	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.30	0.17	-1.77	0.077	-0.24	0.13	-1.82	0.068
North-East	Cmic:Nmic ratio	CWM_leaf_P	RatioCmic_Nmic	~	CWM_leafP_historic	c	-0.04	0.10	-0.41	0.681	-0.05	0.13	-0.41	0.681
North-East	Cmic:Nmic ratio	CWM_leaf_P	RatioCmic_Nmic	~	CWM_leafP_change	d	-0.16	0.11	-1.53	0.126	-0.21	0.13	-1.56	0.119
North-East	Cmic:Nmic ratio	CWM_leaf_P	RatioCmic_Nmic	~	LUI_historic	e	-0.11	0.09	-1.27	0.205	-0.19	0.14	-1.28	0.199
North-East	Cmic:Nmic ratio	CWM_leaf_P	RatioCmic_Nmic	~	LUI_change	f	-0.37	0.15	-2.50	0.012	-0.38	0.14	-2.64	0.008
North-East	Cmic:Nmic ratio	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	Cmic:Nmic ratio	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.05	0.01	5.00	0.000	1.00	0.01	77.51	0.000
North-East	Cmic:Nmic ratio	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.04	0.01	5.00	0.000	0.94	0.07	14.57	0.000
North-East	Cmic:Nmic ratio	CWM_leaf_P	RatioCmic_Nmic	~~	RatioCmic_Nmic		0.02	0.01	5.00	0.000	0.87	0.09	9.80	0.000
North-East	Cmic:Nmic ratio	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	Cmic:Nmic ratio	CWM_leaf_P	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	Cmic:Nmic ratio	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	-0.25	0.800	0.00	0.01	-0.25	0.799
North-East	Cmic:Nmic ratio	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.05	0.04	1.16	0.247	0.05	0.04	1.16	0.244
North-East	Cmic:Nmic ratio	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.11	0.09	-1.28	0.199	-0.19	0.14	-1.30	0.194
North-East	Cmic:Nmic ratio	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.32	0.15	-2.18	0.029	-0.32	0.14	-2.28	0.023
North-East	Cmic:Nmic ratio	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.10	0.08	-1.22	0.221	-0.05	0.14	-0.35	0.729
North-East	Cmic:Nmic ratio	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.32	0.15	-2.18	0.030	-0.24	0.13	-1.83	0.067
North-East	Cmic:Nmic ratio	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.16	0.09	1.72	0.086	0.24	0.13	1.77	0.077
North-East	Cmic:Nmic ratio	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	-0.15	0.15	-1.01	0.311	-0.14	0.14	-1.02	0.306
North-East	Cmic:Nmic ratio	CWM_MycInt	RatioCmic_Nmic	~	CWM_MycInt_historic	c	0.06	0.12	0.50	0.617	0.07	0.14	0.50	0.616
North-East	Cmic:Nmic ratio	CWM_MycInt	RatioCmic_Nmic	~	CWM_MycInt_change	d	0.02	0.12	0.18	0.859	0.02	0.14	0.18	0.859
North-East	Cmic:Nmic ratio	CWM_MycInt	RatioCmic_Nmic	~	LUI_historic	e	-0.12	0.09	-1.33	0.182	-0.20	0.15	-1.35	0.176
North-East	Cmic:Nmic ratio	CWM_MycInt	RatioCmic_Nmic	~	LUI_change	f	-0.34	0.15	-2.33	0.020	-0.35	0.14	-2.44	0.015
North-East	Cmic:Nmic ratio	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	Cmic:Nmic ratio	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.04	0.01	5.00	0.000	0.94	0.06	14.99	0.000
North-East	Cmic:Nmic ratio	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	0.98	0.04	24.93	0.000
North-East	Cmic:Nmic ratio	CWM_MycInt	RatioCmic_Nmic	~~	RatioCmic_Nmic		0.03	0.01	5.00	0.000	0.89	0.08	10.86	0.000
North-East	Cmic:Nmic ratio	CWM_MycInt	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	Cmic:Nmic ratio	CWM_MycInt	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	Cmic:Nmic ratio	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.02	0.48	0.631	0.02	0.03	0.48	0.631
North-East	Cmic:Nmic ratio	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.02	-0.18	0.861	0.00	0.02	-0.18	0.861
North-East	Cmic:Nmic ratio	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.11	0.09	-1.25	0.210	-0.19	0.15	-1.27	0.204
North-East	Cmic:Nmic ratio	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.34	0.15	-2.37	0.018	-0.35	0.14	-2.49	0.013
North-East	Cmic:Nmic ratio	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.10	0.09	-1.19	0.235	-0.04	0.14	-0.25	0.805
North-East	Cmic:Nmic ratio	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.34	0.15	-2.37	0.018	-0.27	0.13	-2.07	0.038
North-East	Cmic:Nmic ratio	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.12	1.61	0.109	0.25	0.15	1.65	0.100
North-East	Cmic:Nmic ratio	Plant_biomass	Plant_biomass	~	LUI_change	b	0.04	0.20	0.19	0.850	0.03	0.15	0.19	0.850
North-East	Cmic:Nmic ratio	Plant_biomass	RatioCmic_Nmic	~	Plant_biomass	c	-0.18	0.10	-1.73	0.083	-0.24	0.13	-1.77	0.076
North-East	Cmic:Nmic ratio	Plant_biomass	RatioCmic_Nmic	~	LUI_historic	e	-0.07	0.09	-0.85	0.396	-0.13	0.15	-0.85	0.394
North-East	Cmic:Nmic ratio	Plant_biomass	RatioCmic_Nmic	~	LUI_change	f	-0.32	0.14	-2.24	0.025	-0.33	0.14	-2.33	0.020
North-East	Cmic:Nmic ratio	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	Cmic:Nmic ratio	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	4.95	0.000	0.94	0.06	14.84	0.000
North-East	Cmic:Nmic ratio	Plant_biomass	RatioCmic_Nmic	~~	RatioCmic_Nmic		0.02	0.01	4.95	0.000	0.86	0.09	9.19	0.000
North-East	Cmic:Nmic ratio	Plant_biomass	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	Cmic:Nmic ratio	Plant_biomass	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	Cmic:Nmic ratio	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	-0.03	0.03	-1.18	0.239	-0.06	0.05	-1.20	0.232
North-East	Cmic:Nmic ratio	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	-0.01	0.04	-0.19	0.851	-0.01	0.04	-0.19	0.851
North-East	Cmic:Nmic ratio	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.11	0.09	-1.23	0.219	-0.19	0.15	-1.25	0.213
North-East	Cmic:Nmic ratio	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.33	0.15	-2.22	0.027	-0.33	0.14	-2.32	0.020
North-East	Cmic:Nmic ratio	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.10	0.09	-1.17	0.243	-0.04	0.14	-0.29	0.770
North-East	Cmic:Nmic ratio	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.32	0.15	-2.21	0.027	-0.25	0.13	-1.90	0.057
North-East	Cmic:Nmic ratio	Lignin_content	Lignin_content	~	LUI_historic	a	0.22	0.12	1.87	0.062	0.29	0.15	1.93	0.054
North-East	Cmic:Nmic ratio	Lignin_content	Lignin_content	~	LUI_change	b	0.22	0.20	1.11	0.265	0.17	0.15	1.13	0.260
North-East	Cmic:Nmic ratio	Lignin_content	RatioCmic_Nmic	~	Lignin_content	c	0.01	0.11	0.12	0.906	0.02	0.14	0.12	0.906
North-East	Cmic:Nmic ratio	Lignin_content	RatioCmic_Nmic	~	LUI_historic	e	-0.11	0.09	-1.22	0.223	-0.19	0.15	-1.24	0.217
North-East	Cmic:Nmic ratio	Lignin_content	RatioCmic_Nmic	~	LUI_change	f	-0.33	0.15	-2.21	0.027	-0.34	0.15	-2.31	0.021
North-East	Cmic:Nmic ratio	Lignin_content	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	Cmic:Nmic ratio	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	4.95	0.000	0.93	0.07	13.39	0.000
North-East	Cmic:Nmic ratio	Lignin_content	RatioCmic_Nmic	~~	RatioCmic_Nmic		0.03	0.01	4.95	0.000	0.91	0.08	11.48	0.000
North-East	Cmic:Nmic ratio	Lignin_content	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	Cmic:Nmic ratio	Lignin_content	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	Cmic:Nmic ratio	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	0.12	0.906	0.01	0.04	0.12	0.906
North-East	Cmic:Nmic ratio	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.02	0.12	0.906	0.00	0.02	0.12	0.906
North-East	Cmic:Nmic ratio	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.11	0.09	-1.23	0.219	-0.19	0.15	-1.25	0.213
North-East	Cmic:Nmic ratio	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.33	0.15	-2.22	0.027	-0.33	0.14	-2.32	0.020
North-East	Cmic:Nmic ratio	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.10	0.09	-1.17	0.243	-0.04	0.14	-0.29	0.770
North-East	Cmic:Nmic ratio	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.32	0.15	-2.21	0.027	-0.25	0.13	-1.90	0.057
North-East	Cmic:Nmic ratio	pH	pH_historic	~	LUI_historic	a	-0.02	0.16	-0.13	0.897	-0.02	0.14	-0.13	0.897
North-East	Cmic:Nmic ratio	pH	pH_change	~	LUI_change	b	0.04	0.10	0.40	0.686	0.06	0.14	0.40	0.686
North-East	Cmic:Nmic ratio	pH	RatioCmic_Nmic	~	pH_historic	c	0.02	0.06	0.28	0.777	0.03	0.12	0.28	0.777
North-East	Cmic:Nmic ratio	pH	RatioCmic_Nmic	~	pH_change	d	-0.66	0.16	-4.13	0.000	-0.48	0.10	-4.60	0.000
North-East	Cmic:Nmic ratio	pH	RatioCmic_Nmic	~	LUI_historic	e	-0.14	0.07	-1.90	0.058	-0.24	0.13	-1.92	0.055
North-East	Cmic:Nmic ratio	pH	RatioCmic_Nmic	~	LUI_change	f	-0.32	0.13	-2.55	0.011	-0.33	0.12	-2.62	0.009
North-East	Cmic:Nmic ratio	pH	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	Cmic:Nmic ratio	pH	pH_historic	~~	pH_historic		0.10	0.02	5.00	0.000	1.00	0.01	193.05	0.000
North-East	Cmic:Nmic ratio	pH	pH_change	~~	pH_change		0.01	0.00	5.00	0.000	1.00	0.02	62.03	0.000
North-East	Cmic:Nmic ratio	pH	RatioCmic_Nmic	~~	RatioCmic_Nmic		0.02	0.00	5.00	0.000	0.66	0.11	6.20	0.000
North-East	Cmic:Nmic ratio	pH	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	Cmic:Nmic ratio	pH	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	Cmic:Nmic ratio	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.00	-0.12	0.906	0.00	0.01	-0.12	0.906
North-East	Cmic:Nmic ratio	pH	LUI_change_in	:=	b*d	LUI_change_in	-0.03	0.07	-0.40	0.688	-0.03	0.07	-0.41	0.686
North-East	Cmic:Nmic ratio	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.14	0.07	-1.90	0.057	-0.24	0.13	-1.93	0.054
North-East	Cmic:Nmic ratio	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.35	0.14	-2.45	0.014	-0.35	0.14	-2.56	0.010
North-East	Cmic:Nmic ratio	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.13	0.07	-1.83	0.068	-0.09	0.13	-0.71	0.476
North-East	Cmic:Nmic ratio	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.34	0.14	-2.44	0.015	-0.25	0.13	-1.87	0.061

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*p*	est.std	se.std	z.std	*p*.std
North-East	Pmic	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	-0.01	0.11	-0.05	0.958	-0.01	0.15	-0.05	0.958
North-East	Pmic	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.36	0.18	-2.04	0.042	-0.29	0.14	-2.13	0.034
North-East	Pmic	CWM_leaf_P	Pmic	~	CWM_leafP_historic	c	0.13	0.14	0.90	0.366	0.12	0.14	0.91	0.363
North-East	Pmic	CWM_leaf_P	Pmic	~	CWM_leafP_change	d	-0.34	0.14	-2.35	0.019	-0.33	0.14	-2.47	0.013
North-East	Pmic	CWM_leaf_P	Pmic	~	LUI_historic	e	-0.01	0.11	-0.09	0.926	-0.01	0.15	-0.09	0.926
North-East	Pmic	CWM_leaf_P	Pmic	~	LUI_change	f	0.09	0.20	0.46	0.646	0.07	0.15	0.46	0.646
North-East	Pmic	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.55	0.011	-0.41	0.12	-3.30	0.001
North-East	Pmic	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.05	0.01	4.80	0.000	1.00	0.00	432.79	0.000
North-East	Pmic	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.04	0.01	4.80	0.000	0.92	0.08	11.80	0.000
North-East	Pmic	CWM_leaf_P	Pmic	~~	Pmic		0.04	0.01	4.80	0.000	0.85	0.10	8.90	0.000
North-East	Pmic	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.08	0.02	4.80	0.000	1.00	0.00	NA	NA
North-East	Pmic	CWM_leaf_P	LUI_change	~~	LUI_change		0.03	0.01	4.80	0.000	1.00	0.00	NA	NA
North-East	Pmic	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	-0.05	0.958	0.00	0.02	-0.05	0.958
North-East	Pmic	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.12	0.08	1.54	0.124	0.10	0.06	1.58	0.113
North-East	Pmic	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.01	0.11	-0.10	0.922	-0.02	0.15	-0.10	0.922
North-East	Pmic	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.21	0.20	1.07	0.286	0.17	0.15	1.08	0.280
North-East	Pmic	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.02	0.11	-0.14	0.891	-0.08	0.14	-0.59	0.556
North-East	Pmic	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.21	0.20	1.07	0.283	0.17	0.14	1.22	0.224
North-East	Pmic	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.20	0.09	2.20	0.028	0.31	0.13	2.31	0.021
North-East	Pmic	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	-0.12	0.15	-0.80	0.421	-0.12	0.15	-0.81	0.418
North-East	Pmic	CWM_MycInt	Pmic	~	CWM_MycInt_historic	c	-0.19	0.16	-1.16	0.247	-0.15	0.13	-1.17	0.244
North-East	Pmic	CWM_MycInt	Pmic	~	CWM_MycInt_change	d	-0.64	0.17	-3.91	0.000	-0.48	0.11	-4.38	0.000
North-East	Pmic	CWM_MycInt	Pmic	~	LUI_historic	e	-0.11	0.12	-0.97	0.333	-0.13	0.14	-0.97	0.331
North-East	Pmic	CWM_MycInt	Pmic	~	LUI_change	f	0.13	0.19	0.71	0.477	0.10	0.13	0.71	0.476
North-East	Pmic	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.55	0.011	-0.41	0.12	-3.30	0.001
North-East	Pmic	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.03	0.01	4.80	0.000	0.91	0.08	11.00	0.000
North-East	Pmic	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	4.80	0.000	0.99	0.03	28.81	0.000
North-East	Pmic	CWM_MycInt	Pmic	~~	Pmic		0.04	0.01	4.80	0.000	0.68	0.11	6.08	0.000
North-East	Pmic	CWM_MycInt	LUI_historic	~~	LUI_historic		0.08	0.02	4.80	0.000	1.00	0.00	NA	NA
North-East	Pmic	CWM_MycInt	LUI_change	~~	LUI_change		0.03	0.01	4.80	0.000	1.00	0.00	NA	NA
North-East	Pmic	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	-0.04	0.04	-1.03	0.305	-0.05	0.04	-1.03	0.302
North-East	Pmic	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.08	0.10	0.79	0.431	0.06	0.07	0.80	0.424
North-East	Pmic	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.15	0.11	-1.34	0.181	-0.18	0.13	-1.35	0.177
North-East	Pmic	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.21	0.21	1.01	0.314	0.15	0.15	1.02	0.308
North-East	Pmic	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.16	0.11	-1.39	0.164	-0.24	0.13	-1.93	0.053
North-East	Pmic	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.21	0.21	1.03	0.305	0.22	0.14	1.62	0.106
North-East	Pmic	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.17	0.12	1.40	0.161	0.22	0.16	1.43	0.152
North-East	Pmic	Plant_biomass	Plant_biomass	~	LUI_change	b	0.05	0.20	0.26	0.798	0.04	0.16	0.26	0.798
North-East	Pmic	Plant_biomass	Pmic	~	Plant_biomass	c	-0.14	0.14	-0.97	0.332	-0.14	0.15	-0.98	0.328
North-East	Pmic	Plant_biomass	Pmic	~	LUI_historic	e	0.03	0.12	0.22	0.829	0.04	0.16	0.22	0.829
North-East	Pmic	Plant_biomass	Pmic	~	LUI_change	f	0.28	0.20	1.41	0.159	0.22	0.16	1.44	0.151
North-East	Pmic	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.52	0.012	-0.41	0.13	-3.26	0.001
North-East	Pmic	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	4.74	0.000	0.96	0.06	15.95	0.000
North-East	Pmic	Plant_biomass	Pmic	~~	Pmic		0.04	0.01	4.74	0.000	0.93	0.07	13.07	0.000
North-East	Pmic	Plant_biomass	LUI_historic	~~	LUI_historic		0.08	0.02	4.74	0.000	1.00	0.00	NA	NA
North-East	Pmic	Plant_biomass	LUI_change	~~	LUI_change		0.03	0.01	4.74	0.000	1.00	0.00	NA	NA
North-East	Pmic	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	-0.02	0.03	-0.80	0.425	-0.03	0.04	-0.80	0.422
North-East	Pmic	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	-0.01	0.03	-0.25	0.805	-0.01	0.02	-0.25	0.805
North-East	Pmic	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.00	0.12	0.02	0.986	0.00	0.16	0.02	0.986
North-East	Pmic	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.27	0.20	1.36	0.174	0.22	0.16	1.39	0.166
North-East	Pmic	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.00	0.12	-0.03	0.977	-0.09	0.15	-0.57	0.566
North-East	Pmic	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.27	0.20	1.37	0.172	0.22	0.14	1.51	0.130
North-East	Pmic	Lignin_content	Lignin_content	~	LUI_historic	a	0.27	0.12	2.16	0.031	0.34	0.15	2.27	0.024
North-East	Pmic	Lignin_content	Lignin_content	~	LUI_change	b	0.20	0.21	0.99	0.322	0.15	0.15	1.00	0.318
North-East	Pmic	Lignin_content	Pmic	~	Lignin_content	c	0.25	0.14	1.79	0.074	0.26	0.14	1.85	0.065
North-East	Pmic	Lignin_content	Pmic	~	LUI_historic	e	-0.06	0.12	-0.53	0.596	-0.09	0.16	-0.53	0.595
North-East	Pmic	Lignin_content	Pmic	~	LUI_change	f	0.22	0.19	1.13	0.259	0.18	0.15	1.14	0.253
North-East	Pmic	Lignin_content	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.52	0.012	-0.41	0.13	-3.26	0.001
North-East	Pmic	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	4.74	0.000	0.91	0.08	10.93	0.000
North-East	Pmic	Lignin_content	Pmic	~~	Pmic		0.04	0.01	4.74	0.000	0.89	0.09	10.13	0.000
North-East	Pmic	Lignin_content	LUI_historic	~~	LUI_historic		0.08	0.02	4.74	0.000	1.00	0.00	NA	NA
North-East	Pmic	Lignin_content	LUI_change	~~	LUI_change		0.03	0.01	4.74	0.000	1.00	0.00	NA	NA
North-East	Pmic	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.07	0.05	1.38	0.168	0.09	0.06	1.40	0.161
North-East	Pmic	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.05	0.06	0.87	0.386	0.04	0.05	0.88	0.380
North-East	Pmic	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.00	0.12	0.02	0.986	0.00	0.16	0.02	0.986
North-East	Pmic	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.27	0.20	1.36	0.174	0.22	0.16	1.39	0.166
North-East	Pmic	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.00	0.12	-0.03	0.977	-0.09	0.15	-0.57	0.566
North-East	Pmic	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.27	0.20	1.37	0.172	0.22	0.14	1.51	0.130
North-East	Pmic	pH	pH_historic	~	LUI_historic	a	-0.05	0.16	-0.28	0.782	-0.04	0.15	-0.28	0.782
North-East	Pmic	pH	pH_change	~	LUI_change	b	0.02	0.11	0.22	0.825	0.03	0.15	0.22	0.825
North-East	Pmic	pH	Pmic	~	pH_historic	c	0.21	0.10	2.19	0.029	0.29	0.13	2.28	0.023
North-East	Pmic	pH	Pmic	~	pH_change	d	0.35	0.25	1.39	0.166	0.19	0.13	1.41	0.160
North-East	Pmic	pH	Pmic	~	LUI_historic	e	0.04	0.12	0.36	0.718	0.05	0.15	0.36	0.717
North-East	Pmic	pH	Pmic	~	LUI_change	f	0.32	0.20	1.61	0.108	0.24	0.14	1.64	0.101
North-East	Pmic	pH	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.55	0.011	-0.41	0.12	-3.30	0.001
North-East	Pmic	pH	pH_historic	~~	pH_historic		0.10	0.02	4.80	0.000	1.00	0.01	83.21	0.000
North-East	Pmic	pH	pH_change	~~	pH_change		0.02	0.00	4.80	0.000	1.00	0.01	104.10	0.000
North-East	Pmic	pH	Pmic	~~	Pmic		0.04	0.01	4.80	0.000	0.83	0.10	8.34	0.000
North-East	Pmic	pH	LUI_historic	~~	LUI_historic		0.08	0.02	4.80	0.000	1.00	0.00	NA	NA
North-East	Pmic	pH	LUI_change	~~	LUI_change		0.03	0.01	4.80	0.000	1.00	0.00	NA	NA
North-East	Pmic	pH	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.04	-0.27	0.784	-0.01	0.04	-0.28	0.783
North-East	Pmic	pH	LUI_change_in	:=	b*d	LUI_change_in	0.01	0.04	0.22	0.827	0.01	0.03	0.22	0.827
North-East	Pmic	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.03	0.12	0.27	0.788	0.04	0.15	0.27	0.788
North-East	Pmic	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.32	0.20	1.62	0.105	0.24	0.15	1.66	0.098
North-East	Pmic	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.03	0.12	0.22	0.827	-0.06	0.15	-0.39	0.694
North-East	Pmic	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.32	0.20	1.62	0.105	0.23	0.14	1.67	0.095

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*p*	est.std	se.std	z.std	*p*.std
North-East	beta-glucosidase	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.03	0.11	0.32	0.747	0.05	0.14	0.32	0.747
North-East	beta-glucosidase	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.30	0.17	-1.77	0.077	-0.24	0.13	-1.82	0.068
North-East	beta-glucosidase	CWM_leaf_P	Glucosidase	~	CWM_leafP_historic	c	0.03	0.14	0.25	0.804	0.03	0.14	0.25	0.804
North-East	beta-glucosidase	CWM_leaf_P	Glucosidase	~	CWM_leafP_change	d	0.05	0.14	0.37	0.708	0.05	0.14	0.38	0.708
North-East	beta-glucosidase	CWM_leaf_P	Glucosidase	~	LUI_historic	e	0.05	0.11	0.48	0.631	0.07	0.15	0.48	0.630
North-East	beta-glucosidase	CWM_leaf_P	Glucosidase	~	LUI_change	f	0.29	0.19	1.51	0.132	0.24	0.15	1.54	0.123
North-East	beta-glucosidase	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	beta-glucosidase	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.05	0.01	5.00	0.000	1.00	0.01	77.51	0.000
North-East	beta-glucosidase	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.04	0.01	5.00	0.000	0.94	0.07	14.57	0.000
North-East	beta-glucosidase	CWM_leaf_P	Glucosidase	~~	Glucosidase		0.04	0.01	5.00	0.000	0.96	0.06	16.66	0.000
North-East	beta-glucosidase	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	beta-glucosidase	CWM_leaf_P	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	beta-glucosidase	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	0.20	0.844	0.00	0.01	0.20	0.844
North-East	beta-glucosidase	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	-0.02	0.04	-0.37	0.714	-0.01	0.04	-0.37	0.714
North-East	beta-glucosidase	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.06	0.11	0.49	0.623	0.08	0.15	0.49	0.622
North-East	beta-glucosidase	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.28	0.19	1.46	0.144	0.22	0.15	1.49	0.136
North-East	beta-glucosidase	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.05	0.11	0.45	0.656	-0.02	0.14	-0.15	0.881
North-East	beta-glucosidase	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.27	0.19	1.46	0.144	0.19	0.14	1.41	0.160
North-East	beta-glucosidase	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.16	0.09	1.72	0.086	0.24	0.13	1.77	0.077
North-East	beta-glucosidase	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	-0.15	0.15	-1.01	0.311	-0.14	0.14	-1.02	0.306
North-East	beta-glucosidase	CWM_MycInt	Glucosidase	~	CWM_MycInt_historic	c	0.20	0.15	1.35	0.177	0.19	0.14	1.37	0.170
North-East	beta-glucosidase	CWM_MycInt	Glucosidase	~	CWM_MycInt_change	d	-0.15	0.16	-0.97	0.332	-0.13	0.14	-0.98	0.328
North-East	beta-glucosidase	CWM_MycInt	Glucosidase	~	LUI_historic	e	-0.03	0.11	-0.23	0.819	-0.04	0.15	-0.23	0.819
North-East	beta-glucosidase	CWM_MycInt	Glucosidase	~	LUI_change	f	0.17	0.18	0.91	0.364	0.14	0.15	0.92	0.360
North-East	beta-glucosidase	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	beta-glucosidase	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.04	0.01	5.00	0.000	0.94	0.06	14.99	0.000
North-East	beta-glucosidase	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	0.98	0.04	24.93	0.000
North-East	beta-glucosidase	CWM_MycInt	Glucosidase	~~	Glucosidase		0.04	0.01	5.00	0.000	0.93	0.07	13.06	0.000
North-East	beta-glucosidase	CWM_MycInt	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	beta-glucosidase	CWM_MycInt	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	beta-glucosidase	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.03	0.03	1.06	0.289	0.05	0.04	1.07	0.285
North-East	beta-glucosidase	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.02	0.03	0.70	0.484	0.02	0.03	0.70	0.481
North-East	beta-glucosidase	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.01	0.11	0.06	0.952	0.01	0.15	0.06	0.952
North-East	beta-glucosidase	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.19	0.18	1.03	0.301	0.16	0.15	1.04	0.297
North-East	beta-glucosidase	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.00	0.11	0.02	0.981	-0.06	0.14	-0.42	0.676
North-East	beta-glucosidase	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.19	0.18	1.04	0.299	0.15	0.14	1.12	0.261
North-East	beta-glucosidase	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.12	1.61	0.109	0.25	0.15	1.65	0.100
North-East	beta-glucosidase	Plant_biomass	Plant_biomass	~	LUI_change	b	0.04	0.20	0.19	0.850	0.03	0.15	0.19	0.850
North-East	beta-glucosidase	Plant_biomass	Glucosidase	~	Plant_biomass	c	0.05	0.13	0.40	0.687	0.06	0.14	0.40	0.687
North-East	beta-glucosidase	Plant_biomass	Glucosidase	~	LUI_historic	e	0.05	0.12	0.40	0.692	0.06	0.16	0.40	0.692
North-East	beta-glucosidase	Plant_biomass	Glucosidase	~	LUI_change	f	0.29	0.19	1.50	0.134	0.23	0.15	1.53	0.126
North-East	beta-glucosidase	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	beta-glucosidase	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	4.95	0.000	0.94	0.06	14.84	0.000
North-East	beta-glucosidase	Plant_biomass	Glucosidase	~~	Glucosidase		0.04	0.01	4.95	0.000	0.95	0.06	15.98	0.000
North-East	beta-glucosidase	Plant_biomass	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	beta-glucosidase	Plant_biomass	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	beta-glucosidase	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.03	0.39	0.696	0.01	0.04	0.39	0.696
North-East	beta-glucosidase	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	0.17	0.864	0.00	0.01	0.17	0.864
North-East	beta-glucosidase	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.06	0.11	0.50	0.619	0.08	0.15	0.50	0.618
North-East	beta-glucosidase	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.29	0.19	1.51	0.132	0.23	0.15	1.54	0.123
North-East	beta-glucosidase	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.05	0.11	0.45	0.653	-0.02	0.14	-0.16	0.870
North-East	beta-glucosidase	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.29	0.19	1.51	0.131	0.20	0.14	1.46	0.145
North-East	beta-glucosidase	Lignin_content	Lignin_content	~	LUI_historic	a	0.22	0.12	1.87	0.062	0.29	0.15	1.93	0.054
North-East	beta-glucosidase	Lignin_content	Lignin_content	~	LUI_change	b	0.22	0.20	1.11	0.265	0.17	0.15	1.13	0.260
North-East	beta-glucosidase	Lignin_content	Glucosidase	~	Lignin_content	c	0.07	0.14	0.52	0.603	0.08	0.14	0.52	0.602
North-East	beta-glucosidase	Lignin_content	Glucosidase	~	LUI_historic	e	0.04	0.12	0.35	0.727	0.06	0.16	0.35	0.727
North-East	beta-glucosidase	Lignin_content	Glucosidase	~	LUI_change	f	0.27	0.19	1.41	0.158	0.22	0.15	1.44	0.150
North-East	beta-glucosidase	Lignin_content	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	beta-glucosidase	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	4.95	0.000	0.93	0.07	13.39	0.000
North-East	beta-glucosidase	Lignin_content	Glucosidase	~~	Glucosidase		0.04	0.01	4.95	0.000	0.95	0.06	15.64	0.000
North-East	beta-glucosidase	Lignin_content	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	beta-glucosidase	Lignin_content	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	beta-glucosidase	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.02	0.03	0.50	0.617	0.02	0.04	0.50	0.616
North-East	beta-glucosidase	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.02	0.03	0.47	0.638	0.01	0.03	0.47	0.637
North-East	beta-glucosidase	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.06	0.11	0.50	0.619	0.08	0.15	0.50	0.618
North-East	beta-glucosidase	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.29	0.19	1.51	0.132	0.23	0.15	1.54	0.123
North-East	beta-glucosidase	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.05	0.11	0.45	0.653	-0.02	0.14	-0.16	0.870
North-East	beta-glucosidase	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.29	0.19	1.51	0.131	0.20	0.14	1.46	0.145
North-East	beta-glucosidase	pH	pH_historic	~	LUI_historic	a	-0.02	0.16	-0.13	0.897	-0.02	0.14	-0.13	0.897
North-East	beta-glucosidase	pH	pH_change	~	LUI_change	b	0.04	0.10	0.40	0.686	0.06	0.14	0.40	0.686
North-East	beta-glucosidase	pH	Glucosidase	~	pH_historic	c	-0.09	0.08	-1.17	0.243	-0.14	0.12	-1.17	0.240
North-East	beta-glucosidase	pH	Glucosidase	~	pH_change	d	0.80	0.20	3.91	0.000	0.47	0.11	4.38	0.000
North-East	beta-glucosidase	pH	Glucosidase	~	LUI_historic	e	0.09	0.09	0.94	0.350	0.12	0.13	0.94	0.348
North-East	beta-glucosidase	pH	Glucosidase	~	LUI_change	f	0.25	0.16	1.57	0.116	0.21	0.13	1.59	0.112
North-East	beta-glucosidase	pH	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	beta-glucosidase	pH	pH_historic	~~	pH_historic		0.10	0.02	5.00	0.000	1.00	0.01	193.05	0.000
North-East	beta-glucosidase	pH	pH_change	~~	pH_change		0.01	0.00	5.00	0.000	1.00	0.02	62.03	0.000
North-East	beta-glucosidase	pH	Glucosidase	~~	Glucosidase		0.03	0.01	5.00	0.000	0.72	0.11	6.73	0.000
North-East	beta-glucosidase	pH	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	beta-glucosidase	pH	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	beta-glucosidase	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	0.13	0.898	0.00	0.02	0.13	0.898
North-East	beta-glucosidase	pH	LUI_change_in	:=	b*d	LUI_change_in	0.03	0.08	0.40	0.688	0.03	0.07	0.40	0.686
North-East	beta-glucosidase	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.09	0.10	0.94	0.345	0.13	0.13	0.95	0.343
North-East	beta-glucosidase	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.28	0.18	1.59	0.112	0.24	0.15	1.62	0.105
North-East	beta-glucosidase	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.08	0.09	0.89	0.371	0.03	0.13	0.20	0.845
North-East	beta-glucosidase	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.28	0.18	1.59	0.113	0.18	0.14	1.33	0.183

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*p*	est.std	se.std	z.std	*p*.std
North-East	beta-xylosidase	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.03	0.11	0.32	0.747	0.05	0.14	0.32	0.747
North-East	beta-xylosidase	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.30	0.17	-1.77	0.077	-0.24	0.13	-1.82	0.068
North-East	beta-xylosidase	CWM_leaf_P	Xylosidase	~	CWM_leafP_historic	c	0.10	0.13	0.77	0.444	0.11	0.14	0.77	0.442
North-East	beta-xylosidase	CWM_leaf_P	Xylosidase	~	CWM_leafP_change	d	0.03	0.13	0.23	0.820	0.03	0.14	0.23	0.820
North-East	beta-xylosidase	CWM_leaf_P	Xylosidase	~	LUI_historic	e	0.03	0.10	0.26	0.795	0.04	0.15	0.26	0.795
North-East	beta-xylosidase	CWM_leaf_P	Xylosidase	~	LUI_change	f	0.28	0.18	1.59	0.111	0.25	0.15	1.63	0.102
North-East	beta-xylosidase	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	beta-xylosidase	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.05	0.01	5.00	0.000	1.00	0.01	77.51	0.000
North-East	beta-xylosidase	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.04	0.01	5.00	0.000	0.94	0.07	14.57	0.000
North-East	beta-xylosidase	CWM_leaf_P	Xylosidase	~~	Xylosidase		0.04	0.01	5.00	0.000	0.94	0.07	14.21	0.000
North-East	beta-xylosidase	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	beta-xylosidase	CWM_leaf_P	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	beta-xylosidase	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	0.30	0.766	0.01	0.02	0.30	0.766
North-East	beta-xylosidase	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	-0.01	0.04	-0.23	0.822	-0.01	0.04	-0.23	0.822
North-East	beta-xylosidase	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.03	0.10	0.29	0.772	0.04	0.15	0.29	0.772
North-East	beta-xylosidase	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.28	0.17	1.58	0.114	0.24	0.15	1.62	0.105
North-East	beta-xylosidase	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.02	0.10	0.24	0.812	-0.06	0.14	-0.42	0.674
North-East	beta-xylosidase	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.27	0.17	1.59	0.112	0.22	0.13	1.65	0.099
North-East	beta-xylosidase	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.16	0.09	1.72	0.086	0.24	0.13	1.77	0.077
North-East	beta-xylosidase	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	-0.15	0.15	-1.01	0.311	-0.14	0.14	-1.02	0.306
North-East	beta-xylosidase	CWM_MycInt	Xylosidase	~	CWM_MycInt_historic	c	0.00	0.14	-0.02	0.981	0.00	0.13	-0.02	0.981
North-East	beta-xylosidase	CWM_MycInt	Xylosidase	~	CWM_MycInt_change	d	-0.32	0.14	-2.27	0.023	-0.30	0.13	-2.37	0.018
North-East	beta-xylosidase	CWM_MycInt	Xylosidase	~	LUI_historic	e	-0.03	0.10	-0.29	0.773	-0.04	0.15	-0.29	0.773
North-East	beta-xylosidase	CWM_MycInt	Xylosidase	~	LUI_change	f	0.21	0.17	1.22	0.222	0.18	0.14	1.24	0.217
North-East	beta-xylosidase	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	beta-xylosidase	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.04	0.01	5.00	0.000	0.94	0.06	14.99	0.000
North-East	beta-xylosidase	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	0.98	0.04	24.94	0.000
North-East	beta-xylosidase	CWM_MycInt	Xylosidase	~~	Xylosidase		0.03	0.01	5.00	0.000	0.85	0.09	9.24	0.000
North-East	beta-xylosidase	CWM_MycInt	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	beta-xylosidase	CWM_MycInt	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	beta-xylosidase	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	-0.02	0.981	0.00	0.03	-0.02	0.981
North-East	beta-xylosidase	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.05	0.05	0.93	0.355	0.04	0.05	0.94	0.348
North-East	beta-xylosidase	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.03	0.10	-0.30	0.764	-0.04	0.15	-0.30	0.764
North-East	beta-xylosidase	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.25	0.17	1.46	0.143	0.22	0.15	1.49	0.135
North-East	beta-xylosidase	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.04	0.10	-0.36	0.719	-0.14	0.13	-1.04	0.300
North-East	beta-xylosidase	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.26	0.17	1.47	0.140	0.24	0.13	1.80	0.073
North-East	beta-xylosidase	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.12	1.61	0.109	0.25	0.15	1.65	0.100
North-East	beta-xylosidase	Plant_biomass	Plant_biomass	~	LUI_change	b	0.04	0.20	0.19	0.850	0.03	0.15	0.19	0.850
North-East	beta-xylosidase	Plant_biomass	Xylosidase	~	Plant_biomass	c	-0.04	0.12	-0.31	0.755	-0.04	0.14	-0.31	0.755
North-East	beta-xylosidase	Plant_biomass	Xylosidase	~	LUI_historic	e	0.04	0.11	0.41	0.681	0.07	0.16	0.41	0.680
North-East	beta-xylosidase	Plant_biomass	Xylosidase	~	LUI_change	f	0.31	0.18	1.75	0.081	0.27	0.15	1.80	0.072
North-East	beta-xylosidase	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	beta-xylosidase	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	4.95	0.000	0.94	0.06	14.84	0.000
North-East	beta-xylosidase	Plant_biomass	Xylosidase	~~	Xylosidase		0.04	0.01	4.95	0.000	0.94	0.07	13.91	0.000
North-East	beta-xylosidase	Plant_biomass	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	beta-xylosidase	Plant_biomass	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	beta-xylosidase	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.02	-0.31	0.759	-0.01	0.04	-0.31	0.759
North-East	beta-xylosidase	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	-0.16	0.872	0.00	0.01	-0.16	0.872
North-East	beta-xylosidase	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.04	0.10	0.35	0.726	0.05	0.15	0.35	0.726
North-East	beta-xylosidase	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.31	0.18	1.74	0.082	0.27	0.15	1.79	0.074
North-East	beta-xylosidase	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.03	0.10	0.29	0.770	-0.06	0.14	-0.43	0.668
North-East	beta-xylosidase	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.31	0.18	1.74	0.082	0.24	0.13	1.81	0.070
North-East	beta-xylosidase	Lignin_content	Lignin_content	~	LUI_historic	a	0.22	0.12	1.87	0.062	0.29	0.15	1.93	0.054
North-East	beta-xylosidase	Lignin_content	Lignin_content	~	LUI_change	b	0.22	0.20	1.11	0.265	0.17	0.15	1.13	0.260
North-East	beta-xylosidase	Lignin_content	Xylosidase	~	Lignin_content	c	0.04	0.13	0.29	0.771	0.04	0.14	0.29	0.771
North-East	beta-xylosidase	Lignin_content	Xylosidase	~	LUI_historic	e	0.03	0.11	0.26	0.792	0.04	0.16	0.26	0.792
North-East	beta-xylosidase	Lignin_content	Xylosidase	~	LUI_change	f	0.30	0.18	1.67	0.095	0.26	0.15	1.72	0.086
North-East	beta-xylosidase	Lignin_content	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	beta-xylosidase	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	4.95	0.000	0.93	0.07	13.39	0.000
North-East	beta-xylosidase	Lignin_content	Xylosidase	~~	Xylosidase		0.04	0.01	4.95	0.000	0.94	0.07	13.93	0.000
North-East	beta-xylosidase	Lignin_content	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	beta-xylosidase	Lignin_content	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	beta-xylosidase	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.03	0.29	0.773	0.01	0.04	0.29	0.773
North-East	beta-xylosidase	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.01	0.03	0.28	0.778	0.01	0.03	0.28	0.778
North-East	beta-xylosidase	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.04	0.10	0.35	0.726	0.05	0.15	0.35	0.726
North-East	beta-xylosidase	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.31	0.18	1.74	0.082	0.27	0.15	1.79	0.074
North-East	beta-xylosidase	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.03	0.10	0.29	0.770	-0.06	0.14	-0.43	0.668
North-East	beta-xylosidase	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.31	0.18	1.74	0.082	0.24	0.13	1.81	0.070
North-East	beta-xylosidase	pH	pH_historic	~	LUI_historic	a	-0.02	0.16	-0.13	0.897	-0.02	0.14	-0.13	0.897
North-East	beta-xylosidase	pH	pH_change	~	LUI_change	b	0.04	0.10	0.40	0.686	0.06	0.14	0.40	0.686
North-East	beta-xylosidase	pH	Xylosidase	~	pH_historic	c	0.05	0.08	0.59	0.557	0.07	0.13	0.59	0.556
North-East	beta-xylosidase	pH	Xylosidase	~	pH_change	d	0.62	0.21	2.99	0.003	0.38	0.12	3.20	0.001
North-East	beta-xylosidase	pH	Xylosidase	~	LUI_historic	e	0.07	0.10	0.77	0.441	0.11	0.14	0.77	0.440
North-East	beta-xylosidase	pH	Xylosidase	~	LUI_change	f	0.32	0.16	1.95	0.052	0.27	0.14	1.99	0.046
North-East	beta-xylosidase	pH	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	beta-xylosidase	pH	pH_historic	~~	pH_historic		0.10	0.02	5.00	0.000	1.00	0.01	193.05	0.000
North-East	beta-xylosidase	pH	pH_change	~~	pH_change		0.01	0.00	5.00	0.000	1.00	0.02	62.03	0.000
North-East	beta-xylosidase	pH	Xylosidase	~~	Xylosidase		0.03	0.01	5.00	0.000	0.79	0.10	7.67	0.000
North-East	beta-xylosidase	pH	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	beta-xylosidase	pH	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	beta-xylosidase	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	-0.13	0.899	0.00	0.01	-0.13	0.899
North-East	beta-xylosidase	pH	LUI_change_in	:=	b*d	LUI_change_in	0.03	0.06	0.40	0.689	0.02	0.05	0.40	0.687
North-East	beta-xylosidase	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.07	0.10	0.76	0.448	0.11	0.14	0.76	0.447
North-East	beta-xylosidase	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.34	0.17	1.96	0.049	0.29	0.14	2.03	0.042
North-East	beta-xylosidase	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.07	0.10	0.69	0.488	-0.02	0.13	-0.15	0.879
North-East	beta-xylosidase	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.34	0.17	1.97	0.049	0.25	0.13	1.86	0.063

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*p*	est.std	se.std	z.std	*p*.std
North-East	chitinase	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.03	0.11	0.32	0.747	0.05	0.14	0.32	0.747
North-East	chitinase	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.30	0.17	-1.77	0.077	-0.24	0.13	-1.82	0.068
North-East	chitinase	CWM_leaf_P	Chitinase	~	CWM_leafP_historic	c	0.26	0.12	2.23	0.025	0.29	0.12	2.32	0.020
North-East	chitinase	CWM_leaf_P	Chitinase	~	CWM_leafP_change	d	0.21	0.12	1.75	0.081	0.23	0.13	1.78	0.075
North-East	chitinase	CWM_leaf_P	Chitinase	~	LUI_historic	e	0.04	0.10	0.39	0.699	0.06	0.14	0.39	0.699
North-East	chitinase	CWM_leaf_P	Chitinase	~	LUI_change	f	0.32	0.17	1.92	0.055	0.28	0.14	1.97	0.049
North-East	chitinase	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	chitinase	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.05	0.01	5.00	0.000	1.00	0.01	77.51	0.000
North-East	chitinase	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.04	0.01	5.00	0.000	0.94	0.07	14.57	0.000
North-East	chitinase	CWM_leaf_P	Chitinase	~~	Chitinase		0.03	0.01	5.00	0.000	0.83	0.10	8.66	0.000
North-East	chitinase	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	chitinase	CWM_leaf_P	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	chitinase	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.03	0.32	0.749	0.01	0.04	0.32	0.749
North-East	chitinase	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	-0.06	0.05	-1.24	0.214	-0.06	0.05	-1.25	0.212
North-East	chitinase	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.05	0.10	0.46	0.645	0.07	0.15	0.46	0.645
North-East	chitinase	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.26	0.17	1.53	0.125	0.22	0.14	1.56	0.118
North-East	chitinase	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.04	0.10	0.41	0.680	-0.03	0.14	-0.20	0.839
North-East	chitinase	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.25	0.17	1.54	0.125	0.19	0.13	1.48	0.139
North-East	chitinase	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.16	0.09	1.72	0.086	0.24	0.13	1.77	0.077
North-East	chitinase	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	-0.15	0.15	-1.01	0.311	-0.14	0.14	-1.02	0.306
North-East	chitinase	CWM_MycInt	Chitinase	~	CWM_MycInt_historic	c	0.12	0.14	0.92	0.359	0.13	0.14	0.92	0.356
North-East	chitinase	CWM_MycInt	Chitinase	~	CWM_MycInt_change	d	-0.09	0.14	-0.67	0.506	-0.09	0.14	-0.67	0.504
North-East	chitinase	CWM_MycInt	Chitinase	~	LUI_historic	e	0.01	0.10	0.08	0.933	0.01	0.15	0.08	0.933
North-East	chitinase	CWM_MycInt	Chitinase	~	LUI_change	f	0.25	0.17	1.51	0.130	0.23	0.15	1.55	0.122
North-East	chitinase	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	chitinase	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.04	0.01	5.00	0.000	0.94	0.06	14.99	0.000
North-East	chitinase	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	0.98	0.04	24.94	0.000
North-East	chitinase	CWM_MycInt	Chitinase	~~	Chitinase		0.03	0.01	5.00	0.000	0.92	0.07	12.94	0.000
North-East	chitinase	CWM_MycInt	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	chitinase	CWM_MycInt	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	chitinase	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.02	0.02	0.81	0.419	0.03	0.04	0.81	0.416
North-East	chitinase	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.01	0.03	0.56	0.578	0.01	0.02	0.56	0.577
North-East	chitinase	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.03	0.10	0.29	0.775	0.04	0.15	0.29	0.775
North-East	chitinase	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.27	0.17	1.61	0.108	0.24	0.15	1.65	0.100
North-East	chitinase	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.02	0.10	0.23	0.817	-0.06	0.14	-0.44	0.662
North-East	chitinase	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.26	0.16	1.61	0.107	0.22	0.13	1.68	0.093
North-East	chitinase	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.12	1.61	0.109	0.25	0.15	1.65	0.100
North-East	chitinase	Plant_biomass	Plant_biomass	~	LUI_change	b	0.04	0.20	0.19	0.850	0.03	0.15	0.19	0.850
North-East	chitinase	Plant_biomass	Chitinase	~	Plant_biomass	c	-0.05	0.12	-0.44	0.660	-0.06	0.14	-0.44	0.660
North-East	chitinase	Plant_biomass	Chitinase	~	LUI_historic	e	0.07	0.10	0.68	0.499	0.11	0.16	0.68	0.498
North-East	chitinase	Plant_biomass	Chitinase	~	LUI_change	f	0.33	0.17	1.96	0.050	0.30	0.15	2.04	0.042
North-East	chitinase	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	chitinase	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	4.95	0.000	0.94	0.06	14.84	0.000
North-East	chitinase	Plant_biomass	Chitinase	~~	Chitinase		0.03	0.01	4.95	0.000	0.92	0.07	12.63	0.000
North-East	chitinase	Plant_biomass	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	chitinase	Plant_biomass	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	chitinase	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.02	-0.42	0.672	-0.02	0.04	-0.42	0.671
North-East	chitinase	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	-0.17	0.862	0.00	0.01	-0.17	0.862
North-East	chitinase	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.06	0.10	0.59	0.554	0.09	0.15	0.59	0.553
North-East	chitinase	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.33	0.17	1.95	0.052	0.30	0.15	2.02	0.043
North-East	chitinase	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.05	0.10	0.53	0.597	-0.04	0.14	-0.27	0.791
North-East	chitinase	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.33	0.17	1.95	0.051	0.26	0.13	1.93	0.053
North-East	chitinase	Lignin_content	Lignin_content	~	LUI_historic	a	0.22	0.12	1.87	0.062	0.29	0.15	1.93	0.054
North-East	chitinase	Lignin_content	Lignin_content	~	LUI_change	b	0.22	0.20	1.11	0.265	0.17	0.15	1.13	0.260
North-East	chitinase	Lignin_content	Chitinase	~	Lignin_content	c	0.04	0.12	0.36	0.718	0.05	0.14	0.36	0.718
North-East	chitinase	Lignin_content	Chitinase	~	LUI_historic	e	0.05	0.10	0.48	0.632	0.08	0.16	0.48	0.631
North-East	chitinase	Lignin_content	Chitinase	~	LUI_change	f	0.32	0.17	1.87	0.062	0.29	0.15	1.93	0.053
North-East	chitinase	Lignin_content	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	chitinase	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	4.95	0.000	0.93	0.07	13.39	0.000
North-East	chitinase	Lignin_content	Chitinase	~~	Chitinase		0.03	0.01	4.95	0.000	0.92	0.07	12.73	0.000
North-East	chitinase	Lignin_content	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	chitinase	Lignin_content	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	chitinase	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.03	0.36	0.723	0.02	0.04	0.36	0.723
North-East	chitinase	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.01	0.03	0.34	0.731	0.01	0.03	0.34	0.731
North-East	chitinase	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.06	0.10	0.59	0.554	0.09	0.15	0.59	0.553
North-East	chitinase	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.33	0.17	1.95	0.052	0.30	0.15	2.02	0.043
North-East	chitinase	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.05	0.10	0.53	0.597	-0.04	0.14	-0.27	0.791
North-East	chitinase	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.33	0.17	1.95	0.051	0.26	0.13	1.93	0.053
North-East	chitinase	pH	pH_historic	~	LUI_historic	a	-0.02	0.16	-0.13	0.897	-0.02	0.14	-0.13	0.897
North-East	chitinase	pH	pH_change	~	LUI_change	b	0.04	0.10	0.40	0.686	0.06	0.14	0.40	0.686
North-East	chitinase	pH	Chitinase	~	pH_historic	c	0.03	0.08	0.35	0.727	0.05	0.13	0.35	0.726
North-East	chitinase	pH	Chitinase	~	pH_change	d	0.49	0.20	2.38	0.017	0.31	0.12	2.48	0.013
North-East	chitinase	pH	Chitinase	~	LUI_historic	e	0.09	0.09	0.92	0.356	0.13	0.14	0.93	0.354
North-East	chitinase	pH	Chitinase	~	LUI_change	f	0.33	0.16	2.08	0.038	0.30	0.14	2.15	0.032
North-East	chitinase	pH	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	chitinase	pH	pH_historic	~~	pH_historic		0.10	0.02	5.00	0.000	1.00	0.01	193.05	0.000
North-East	chitinase	pH	pH_change	~~	pH_change		0.01	0.00	5.00	0.000	1.00	0.02	62.03	0.000
North-East	chitinase	pH	Chitinase	~~	Chitinase		0.03	0.01	5.00	0.000	0.83	0.10	8.48	0.000
North-East	chitinase	pH	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	chitinase	pH	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	chitinase	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.00	-0.12	0.903	0.00	0.01	-0.12	0.903
North-East	chitinase	pH	LUI_change_in	:=	b*d	LUI_change_in	0.02	0.05	0.40	0.691	0.02	0.04	0.40	0.689
North-East	chitinase	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.09	0.09	0.92	0.360	0.13	0.14	0.92	0.357
North-East	chitinase	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.35	0.17	2.11	0.035	0.31	0.14	2.20	0.028
North-East	chitinase	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.08	0.09	0.85	0.395	-0.01	0.14	-0.03	0.973
North-East	chitinase	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.35	0.17	2.11	0.035	0.26	0.13	1.95	0.051

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*p*	est.std	se.std	z.std	*p*.std
North-East	urease	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.03	0.11	0.32	0.747	0.05	0.14	0.32	0.747
North-East	urease	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.30	0.17	-1.77	0.077	-0.24	0.13	-1.82	0.068
North-East	urease	CWM_leaf_P	Urease	~	CWM_leafP_historic	c	0.10	0.12	0.84	0.400	0.12	0.14	0.85	0.397
North-East	urease	CWM_leaf_P	Urease	~	CWM_leafP_change	d	0.00	0.12	-0.03	0.976	0.00	0.14	-0.03	0.976
North-East	urease	CWM_leaf_P	Urease	~	LUI_historic	e	0.07	0.10	0.73	0.463	0.11	0.15	0.74	0.461
North-East	urease	CWM_leaf_P	Urease	~	LUI_change	f	-0.06	0.17	-0.37	0.711	-0.06	0.16	-0.37	0.711
North-East	urease	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	urease	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.05	0.01	5.00	0.000	1.00	0.01	77.51	0.000
North-East	urease	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.04	0.01	5.00	0.000	0.94	0.07	14.57	0.000
North-East	urease	CWM_leaf_P	Urease	~~	Urease		0.03	0.01	5.00	0.000	0.96	0.05	18.45	0.000
North-East	urease	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	urease	CWM_leaf_P	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	urease	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	0.30	0.763	0.01	0.02	0.30	0.763
North-East	urease	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.04	0.03	0.976	0.00	0.04	0.03	0.976
North-East	urease	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.07	0.10	0.77	0.444	0.12	0.15	0.77	0.442
North-East	urease	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.06	0.16	-0.37	0.710	-0.06	0.15	-0.37	0.709
North-East	urease	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.08	0.10	0.79	0.430	0.14	0.14	1.03	0.302
North-East	urease	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.06	0.16	-0.38	0.701	-0.11	0.14	-0.78	0.436
North-East	urease	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.16	0.09	1.72	0.086	0.24	0.13	1.77	0.077
North-East	urease	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	-0.15	0.15	-1.01	0.311	-0.14	0.14	-1.02	0.306
North-East	urease	CWM_MycInt	Urease	~	CWM_MycInt_historic	c	0.02	0.13	0.17	0.867	0.02	0.14	0.17	0.867
North-East	urease	CWM_MycInt	Urease	~	CWM_MycInt_change	d	-0.25	0.14	-1.83	0.068	-0.25	0.13	-1.88	0.060
North-East	urease	CWM_MycInt	Urease	~	LUI_historic	e	0.03	0.10	0.26	0.792	0.04	0.15	0.26	0.792
North-East	urease	CWM_MycInt	Urease	~	LUI_change	f	-0.12	0.16	-0.72	0.472	-0.11	0.15	-0.72	0.470
North-East	urease	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	urease	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.04	0.01	5.00	0.000	0.94	0.06	14.99	0.000
North-East	urease	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	0.98	0.04	24.93	0.000
North-East	urease	CWM_MycInt	Urease	~~	Urease		0.03	0.01	5.00	0.000	0.93	0.07	13.11	0.000
North-East	urease	CWM_MycInt	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	urease	CWM_MycInt	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	urease	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	0.17	0.867	0.01	0.03	0.17	0.867
North-East	urease	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.04	0.04	0.89	0.376	0.04	0.04	0.89	0.374
North-East	urease	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.03	0.09	0.31	0.760	0.05	0.15	0.31	0.759
North-East	urease	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.08	0.16	-0.48	0.633	-0.07	0.16	-0.48	0.633
North-East	urease	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.03	0.09	0.33	0.743	0.08	0.14	0.57	0.569
North-East	urease	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.08	0.16	-0.48	0.629	-0.09	0.14	-0.67	0.503
North-East	urease	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.12	1.61	0.109	0.25	0.15	1.65	0.100
North-East	urease	Plant_biomass	Plant_biomass	~	LUI_change	b	0.04	0.20	0.19	0.850	0.03	0.15	0.19	0.850
North-East	urease	Plant_biomass	Urease	~	Plant_biomass	c	0.04	0.12	0.32	0.748	0.05	0.15	0.32	0.748
North-East	urease	Plant_biomass	Urease	~	LUI_historic	e	0.07	0.10	0.74	0.458	0.12	0.16	0.75	0.455
North-East	urease	Plant_biomass	Urease	~	LUI_change	f	-0.03	0.17	-0.19	0.852	-0.03	0.16	-0.19	0.852
North-East	urease	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	urease	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	4.95	0.000	0.94	0.06	14.84	0.000
North-East	urease	Plant_biomass	Urease	~~	Urease		0.03	0.01	4.95	0.000	0.98	0.04	23.05	0.000
North-East	urease	Plant_biomass	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	urease	Plant_biomass	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	urease	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.02	0.32	0.753	0.01	0.04	0.32	0.753
North-East	urease	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	0.16	0.871	0.00	0.01	0.16	0.871
North-East	urease	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.08	0.10	0.84	0.404	0.13	0.16	0.84	0.400
North-East	urease	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.03	0.17	-0.18	0.859	-0.03	0.16	-0.18	0.859
North-East	urease	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.08	0.10	0.85	0.393	0.14	0.14	1.02	0.308
North-East	urease	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.03	0.16	-0.19	0.850	-0.08	0.14	-0.59	0.553
North-East	urease	Lignin_content	Lignin_content	~	LUI_historic	a	0.22	0.12	1.87	0.062	0.29	0.15	1.93	0.054
North-East	urease	Lignin_content	Lignin_content	~	LUI_change	b	0.22	0.20	1.11	0.265	0.17	0.15	1.13	0.260
North-East	urease	Lignin_content	Urease	~	Lignin_content	c	0.04	0.12	0.31	0.757	0.05	0.15	0.31	0.757
North-East	urease	Lignin_content	Urease	~	LUI_historic	e	0.07	0.10	0.73	0.467	0.12	0.16	0.73	0.464
North-East	urease	Lignin_content	Urease	~	LUI_change	f	-0.04	0.17	-0.22	0.823	-0.04	0.16	-0.22	0.823
North-East	urease	Lignin_content	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	urease	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	4.95	0.000	0.93	0.07	13.39	0.000
North-East	urease	Lignin_content	Urease	~~	Urease		0.03	0.01	4.95	0.000	0.98	0.04	23.12	0.000
North-East	urease	Lignin_content	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	urease	Lignin_content	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	urease	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.03	0.31	0.760	0.01	0.04	0.31	0.760
North-East	urease	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.01	0.03	0.30	0.765	0.01	0.03	0.30	0.765
North-East	urease	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.08	0.10	0.84	0.404	0.13	0.16	0.84	0.400
North-East	urease	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.03	0.17	-0.18	0.859	-0.03	0.16	-0.18	0.859
North-East	urease	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.08	0.10	0.85	0.393	0.14	0.14	1.02	0.308
North-East	urease	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.03	0.16	-0.19	0.850	-0.08	0.14	-0.59	0.553
North-East	urease	pH	pH_historic	~	LUI_historic	a	-0.02	0.16	-0.13	0.897	-0.02	0.14	-0.13	0.897
North-East	urease	pH	pH_change	~	LUI_change	b	0.04	0.10	0.40	0.686	0.06	0.14	0.40	0.686
North-East	urease	pH	Urease	~	pH_historic	c	0.27	0.06	4.19	0.000	0.42	0.10	4.38	0.000
North-East	urease	pH	Urease	~	pH_change	d	0.90	0.17	5.34	0.000	0.54	0.09	5.96	0.000
North-East	urease	pH	Urease	~	LUI_historic	e	0.16	0.08	2.03	0.042	0.23	0.11	2.04	0.041
North-East	urease	pH	Urease	~	LUI_change	f	0.06	0.13	0.45	0.652	0.05	0.11	0.45	0.652
North-East	urease	pH	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	urease	pH	pH_historic	~~	pH_historic		0.10	0.02	5.00	0.000	1.00	0.01	193.05	0.000
North-East	urease	pH	pH_change	~~	pH_change		0.01	0.00	5.00	0.000	1.00	0.02	62.03	0.000
North-East	urease	pH	Urease	~~	Urease		0.02	0.00	5.00	0.000	0.50	0.09	5.34	0.000
North-East	urease	pH	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	urease	pH	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	urease	pH	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.04	-0.13	0.897	-0.01	0.06	-0.13	0.897
North-East	urease	pH	LUI_change_in	:=	b*d	LUI_change_in	0.04	0.09	0.40	0.687	0.03	0.08	0.40	0.687
North-East	urease	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.15	0.09	1.73	0.084	0.22	0.12	1.75	0.080
North-East	urease	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.10	0.16	0.60	0.548	0.08	0.13	0.60	0.548
North-East	urease	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.15	0.09	1.73	0.084	0.18	0.12	1.52	0.127
North-East	urease	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.09	0.16	0.58	0.560	-0.01	0.13	-0.10	0.920

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*p*	est.std	se.std	z.std	*p*.std
North-East	DEA	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.03	0.11	0.32	0.747	0.05	0.14	0.32	0.747
North-East	DEA	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.30	0.17	-1.77	0.077	-0.24	0.13	-1.82	0.068
North-East	DEA	CWM_leaf_P	DEA	~	CWM_leafP_historic	c	0.41	0.15	2.81	0.005	0.37	0.12	3.02	0.003
North-East	DEA	CWM_leaf_P	DEA	~	CWM_leafP_change	d	0.13	0.15	0.88	0.379	0.12	0.13	0.88	0.377
North-East	DEA	CWM_leaf_P	DEA	~	LUI_historic	e	-0.06	0.12	-0.54	0.591	-0.08	0.14	-0.54	0.591
North-East	DEA	CWM_leaf_P	DEA	~	LUI_change	f	-0.04	0.21	-0.19	0.850	-0.03	0.15	-0.19	0.850
North-East	DEA	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	DEA	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.05	0.01	5.00	0.000	1.00	0.01	77.51	0.000
North-East	DEA	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.04	0.01	5.00	0.000	0.94	0.07	14.57	0.000
North-East	DEA	CWM_leaf_P	DEA	~~	DEA		0.05	0.01	5.00	0.000	0.85	0.09	9.16	0.000
North-East	DEA	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	DEA	CWM_leaf_P	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	DEA	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.04	0.32	0.748	0.02	0.05	0.32	0.748
North-East	DEA	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	-0.04	0.05	-0.79	0.431	-0.03	0.04	-0.79	0.429
North-East	DEA	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.05	0.13	-0.40	0.692	-0.06	0.15	-0.40	0.691
North-East	DEA	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.08	0.20	-0.39	0.697	-0.06	0.15	-0.39	0.696
North-East	DEA	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.05	0.12	-0.39	0.697	-0.04	0.14	-0.26	0.795
North-East	DEA	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.08	0.20	-0.39	0.699	-0.03	0.13	-0.23	0.820
North-East	DEA	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.16	0.09	1.72	0.086	0.24	0.13	1.77	0.077
North-East	DEA	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	-0.15	0.15	-1.01	0.311	-0.14	0.14	-1.02	0.306
North-East	DEA	CWM_MycInt	DEA	~	CWM_MycInt_historic	c	-0.34	0.16	-2.15	0.032	-0.26	0.12	-2.20	0.028
North-East	DEA	CWM_MycInt	DEA	~	CWM_MycInt_change	d	-0.65	0.16	-3.97	0.000	-0.47	0.11	-4.44	0.000
North-East	DEA	CWM_MycInt	DEA	~	LUI_historic	e	-0.07	0.12	-0.63	0.528	-0.08	0.13	-0.63	0.527
North-East	DEA	CWM_MycInt	DEA	~	LUI_change	f	-0.04	0.19	-0.22	0.825	-0.03	0.13	-0.22	0.825
North-East	DEA	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	DEA	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.04	0.01	5.00	0.000	0.94	0.06	14.99	0.000
North-East	DEA	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	0.98	0.04	24.93	0.000
North-East	DEA	CWM_MycInt	DEA	~~	DEA		0.04	0.01	5.00	0.000	0.69	0.11	6.55	0.000
North-East	DEA	CWM_MycInt	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	DEA	CWM_MycInt	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	DEA	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	-0.05	0.04	-1.34	0.180	-0.06	0.05	-1.36	0.174
North-East	DEA	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.10	0.10	0.98	0.326	0.07	0.07	0.99	0.321
North-East	DEA	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.13	0.12	-1.08	0.281	-0.15	0.13	-1.08	0.278
North-East	DEA	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.06	0.22	0.26	0.795	0.04	0.15	0.26	0.795
North-East	DEA	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.13	0.12	-1.10	0.270	-0.16	0.13	-1.30	0.195
North-East	DEA	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.06	0.22	0.27	0.785	0.10	0.14	0.74	0.461
North-East	DEA	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.12	1.61	0.109	0.25	0.15	1.65	0.100
North-East	DEA	Plant_biomass	Plant_biomass	~	LUI_change	b	0.04	0.20	0.19	0.850	0.03	0.15	0.19	0.850
North-East	DEA	Plant_biomass	DEA	~	Plant_biomass	c	-0.09	0.15	-0.59	0.555	-0.09	0.15	-0.59	0.553
North-East	DEA	Plant_biomass	DEA	~	LUI_historic	e	-0.01	0.13	-0.05	0.957	-0.01	0.16	-0.05	0.957
North-East	DEA	Plant_biomass	DEA	~	LUI_change	f	0.05	0.21	0.22	0.824	0.04	0.16	0.22	0.824
North-East	DEA	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	DEA	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	4.95	0.000	0.94	0.06	14.84	0.000
North-East	DEA	Plant_biomass	DEA	~~	DEA		0.05	0.01	4.95	0.000	0.99	0.03	35.23	0.000
North-East	DEA	Plant_biomass	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	DEA	Plant_biomass	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	DEA	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	-0.02	0.03	-0.56	0.579	-0.02	0.04	-0.56	0.578
North-East	DEA	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.02	-0.18	0.857	0.00	0.01	-0.18	0.857
North-East	DEA	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.02	0.12	-0.19	0.849	-0.03	0.16	-0.19	0.849
North-East	DEA	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.04	0.21	0.21	0.837	0.03	0.16	0.21	0.836
North-East	DEA	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.03	0.12	-0.20	0.841	-0.04	0.14	-0.31	0.757
North-East	DEA	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.04	0.21	0.21	0.834	0.05	0.14	0.32	0.749
North-East	DEA	Lignin_content	Lignin_content	~	LUI_historic	a	0.22	0.12	1.87	0.062	0.29	0.15	1.93	0.054
North-East	DEA	Lignin_content	Lignin_content	~	LUI_change	b	0.22	0.20	1.11	0.265	0.17	0.15	1.13	0.260
North-East	DEA	Lignin_content	DEA	~	Lignin_content	c	-0.06	0.15	-0.38	0.702	-0.06	0.15	-0.38	0.702
North-East	DEA	Lignin_content	DEA	~	LUI_historic	e	-0.01	0.13	-0.09	0.932	-0.01	0.16	-0.09	0.932
North-East	DEA	Lignin_content	DEA	~	LUI_change	f	0.06	0.21	0.26	0.792	0.04	0.16	0.26	0.792
North-East	DEA	Lignin_content	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	DEA	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	4.95	0.000	0.93	0.07	13.39	0.000
North-East	DEA	Lignin_content	DEA	~~	DEA		0.05	0.01	4.95	0.000	0.99	0.02	46.04	0.000
North-East	DEA	Lignin_content	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	DEA	Lignin_content	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	DEA	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.03	-0.38	0.708	-0.02	0.04	-0.38	0.708
North-East	DEA	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	-0.01	0.04	-0.36	0.718	-0.01	0.03	-0.36	0.717
North-East	DEA	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.02	0.12	-0.19	0.849	-0.03	0.16	-0.19	0.849
North-East	DEA	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.04	0.21	0.21	0.837	0.03	0.16	0.21	0.836
North-East	DEA	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.03	0.12	-0.20	0.841	-0.04	0.14	-0.31	0.757
North-East	DEA	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.04	0.21	0.21	0.834	0.05	0.14	0.32	0.749
North-East	DEA	pH	pH_historic	~	LUI_historic	a	-0.02	0.16	-0.13	0.897	-0.02	0.14	-0.13	0.897
North-East	DEA	pH	pH_change	~	LUI_change	b	0.04	0.10	0.40	0.686	0.06	0.14	0.40	0.686
North-East	DEA	pH	DEA	~	pH_historic	c	0.50	0.08	6.27	0.000	0.62	0.08	7.55	0.000
North-East	DEA	pH	DEA	~	pH_change	d	0.75	0.21	3.55	0.000	0.35	0.10	3.62	0.000
North-East	DEA	pH	DEA	~	LUI_historic	e	0.07	0.10	0.71	0.476	0.08	0.11	0.71	0.476
North-East	DEA	pH	DEA	~	LUI_change	f	0.21	0.16	1.25	0.212	0.14	0.11	1.25	0.211
North-East	DEA	pH	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	DEA	pH	pH_historic	~~	pH_historic		0.10	0.02	5.00	0.000	1.00	0.01	193.05	0.000
North-East	DEA	pH	pH_change	~~	pH_change		0.01	0.00	5.00	0.000	1.00	0.02	62.03	0.000
North-East	DEA	pH	DEA	~~	DEA		0.03	0.01	5.00	0.000	0.48	0.09	5.18	0.000
North-East	DEA	pH	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	DEA	pH	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	DEA	pH	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.08	-0.13	0.897	-0.01	0.09	-0.13	0.897
North-East	DEA	pH	LUI_change_in	:=	b*d	LUI_change_in	0.03	0.08	0.40	0.688	0.02	0.05	0.40	0.688
North-East	DEA	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.06	0.12	0.48	0.634	0.07	0.14	0.48	0.634
North-East	DEA	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.24	0.18	1.31	0.192	0.16	0.12	1.31	0.190
North-East	DEA	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.05	0.12	0.44	0.660	0.00	0.13	-0.01	0.994
North-East	DEA	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.23	0.18	1.31	0.192	0.13	0.12	1.10	0.272

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*p*	est.std	se.std	z.std	*p*.std
North-East	phosphatase	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.03	0.11	0.32	0.747	0.05	0.14	0.32	0.747
North-East	phosphatase	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.30	0.17	-1.77	0.077	-0.24	0.13	-1.82	0.068
North-East	phosphatase	CWM_leaf_P	Phosphatase	~	CWM_leafP_historic	c	-0.19	0.08	-2.31	0.021	-0.28	0.12	-2.39	0.017
North-East	phosphatase	CWM_leaf_P	Phosphatase	~	CWM_leafP_change	d	0.04	0.08	0.47	0.640	0.06	0.13	0.47	0.640
North-East	phosphatase	CWM_leaf_P	Phosphatase	~	LUI_historic	e	0.12	0.07	1.80	0.072	0.24	0.13	1.83	0.067
North-East	phosphatase	CWM_leaf_P	Phosphatase	~	LUI_change	f	0.38	0.11	3.36	0.001	0.47	0.13	3.63	0.000
North-East	phosphatase	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	phosphatase	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.05	0.01	5.00	0.000	1.00	0.01	77.51	0.000
North-East	phosphatase	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.04	0.01	5.00	0.000	0.94	0.07	14.57	0.000
North-East	phosphatase	CWM_leaf_P	Phosphatase	~~	Phosphatase		0.02	0.00	5.00	0.000	0.75	0.10	7.25	0.000
North-East	phosphatase	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	phosphatase	CWM_leaf_P	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	phosphatase	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.02	-0.32	0.749	-0.01	0.04	-0.32	0.749
North-East	phosphatase	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	-0.01	0.03	-0.45	0.651	-0.01	0.03	-0.45	0.651
North-East	phosphatase	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.11	0.07	1.64	0.102	0.23	0.14	1.66	0.097
North-East	phosphatase	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.37	0.11	3.33	0.001	0.45	0.13	3.60	0.000
North-East	phosphatase	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.11	0.07	1.54	0.123	0.04	0.14	0.26	0.796
North-East	phosphatase	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.37	0.11	3.33	0.001	0.35	0.12	2.94	0.003
North-East	phosphatase	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.16	0.09	1.72	0.086	0.24	0.13	1.77	0.077
North-East	phosphatase	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	-0.15	0.15	-1.01	0.311	-0.14	0.14	-1.02	0.306
North-East	phosphatase	CWM_MycInt	Phosphatase	~	CWM_MycInt_historic	c	-0.13	0.10	-1.39	0.166	-0.18	0.13	-1.40	0.161
North-East	phosphatase	CWM_MycInt	Phosphatase	~	CWM_MycInt_change	d	-0.09	0.10	-0.94	0.349	-0.12	0.13	-0.94	0.346
North-East	phosphatase	CWM_MycInt	Phosphatase	~	LUI_historic	e	0.11	0.07	1.58	0.114	0.23	0.14	1.61	0.108
North-East	phosphatase	CWM_MycInt	Phosphatase	~	LUI_change	f	0.34	0.12	2.87	0.004	0.41	0.13	3.06	0.002
North-East	phosphatase	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	phosphatase	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.04	0.01	5.00	0.000	0.94	0.06	14.99	0.000
North-East	phosphatase	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	0.98	0.04	24.93	0.000
North-East	phosphatase	CWM_MycInt	Phosphatase	~~	Phosphatase		0.02	0.00	5.00	0.000	0.81	0.10	8.19	0.000
North-East	phosphatase	CWM_MycInt	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	phosphatase	CWM_MycInt	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	phosphatase	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	-0.02	0.02	-1.08	0.281	-0.04	0.04	-1.09	0.278
North-East	phosphatase	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.01	0.02	0.69	0.492	0.02	0.03	0.69	0.489
North-East	phosphatase	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.09	0.07	1.30	0.195	0.19	0.14	1.31	0.191
North-East	phosphatase	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.35	0.12	2.99	0.003	0.42	0.13	3.22	0.001
North-East	phosphatase	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.08	0.07	1.21	0.228	0.00	0.14	0.02	0.986
North-East	phosphatase	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.35	0.12	2.99	0.003	0.35	0.12	2.80	0.005
North-East	phosphatase	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.12	1.61	0.109	0.25	0.15	1.65	0.100
North-East	phosphatase	Plant_biomass	Plant_biomass	~	LUI_change	b	0.04	0.20	0.19	0.850	0.03	0.15	0.19	0.850
North-East	phosphatase	Plant_biomass	Phosphatase	~	Plant_biomass	c	0.02	0.09	0.22	0.824	0.03	0.14	0.22	0.824
North-East	phosphatase	Plant_biomass	Phosphatase	~	LUI_historic	e	0.09	0.07	1.30	0.194	0.20	0.15	1.32	0.188
North-East	phosphatase	Plant_biomass	Phosphatase	~	LUI_change	f	0.32	0.12	2.64	0.008	0.39	0.14	2.81	0.005
North-East	phosphatase	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	phosphatase	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	4.95	0.000	0.94	0.06	14.84	0.000
North-East	phosphatase	Plant_biomass	Phosphatase	~~	Phosphatase		0.02	0.00	4.95	0.000	0.87	0.09	9.82	0.000
North-East	phosphatase	Plant_biomass	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	phosphatase	Plant_biomass	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	phosphatase	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	0.22	0.826	0.01	0.03	0.22	0.826
North-East	phosphatase	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	0.14	0.886	0.00	0.01	0.14	0.886
North-East	phosphatase	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.10	0.07	1.38	0.167	0.21	0.15	1.40	0.161
North-East	phosphatase	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.32	0.12	2.65	0.008	0.39	0.14	2.82	0.005
North-East	phosphatase	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.09	0.07	1.31	0.192	0.04	0.14	0.25	0.801
North-East	phosphatase	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.32	0.12	2.64	0.008	0.30	0.13	2.34	0.019
North-East	phosphatase	Lignin_content	Lignin_content	~	LUI_historic	a	0.22	0.12	1.87	0.062	0.29	0.15	1.93	0.054
North-East	phosphatase	Lignin_content	Lignin_content	~	LUI_change	b	0.22	0.20	1.11	0.265	0.17	0.15	1.13	0.260
North-East	phosphatase	Lignin_content	Phosphatase	~	Lignin_content	c	0.01	0.09	0.09	0.926	0.01	0.14	0.09	0.926
North-East	phosphatase	Lignin_content	Phosphatase	~	LUI_historic	e	0.10	0.07	1.31	0.189	0.20	0.15	1.33	0.184
North-East	phosphatase	Lignin_content	Phosphatase	~	LUI_change	f	0.32	0.12	2.60	0.009	0.39	0.14	2.76	0.006
North-East	phosphatase	Lignin_content	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	phosphatase	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	4.95	0.000	0.93	0.07	13.39	0.000
North-East	phosphatase	Lignin_content	Phosphatase	~~	Phosphatase		0.02	0.00	4.95	0.000	0.87	0.09	9.85	0.000
North-East	phosphatase	Lignin_content	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	phosphatase	Lignin_content	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	phosphatase	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	0.09	0.926	0.00	0.04	0.09	0.926
North-East	phosphatase	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.02	0.09	0.927	0.00	0.02	0.09	0.927
North-East	phosphatase	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.10	0.07	1.38	0.167	0.21	0.15	1.40	0.161
North-East	phosphatase	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.32	0.12	2.65	0.008	0.39	0.14	2.82	0.005
North-East	phosphatase	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.09	0.07	1.31	0.192	0.04	0.14	0.25	0.801
North-East	phosphatase	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.32	0.12	2.64	0.008	0.30	0.13	2.34	0.019
North-East	phosphatase	pH	pH_historic	~	LUI_historic	a	-0.02	0.16	-0.13	0.897	-0.02	0.14	-0.13	0.897
North-East	phosphatase	pH	pH_change	~	LUI_change	b	0.04	0.10	0.40	0.686	0.06	0.14	0.40	0.686
North-East	phosphatase	pH	Phosphatase	~	pH_historic	c	-0.11	0.05	-2.00	0.046	-0.25	0.12	-2.05	0.041
North-East	phosphatase	pH	Phosphatase	~	pH_change	d	-0.38	0.14	-2.61	0.009	-0.32	0.12	-2.73	0.006
North-East	phosphatase	pH	Phosphatase	~	LUI_historic	e	0.07	0.07	1.01	0.315	0.14	0.14	1.01	0.312
North-East	phosphatase	pH	Phosphatase	~	LUI_change	f	0.28	0.11	2.52	0.012	0.34	0.13	2.62	0.009
North-East	phosphatase	pH	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	phosphatase	pH	pH_historic	~~	pH_historic		0.10	0.02	5.00	0.000	1.00	0.01	193.05	0.000
North-East	phosphatase	pH	pH_change	~~	pH_change		0.01	0.00	5.00	0.000	1.00	0.02	62.03	0.000
North-East	phosphatase	pH	Phosphatase	~~	Phosphatase		0.02	0.00	5.00	0.000	0.75	0.10	7.29	0.000
North-East	phosphatase	pH	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	phosphatase	pH	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	phosphatase	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	0.13	0.897	0.00	0.04	0.13	0.897
North-East	phosphatase	pH	LUI_change_in	:=	b*d	LUI_change_in	-0.02	0.04	-0.40	0.690	-0.02	0.05	-0.40	0.691
North-East	phosphatase	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.07	0.07	1.01	0.314	0.14	0.14	1.01	0.312
North-East	phosphatase	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.27	0.12	2.27	0.023	0.33	0.14	2.36	0.018
North-East	phosphatase	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.06	0.07	0.94	0.349	0.00	0.14	0.01	0.993
North-East	phosphatase	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.27	0.12	2.27	0.023	0.26	0.13	2.06	0.040

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*p*	est.std	se.std	z.std	*p*.std
North-East	bacteria	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.03	0.11	0.32	0.747	0.05	0.14	0.32	0.747
North-East	bacteria	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.30	0.17	-1.77	0.077	-0.24	0.13	-1.82	0.068
North-East	bacteria	CWM_leaf_P	bactotal	~	CWM_leafP_historic	c	0.23	0.12	2.01	0.045	0.26	0.13	2.07	0.038
North-East	bacteria	CWM_leaf_P	bactotal	~	CWM_leafP_change	d	0.16	0.12	1.32	0.186	0.18	0.13	1.34	0.181
North-East	bacteria	CWM_leaf_P	bactotal	~	LUI_historic	e	0.00	0.09	0.03	0.975	0.01	0.15	0.03	0.975
North-East	bacteria	CWM_leaf_P	bactotal	~	LUI_change	f	0.25	0.16	1.56	0.120	0.23	0.15	1.58	0.113
North-East	bacteria	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	bacteria	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.05	0.01	5.00	0.000	1.00	0.01	77.51	0.000
North-East	bacteria	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.04	0.01	5.00	0.000	0.94	0.07	14.57	0.000
North-East	bacteria	CWM_leaf_P	bactotal	~~	bactotal		0.03	0.01	5.00	0.000	0.87	0.09	9.84	0.000
North-East	bacteria	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	bacteria	CWM_leaf_P	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	bacteria	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.02	0.32	0.750	0.01	0.04	0.32	0.750
North-East	bacteria	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	-0.05	0.05	-1.06	0.290	-0.04	0.04	-1.07	0.287
North-East	bacteria	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.01	0.10	0.11	0.912	0.02	0.15	0.11	0.912
North-East	bacteria	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.21	0.16	1.28	0.201	0.19	0.15	1.30	0.195
North-East	bacteria	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.01	0.10	0.07	0.947	-0.07	0.14	-0.47	0.641
North-East	bacteria	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.21	0.16	1.28	0.200	0.18	0.13	1.37	0.171
North-East	bacteria	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.16	0.09	1.72	0.086	0.24	0.13	1.77	0.077
North-East	bacteria	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	-0.15	0.15	-1.01	0.311	-0.14	0.14	-1.02	0.306
North-East	bacteria	CWM_MycInt	bactotal	~	CWM_MycInt_historic	c	0.46	0.12	3.75	0.000	0.45	0.11	4.10	0.000
North-East	bacteria	CWM_MycInt	bactotal	~	CWM_MycInt_change	d	0.36	0.13	2.79	0.005	0.33	0.11	2.90	0.004
North-East	bacteria	CWM_MycInt	bactotal	~	LUI_historic	e	-0.02	0.09	-0.22	0.827	-0.03	0.13	-0.22	0.827
North-East	bacteria	CWM_MycInt	bactotal	~	LUI_change	f	0.21	0.15	1.38	0.169	0.18	0.13	1.39	0.166
North-East	bacteria	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	bacteria	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.04	0.01	5.00	0.000	0.94	0.06	14.99	0.000
North-East	bacteria	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	0.98	0.04	24.94	0.000
North-East	bacteria	CWM_MycInt	bactotal	~~	bactotal		0.03	0.01	5.00	0.000	0.69	0.11	6.56	0.000
North-East	bacteria	CWM_MycInt	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	bacteria	CWM_MycInt	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	bacteria	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.07	0.05	1.56	0.119	0.11	0.07	1.58	0.115
North-East	bacteria	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	-0.05	0.06	-0.95	0.341	-0.05	0.05	-0.95	0.341
North-East	bacteria	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.05	0.10	0.54	0.590	0.08	0.14	0.54	0.590
North-East	bacteria	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.15	0.16	0.97	0.333	0.13	0.14	0.97	0.331
North-East	bacteria	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.05	0.10	0.51	0.609	0.02	0.14	0.15	0.882
North-East	bacteria	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.15	0.16	0.97	0.334	0.10	0.13	0.78	0.437
North-East	bacteria	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.12	1.61	0.109	0.25	0.15	1.65	0.100
North-East	bacteria	Plant_biomass	Plant_biomass	~	LUI_change	b	0.04	0.20	0.19	0.850	0.03	0.15	0.19	0.850
North-East	bacteria	Plant_biomass	bactotal	~	Plant_biomass	c	0.19	0.11	1.65	0.099	0.23	0.14	1.69	0.092
North-East	bacteria	Plant_biomass	bactotal	~	LUI_historic	e	-0.01	0.10	-0.14	0.888	-0.02	0.15	-0.14	0.888
North-East	bacteria	Plant_biomass	bactotal	~	LUI_change	f	0.26	0.16	1.61	0.108	0.24	0.15	1.65	0.100
North-East	bacteria	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	bacteria	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	4.95	0.000	0.94	0.06	14.84	0.000
North-East	bacteria	Plant_biomass	bactotal	~~	bactotal		0.03	0.01	4.95	0.000	0.90	0.08	10.81	0.000
North-East	bacteria	Plant_biomass	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	bacteria	Plant_biomass	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	bacteria	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.04	0.03	1.15	0.250	0.06	0.05	1.16	0.245
North-East	bacteria	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.01	0.04	0.19	0.851	0.01	0.04	0.19	0.851
North-East	bacteria	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.02	0.10	0.23	0.820	0.04	0.15	0.23	0.820
North-East	bacteria	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.27	0.17	1.61	0.107	0.25	0.15	1.65	0.099
North-East	bacteria	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.02	0.10	0.17	0.863	-0.07	0.14	-0.50	0.614
North-East	bacteria	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.27	0.16	1.62	0.106	0.23	0.14	1.72	0.085
North-East	bacteria	Lignin_content	Lignin_content	~	LUI_historic	a	0.22	0.12	1.87	0.062	0.29	0.15	1.93	0.054
North-East	bacteria	Lignin_content	Lignin_content	~	LUI_change	b	0.22	0.20	1.11	0.265	0.17	0.15	1.13	0.260
North-East	bacteria	Lignin_content	bactotal	~	Lignin_content	c	0.00	0.12	-0.04	0.970	-0.01	0.14	-0.04	0.970
North-East	bacteria	Lignin_content	bactotal	~	LUI_historic	e	0.02	0.10	0.23	0.818	0.04	0.16	0.23	0.818
North-East	bacteria	Lignin_content	bactotal	~	LUI_change	f	0.27	0.17	1.60	0.111	0.25	0.15	1.64	0.102
North-East	bacteria	Lignin_content	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	bacteria	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	4.95	0.000	0.93	0.07	13.39	0.000
North-East	bacteria	Lignin_content	bactotal	~~	bactotal		0.03	0.01	4.95	0.000	0.95	0.06	14.90	0.000
North-East	bacteria	Lignin_content	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	bacteria	Lignin_content	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	bacteria	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.03	-0.04	0.970	0.00	0.04	-0.04	0.970
North-East	bacteria	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.03	-0.04	0.970	0.00	0.03	-0.04	0.970
North-East	bacteria	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.02	0.10	0.23	0.820	0.04	0.15	0.23	0.820
North-East	bacteria	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.27	0.17	1.61	0.107	0.25	0.15	1.65	0.099
North-East	bacteria	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.02	0.10	0.17	0.863	-0.07	0.14	-0.50	0.614
North-East	bacteria	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.27	0.16	1.62	0.106	0.23	0.14	1.72	0.085
North-East	bacteria	pH	pH_historic	~	LUI_historic	a	-0.02	0.16	-0.13	0.897	-0.02	0.14	-0.13	0.897
North-East	bacteria	pH	pH_change	~	LUI_change	b	0.04	0.10	0.40	0.686	0.06	0.14	0.40	0.686
North-East	bacteria	pH	bactotal	~	pH_historic	c	0.01	0.08	0.08	0.938	0.01	0.14	0.08	0.938
North-East	bacteria	pH	bactotal	~	pH_change	d	0.09	0.21	0.42	0.678	0.06	0.14	0.42	0.678
North-East	bacteria	pH	bactotal	~	LUI_historic	e	0.03	0.10	0.29	0.774	0.04	0.15	0.29	0.774
North-East	bacteria	pH	bactotal	~	LUI_change	f	0.27	0.16	1.65	0.099	0.25	0.15	1.69	0.090
North-East	bacteria	pH	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	bacteria	pH	pH_historic	~~	pH_historic		0.10	0.02	5.00	0.000	1.00	0.01	193.05	0.000
North-East	bacteria	pH	pH_change	~~	pH_change		0.01	0.00	5.00	0.000	1.00	0.02	62.03	0.000
North-East	bacteria	pH	bactotal	~~	bactotal		0.03	0.01	5.00	0.000	0.94	0.07	14.39	0.000
North-East	bacteria	pH	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	bacteria	pH	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	bacteria	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.00	-0.07	0.947	0.00	0.00	-0.07	0.947
North-East	bacteria	pH	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	0.29	0.772	0.00	0.01	0.29	0.772
North-East	bacteria	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.03	0.10	0.29	0.775	0.04	0.15	0.29	0.775
North-East	bacteria	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.27	0.16	1.67	0.095	0.25	0.15	1.72	0.086
North-East	bacteria	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.02	0.10	0.23	0.818	-0.07	0.14	-0.47	0.638
North-East	bacteria	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.27	0.16	1.68	0.094	0.24	0.13	1.76	0.078

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*p*	est.std	se.std	z.std	*p*.std
North-East	fungi:bacteria ratio	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.03	0.11	0.32	0.747	0.05	0.14	0.32	0.747
North-East	fungi:bacteria ratio	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.30	0.17	-1.77	0.077	-0.24	0.13	-1.82	0.068
North-East	fungi:bacteria ratio	CWM_leaf_P	fungi_bac	~	CWM_leafP_historic	c	-0.24	0.11	-2.31	0.021	-0.29	0.12	-2.40	0.016
North-East	fungi:bacteria ratio	CWM_leaf_P	fungi_bac	~	CWM_leafP_change	d	-0.26	0.11	-2.41	0.016	-0.31	0.12	-2.52	0.012
North-East	fungi:bacteria ratio	CWM_leaf_P	fungi_bac	~	LUI_historic	e	0.06	0.09	0.69	0.487	0.10	0.14	0.70	0.486
North-East	fungi:bacteria ratio	CWM_leaf_P	fungi_bac	~	LUI_change	f	0.13	0.15	0.86	0.390	0.12	0.14	0.86	0.388
North-East	fungi:bacteria ratio	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	fungi:bacteria ratio	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.05	0.01	5.00	0.000	1.00	0.01	77.51	0.000
North-East	fungi:bacteria ratio	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.04	0.01	5.00	0.000	0.94	0.07	14.57	0.000
North-East	fungi:bacteria ratio	CWM_leaf_P	fungi_bac	~~	fungi_bac		0.03	0.01	5.00	0.000	0.79	0.10	7.95	0.000
North-East	fungi:bacteria ratio	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	fungi:bacteria ratio	CWM_leaf_P	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	fungi:bacteria ratio	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.03	-0.32	0.749	-0.01	0.04	-0.32	0.749
North-East	fungi:bacteria ratio	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.08	0.06	1.43	0.154	0.08	0.05	1.46	0.145
North-East	fungi:bacteria ratio	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.05	0.09	0.58	0.565	0.08	0.15	0.58	0.564
North-East	fungi:bacteria ratio	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.21	0.15	1.36	0.173	0.20	0.14	1.38	0.167
North-East	fungi:bacteria ratio	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.05	0.09	0.53	0.593	0.00	0.14	-0.01	0.989
North-East	fungi:bacteria ratio	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.21	0.15	1.36	0.173	0.16	0.13	1.22	0.221
North-East	fungi:bacteria ratio	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.16	0.09	1.72	0.086	0.24	0.13	1.77	0.077
North-East	fungi:bacteria ratio	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	-0.15	0.15	-1.01	0.311	-0.14	0.14	-1.02	0.306
North-East	fungi:bacteria ratio	CWM_MycInt	fungi_bac	~	CWM_MycInt_historic	c	-0.19	0.12	-1.56	0.120	-0.22	0.14	-1.59	0.112
North-East	fungi:bacteria ratio	CWM_MycInt	fungi_bac	~	CWM_MycInt_change	d	-0.02	0.13	-0.17	0.869	-0.02	0.14	-0.17	0.869
North-East	fungi:bacteria ratio	CWM_MycInt	fungi_bac	~	LUI_historic	e	0.09	0.09	0.95	0.343	0.15	0.15	0.96	0.339
North-East	fungi:bacteria ratio	CWM_MycInt	fungi_bac	~	LUI_change	f	0.21	0.15	1.39	0.166	0.21	0.15	1.41	0.159
North-East	fungi:bacteria ratio	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	fungi:bacteria ratio	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.04	0.01	5.00	0.000	0.94	0.06	14.99	0.000
North-East	fungi:bacteria ratio	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	0.98	0.04	24.94	0.000
North-East	fungi:bacteria ratio	CWM_MycInt	fungi_bac	~~	fungi_bac		0.03	0.01	5.00	0.000	0.92	0.07	12.48	0.000
North-East	fungi:bacteria ratio	CWM_MycInt	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	fungi:bacteria ratio	CWM_MycInt	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	fungi:bacteria ratio	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	-0.03	0.03	-1.15	0.249	-0.05	0.04	-1.17	0.244
North-East	fungi:bacteria ratio	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.02	0.16	0.871	0.00	0.02	0.16	0.871
North-East	fungi:bacteria ratio	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.06	0.09	0.62	0.537	0.10	0.15	0.62	0.535
North-East	fungi:bacteria ratio	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.21	0.15	1.42	0.156	0.21	0.15	1.44	0.149
North-East	fungi:bacteria ratio	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.05	0.09	0.58	0.564	0.00	0.14	0.02	0.984
North-East	fungi:bacteria ratio	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.21	0.15	1.42	0.156	0.17	0.14	1.28	0.201
North-East	fungi:bacteria ratio	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.12	1.61	0.109	0.25	0.15	1.65	0.100
North-East	fungi:bacteria ratio	Plant_biomass	Plant_biomass	~	LUI_change	b	0.04	0.20	0.19	0.850	0.03	0.15	0.19	0.850
North-East	fungi:bacteria ratio	Plant_biomass	fungi_bac	~	Plant_biomass	c	-0.08	0.10	-0.81	0.415	-0.12	0.14	-0.82	0.412
North-East	fungi:bacteria ratio	Plant_biomass	fungi_bac	~	LUI_historic	e	0.06	0.09	0.70	0.486	0.11	0.16	0.70	0.484
North-East	fungi:bacteria ratio	Plant_biomass	fungi_bac	~	LUI_change	f	0.17	0.14	1.17	0.241	0.18	0.15	1.19	0.234
North-East	fungi:bacteria ratio	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	fungi:bacteria ratio	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	4.95	0.000	0.94	0.06	14.84	0.000
North-East	fungi:bacteria ratio	Plant_biomass	fungi_bac	~~	fungi_bac		0.02	0.01	4.95	0.000	0.96	0.05	17.71	0.000
North-East	fungi:bacteria ratio	Plant_biomass	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	fungi:bacteria ratio	Plant_biomass	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	fungi:bacteria ratio	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	-0.02	0.02	-0.73	0.468	-0.03	0.04	-0.73	0.466
North-East	fungi:bacteria ratio	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.02	-0.18	0.854	0.00	0.02	-0.18	0.854
North-East	fungi:bacteria ratio	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.05	0.09	0.53	0.600	0.08	0.16	0.53	0.599
North-East	fungi:bacteria ratio	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.17	0.14	1.14	0.252	0.18	0.15	1.16	0.246
North-East	fungi:bacteria ratio	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.04	0.08	0.49	0.623	0.01	0.14	0.04	0.972
North-East	fungi:bacteria ratio	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.16	0.14	1.14	0.253	0.14	0.14	1.03	0.305
North-East	fungi:bacteria ratio	Lignin_content	Lignin_content	~	LUI_historic	a	0.22	0.12	1.87	0.062	0.29	0.15	1.93	0.054
North-East	fungi:bacteria ratio	Lignin_content	Lignin_content	~	LUI_change	b	0.22	0.20	1.11	0.265	0.17	0.15	1.13	0.260
North-East	fungi:bacteria ratio	Lignin_content	fungi_bac	~	Lignin_content	c	0.11	0.10	1.08	0.279	0.16	0.14	1.10	0.274
North-East	fungi:bacteria ratio	Lignin_content	fungi_bac	~	LUI_historic	e	0.02	0.09	0.24	0.814	0.04	0.16	0.24	0.814
North-East	fungi:bacteria ratio	Lignin_content	fungi_bac	~	LUI_change	f	0.14	0.15	0.97	0.330	0.15	0.16	0.98	0.326
North-East	fungi:bacteria ratio	Lignin_content	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	fungi:bacteria ratio	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	4.95	0.000	0.93	0.07	13.39	0.000
North-East	fungi:bacteria ratio	Lignin_content	fungi_bac	~~	fungi_bac		0.02	0.01	4.95	0.000	0.95	0.06	15.84	0.000
North-East	fungi:bacteria ratio	Lignin_content	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	fungi:bacteria ratio	Lignin_content	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	fungi:bacteria ratio	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.02	0.03	0.94	0.349	0.05	0.05	0.95	0.345
North-East	fungi:bacteria ratio	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.03	0.03	0.78	0.437	0.03	0.03	0.78	0.434
North-East	fungi:bacteria ratio	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.05	0.09	0.53	0.600	0.08	0.16	0.53	0.599
North-East	fungi:bacteria ratio	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.17	0.14	1.14	0.252	0.18	0.15	1.16	0.246
North-East	fungi:bacteria ratio	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.04	0.08	0.49	0.623	0.01	0.14	0.04	0.972
North-East	fungi:bacteria ratio	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.16	0.14	1.14	0.253	0.14	0.14	1.03	0.305
North-East	fungi:bacteria ratio	pH	pH_historic	~	LUI_historic	a	-0.02	0.16	-0.13	0.897	-0.02	0.14	-0.13	0.897
North-East	fungi:bacteria ratio	pH	pH_change	~	LUI_change	b	0.04	0.10	0.40	0.686	0.06	0.14	0.40	0.686
North-East	fungi:bacteria ratio	pH	fungi_bac	~	pH_historic	c	-0.08	0.07	-1.05	0.295	-0.14	0.13	-1.06	0.291
North-East	fungi:bacteria ratio	pH	fungi_bac	~	pH_change	d	-0.35	0.19	-1.86	0.064	-0.25	0.13	-1.91	0.056
North-East	fungi:bacteria ratio	pH	fungi_bac	~	LUI_historic	e	0.02	0.09	0.18	0.859	0.03	0.15	0.18	0.859
North-East	fungi:bacteria ratio	pH	fungi_bac	~	LUI_change	f	0.12	0.15	0.82	0.415	0.12	0.15	0.82	0.412
North-East	fungi:bacteria ratio	pH	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	fungi:bacteria ratio	pH	pH_historic	~~	pH_historic		0.10	0.02	5.00	0.000	1.00	0.01	193.05	0.000
North-East	fungi:bacteria ratio	pH	pH_change	~~	pH_change		0.01	0.00	5.00	0.000	1.00	0.02	62.03	0.000
North-East	fungi:bacteria ratio	pH	fungi_bac	~~	fungi_bac		0.03	0.01	5.00	0.000	0.91	0.08	11.74	0.000
North-East	fungi:bacteria ratio	pH	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	fungi:bacteria ratio	pH	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	fungi:bacteria ratio	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	0.13	0.898	0.00	0.02	0.13	0.898
North-East	fungi:bacteria ratio	pH	LUI_change_in	:=	b*d	LUI_change_in	-0.01	0.04	-0.39	0.693	-0.01	0.04	-0.39	0.693
North-East	fungi:bacteria ratio	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.02	0.09	0.19	0.846	0.03	0.15	0.19	0.846
North-East	fungi:bacteria ratio	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.11	0.15	0.70	0.483	0.11	0.15	0.71	0.481
North-East	fungi:bacteria ratio	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.02	0.09	0.17	0.864	-0.02	0.14	-0.13	0.901
North-East	fungi:bacteria ratio	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.11	0.15	0.70	0.482	0.10	0.14	0.68	0.494

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*p*	est.std	se.std	z.std	*p*.std
North-East	fungi	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.03	0.11	0.32	0.747	0.05	0.14	0.32	0.747
North-East	fungi	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.30	0.17	-1.77	0.077	-0.24	0.13	-1.82	0.068
North-East	fungi	CWM_leaf_P	fungi	~	CWM_leafP_historic	c	-0.03	0.11	-0.25	0.804	-0.03	0.13	-0.25	0.804
North-East	fungi	CWM_leaf_P	fungi	~	CWM_leafP_change	d	-0.08	0.11	-0.72	0.471	-0.10	0.14	-0.72	0.469
North-East	fungi	CWM_leaf_P	fungi	~	LUI_historic	e	0.07	0.09	0.85	0.396	0.13	0.15	0.85	0.393
North-East	fungi	CWM_leaf_P	fungi	~	LUI_change	f	0.30	0.15	2.03	0.042	0.31	0.15	2.11	0.035
North-East	fungi	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	fungi	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.05	0.01	5.00	0.000	1.00	0.01	77.51	0.000
North-East	fungi	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.04	0.01	5.00	0.000	0.94	0.07	14.57	0.000
North-East	fungi	CWM_leaf_P	fungi	~~	fungi		0.03	0.01	5.00	0.000	0.90	0.08	11.12	0.000
North-East	fungi	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	fungi	CWM_leaf_P	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	fungi	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.00	-0.20	0.844	0.00	0.01	-0.20	0.844
North-East	fungi	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.02	0.04	0.67	0.504	0.02	0.04	0.67	0.502
North-East	fungi	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.07	0.09	0.84	0.401	0.13	0.15	0.84	0.398
North-East	fungi	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.33	0.15	2.23	0.025	0.33	0.14	2.34	0.019
North-East	fungi	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.07	0.09	0.77	0.441	-0.02	0.14	-0.13	0.894
North-East	fungi	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.33	0.15	2.24	0.025	0.28	0.13	2.15	0.032
North-East	fungi	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.16	0.09	1.72	0.086	0.24	0.13	1.77	0.077
North-East	fungi	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	-0.15	0.15	-1.01	0.311	-0.14	0.14	-1.02	0.306
North-East	fungi	CWM_MycInt	fungi	~	CWM_MycInt_historic	c	0.36	0.11	3.25	0.001	0.39	0.11	3.46	0.001
North-East	fungi	CWM_MycInt	fungi	~	CWM_MycInt_change	d	0.35	0.12	2.98	0.003	0.35	0.11	3.12	0.002
North-East	fungi	CWM_MycInt	fungi	~	LUI_historic	e	0.05	0.08	0.64	0.522	0.09	0.13	0.64	0.521
North-East	fungi	CWM_MycInt	fungi	~	LUI_change	f	0.30	0.14	2.14	0.032	0.28	0.13	2.19	0.029
North-East	fungi	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	fungi	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.04	0.01	5.00	0.000	0.94	0.06	14.99	0.000
North-East	fungi	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	0.98	0.04	24.94	0.000
North-East	fungi	CWM_MycInt	fungi	~~	fungi		0.02	0.00	5.00	0.000	0.68	0.10	6.58	0.000
North-East	fungi	CWM_MycInt	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	fungi	CWM_MycInt	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	fungi	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.06	0.04	1.52	0.129	0.09	0.06	1.54	0.123
North-East	fungi	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	-0.05	0.06	-0.96	0.338	-0.05	0.05	-0.96	0.339
North-East	fungi	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.11	0.09	1.26	0.207	0.18	0.14	1.27	0.203
North-East	fungi	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.24	0.15	1.66	0.097	0.23	0.14	1.69	0.091
North-East	fungi	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.11	0.09	1.22	0.223	0.08	0.13	0.59	0.559
North-East	fungi	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.24	0.15	1.65	0.098	0.15	0.13	1.19	0.236
North-East	fungi	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.12	1.61	0.109	0.25	0.15	1.65	0.100
North-East	fungi	Plant_biomass	Plant_biomass	~	LUI_change	b	0.04	0.20	0.19	0.850	0.03	0.15	0.19	0.850
North-East	fungi	Plant_biomass	fungi	~	Plant_biomass	c	0.08	0.10	0.74	0.460	0.10	0.14	0.74	0.458
North-East	fungi	Plant_biomass	fungi	~	LUI_historic	e	0.06	0.09	0.66	0.510	0.10	0.15	0.66	0.509
North-East	fungi	Plant_biomass	fungi	~	LUI_change	f	0.32	0.15	2.19	0.028	0.33	0.14	2.29	0.022
North-East	fungi	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	fungi	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	4.95	0.000	0.94	0.06	14.84	0.000
North-East	fungi	Plant_biomass	fungi	~~	fungi		0.03	0.01	4.95	0.000	0.90	0.08	11.06	0.000
North-East	fungi	Plant_biomass	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	fungi	Plant_biomass	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	fungi	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.02	0.02	0.67	0.502	0.03	0.04	0.67	0.501
North-East	fungi	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.02	0.18	0.855	0.00	0.02	0.18	0.855
North-East	fungi	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.07	0.09	0.84	0.401	0.13	0.15	0.85	0.398
North-East	fungi	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.33	0.15	2.20	0.028	0.33	0.14	2.30	0.021
North-East	fungi	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.07	0.09	0.77	0.440	-0.02	0.14	-0.11	0.910
North-East	fungi	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.32	0.15	2.20	0.028	0.28	0.13	2.10	0.035
North-East	fungi	Lignin_content	Lignin_content	~	LUI_historic	a	0.22	0.12	1.87	0.062	0.29	0.15	1.93	0.054
North-East	fungi	Lignin_content	Lignin_content	~	LUI_change	b	0.22	0.20	1.11	0.265	0.17	0.15	1.13	0.260
North-East	fungi	Lignin_content	fungi	~	Lignin_content	c	0.05	0.11	0.52	0.604	0.07	0.14	0.52	0.603
North-East	fungi	Lignin_content	fungi	~	LUI_historic	e	0.06	0.09	0.68	0.496	0.11	0.16	0.68	0.494
North-East	fungi	Lignin_content	fungi	~	LUI_change	f	0.31	0.15	2.10	0.036	0.32	0.15	2.19	0.029
North-East	fungi	Lignin_content	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	fungi	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	4.95	0.000	0.93	0.07	13.39	0.000
North-East	fungi	Lignin_content	fungi	~~	fungi		0.03	0.01	4.95	0.000	0.91	0.08	11.35	0.000
North-East	fungi	Lignin_content	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	fungi	Lignin_content	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	fungi	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.02	0.50	0.617	0.02	0.04	0.50	0.617
North-East	fungi	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.01	0.03	0.47	0.638	0.01	0.03	0.47	0.637
North-East	fungi	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.07	0.09	0.84	0.401	0.13	0.15	0.85	0.398
North-East	fungi	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.33	0.15	2.20	0.028	0.33	0.14	2.30	0.021
North-East	fungi	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.07	0.09	0.77	0.440	-0.02	0.14	-0.11	0.910
North-East	fungi	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.32	0.15	2.20	0.028	0.28	0.13	2.10	0.035
North-East	fungi	pH	pH_historic	~	LUI_historic	a	-0.02	0.16	-0.13	0.897	-0.02	0.14	-0.13	0.897
North-East	fungi	pH	pH_change	~	LUI_change	b	0.04	0.10	0.40	0.686	0.06	0.14	0.40	0.686
North-East	fungi	pH	fungi	~	pH_historic	c	-0.08	0.07	-1.07	0.287	-0.14	0.13	-1.08	0.282
North-East	fungi	pH	fungi	~	pH_change	d	-0.01	0.19	-0.06	0.956	-0.01	0.14	-0.06	0.956
North-East	fungi	pH	fungi	~	LUI_historic	e	0.06	0.09	0.75	0.454	0.11	0.15	0.75	0.452
North-East	fungi	pH	fungi	~	LUI_change	f	0.30	0.15	2.04	0.042	0.30	0.14	2.12	0.034
North-East	fungi	pH	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	fungi	pH	pH_historic	~~	pH_historic		0.10	0.02	5.00	0.000	1.00	0.01	193.05	0.000
North-East	fungi	pH	pH_change	~~	pH_change		0.01	0.00	5.00	0.000	1.00	0.02	62.03	0.000
North-East	fungi	pH	fungi	~~	fungi		0.03	0.01	5.00	0.000	0.90	0.08	11.51	0.000
North-East	fungi	pH	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	fungi	pH	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	fungi	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	0.13	0.898	0.00	0.02	0.13	0.898
North-East	fungi	pH	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	-0.06	0.956	0.00	0.01	-0.06	0.956
North-East	fungi	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.07	0.09	0.76	0.447	0.11	0.15	0.76	0.445
North-East	fungi	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.30	0.15	2.04	0.042	0.30	0.14	2.12	0.034
North-East	fungi	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.06	0.09	0.70	0.485	-0.02	0.14	-0.12	0.907
North-East	fungi	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.29	0.14	2.04	0.042	0.25	0.13	1.94	0.053

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*p*	est.std	se.std	z.std	*p*.std
North-East	ergosterol	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.03	0.11	0.32	0.747	0.05	0.14	0.32	0.747
North-East	ergosterol	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.30	0.17	-1.77	0.077	-0.24	0.13	-1.82	0.068
North-East	ergosterol	CWM_leaf_P	Ergosterol	~	CWM_leafP_historic	c	-0.12	0.09	-1.33	0.183	-0.17	0.13	-1.35	0.178
North-East	ergosterol	CWM_leaf_P	Ergosterol	~	CWM_leafP_change	d	0.04	0.09	0.43	0.664	0.06	0.13	0.44	0.664
North-East	ergosterol	CWM_leaf_P	Ergosterol	~	LUI_historic	e	0.06	0.07	0.87	0.383	0.12	0.14	0.88	0.380
North-East	ergosterol	CWM_leaf_P	Ergosterol	~	LUI_change	f	0.36	0.13	2.91	0.004	0.43	0.14	3.13	0.002
North-East	ergosterol	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	ergosterol	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.05	0.01	5.00	0.000	1.00	0.01	77.51	0.000
North-East	ergosterol	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.04	0.01	5.00	0.000	0.94	0.07	14.57	0.000
North-East	ergosterol	CWM_leaf_P	Ergosterol	~~	Ergosterol		0.02	0.00	5.00	0.000	0.83	0.10	8.59	0.000
North-East	ergosterol	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	ergosterol	CWM_leaf_P	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	ergosterol	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	-0.31	0.754	-0.01	0.03	-0.31	0.753
North-East	ergosterol	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	-0.01	0.03	-0.42	0.673	-0.01	0.03	-0.42	0.673
North-East	ergosterol	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.06	0.07	0.81	0.419	0.12	0.14	0.81	0.417
North-East	ergosterol	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.35	0.12	2.88	0.004	0.41	0.13	3.09	0.002
North-East	ergosterol	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.05	0.07	0.72	0.474	-0.06	0.14	-0.43	0.667
North-East	ergosterol	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.35	0.12	2.89	0.004	0.36	0.12	2.97	0.003
North-East	ergosterol	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.16	0.09	1.72	0.086	0.24	0.13	1.77	0.077
North-East	ergosterol	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	-0.15	0.15	-1.01	0.311	-0.14	0.14	-1.02	0.306
North-East	ergosterol	CWM_MycInt	Ergosterol	~	CWM_MycInt_historic	c	0.11	0.10	1.04	0.301	0.14	0.13	1.04	0.297
North-East	ergosterol	CWM_MycInt	Ergosterol	~	CWM_MycInt_change	d	0.13	0.11	1.19	0.236	0.16	0.13	1.20	0.231
North-East	ergosterol	CWM_MycInt	Ergosterol	~	LUI_historic	e	0.05	0.08	0.65	0.514	0.10	0.15	0.66	0.513
North-East	ergosterol	CWM_MycInt	Ergosterol	~	LUI_change	f	0.32	0.13	2.55	0.011	0.37	0.14	2.70	0.007
North-East	ergosterol	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	ergosterol	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.04	0.01	5.00	0.000	0.94	0.06	14.99	0.000
North-East	ergosterol	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	0.98	0.04	24.93	0.000
North-East	ergosterol	CWM_MycInt	Ergosterol	~~	Ergosterol		0.02	0.00	5.00	0.000	0.86	0.09	9.43	0.000
North-East	ergosterol	CWM_MycInt	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	ergosterol	CWM_MycInt	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	ergosterol	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.02	0.02	0.89	0.376	0.03	0.04	0.89	0.373
North-East	ergosterol	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	-0.02	0.03	-0.77	0.441	-0.02	0.03	-0.77	0.441
North-East	ergosterol	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.07	0.07	0.89	0.375	0.13	0.15	0.89	0.372
North-East	ergosterol	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.30	0.13	2.39	0.017	0.35	0.14	2.52	0.012
North-East	ergosterol	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.06	0.07	0.81	0.416	-0.02	0.14	-0.15	0.879
North-East	ergosterol	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.30	0.12	2.39	0.017	0.30	0.13	2.30	0.021
North-East	ergosterol	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.12	1.61	0.109	0.25	0.15	1.65	0.100
North-East	ergosterol	Plant_biomass	Plant_biomass	~	LUI_change	b	0.04	0.20	0.19	0.850	0.03	0.15	0.19	0.850
North-East	ergosterol	Plant_biomass	Ergosterol	~	Plant_biomass	c	0.22	0.08	2.67	0.008	0.34	0.12	2.81	0.005
North-East	ergosterol	Plant_biomass	Ergosterol	~	LUI_historic	e	0.01	0.07	0.10	0.919	0.02	0.14	0.10	0.919
North-East	ergosterol	Plant_biomass	Ergosterol	~	LUI_change	f	0.31	0.12	2.65	0.008	0.37	0.13	2.79	0.005
North-East	ergosterol	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	ergosterol	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	4.95	0.000	0.94	0.06	14.84	0.000
North-East	ergosterol	Plant_biomass	Ergosterol	~~	Ergosterol		0.02	0.00	4.95	0.000	0.77	0.11	7.26	0.000
North-East	ergosterol	Plant_biomass	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	ergosterol	Plant_biomass	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	ergosterol	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.04	0.03	1.38	0.169	0.09	0.06	1.40	0.162
North-East	ergosterol	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.01	0.05	0.19	0.851	0.01	0.05	0.19	0.850
North-East	ergosterol	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.05	0.07	0.67	0.503	0.10	0.15	0.67	0.501
North-East	ergosterol	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.32	0.13	2.55	0.011	0.38	0.14	2.71	0.007
North-East	ergosterol	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.04	0.07	0.59	0.557	-0.06	0.14	-0.45	0.656
North-East	ergosterol	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.32	0.13	2.55	0.011	0.34	0.13	2.65	0.008
North-East	ergosterol	Lignin_content	Lignin_content	~	LUI_historic	a	0.22	0.12	1.87	0.062	0.29	0.15	1.93	0.054
North-East	ergosterol	Lignin_content	Lignin_content	~	LUI_change	b	0.22	0.20	1.11	0.265	0.17	0.15	1.13	0.260
North-East	ergosterol	Lignin_content	Ergosterol	~	Lignin_content	c	0.12	0.09	1.34	0.181	0.18	0.13	1.36	0.175
North-East	ergosterol	Lignin_content	Ergosterol	~	LUI_historic	e	0.02	0.08	0.32	0.753	0.05	0.15	0.32	0.752
North-East	ergosterol	Lignin_content	Ergosterol	~	LUI_change	f	0.30	0.13	2.35	0.019	0.35	0.14	2.47	0.014
North-East	ergosterol	Lignin_content	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	ergosterol	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	4.95	0.000	0.93	0.07	13.39	0.000
North-East	ergosterol	Lignin_content	Ergosterol	~~	Ergosterol		0.02	0.00	4.95	0.000	0.85	0.09	8.99	0.000
North-East	ergosterol	Lignin_content	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	ergosterol	Lignin_content	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	ergosterol	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.03	0.02	1.09	0.277	0.05	0.05	1.10	0.273
North-East	ergosterol	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.03	0.03	0.86	0.392	0.03	0.04	0.87	0.386
North-East	ergosterol	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.05	0.07	0.67	0.503	0.10	0.15	0.67	0.501
North-East	ergosterol	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.32	0.13	2.55	0.011	0.38	0.14	2.71	0.007
North-East	ergosterol	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.04	0.07	0.59	0.557	-0.06	0.14	-0.45	0.656
North-East	ergosterol	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.32	0.13	2.55	0.011	0.34	0.13	2.65	0.008
North-East	ergosterol	pH	pH_historic	~	LUI_historic	a	-0.02	0.16	-0.13	0.897	-0.02	0.14	-0.13	0.897
North-East	ergosterol	pH	pH_change	~	LUI_change	b	0.04	0.10	0.40	0.686	0.06	0.14	0.40	0.686
North-East	ergosterol	pH	Ergosterol	~	pH_historic	c	-0.12	0.05	-2.26	0.024	-0.27	0.12	-2.32	0.020
North-East	ergosterol	pH	Ergosterol	~	pH_change	d	0.38	0.14	2.72	0.007	0.33	0.12	2.84	0.005
North-East	ergosterol	pH	Ergosterol	~	LUI_historic	e	0.06	0.06	0.89	0.375	0.12	0.13	0.89	0.373
North-East	ergosterol	pH	Ergosterol	~	LUI_change	f	0.28	0.11	2.56	0.010	0.34	0.13	2.66	0.008
North-East	ergosterol	pH	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	ergosterol	pH	pH_historic	~~	pH_historic		0.10	0.02	5.00	0.000	1.00	0.01	193.05	0.000
North-East	ergosterol	pH	pH_change	~~	pH_change		0.01	0.00	5.00	0.000	1.00	0.02	62.03	0.000
North-East	ergosterol	pH	Ergosterol	~~	Ergosterol		0.01	0.00	5.00	0.000	0.72	0.11	6.83	0.000
North-East	ergosterol	pH	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	ergosterol	pH	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	ergosterol	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	0.13	0.897	0.01	0.04	0.13	0.897
North-East	ergosterol	pH	LUI_change_in	:=	b*d	LUI_change_in	0.02	0.04	0.40	0.690	0.02	0.05	0.40	0.688
North-East	ergosterol	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.06	0.07	0.89	0.374	0.12	0.14	0.89	0.373
North-East	ergosterol	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.29	0.11	2.56	0.011	0.36	0.13	2.68	0.007
North-East	ergosterol	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.05	0.07	0.81	0.420	-0.03	0.14	-0.24	0.814
North-East	ergosterol	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.29	0.11	2.56	0.011	0.31	0.12	2.46	0.014

Table S7-6.3: R^2 values of SEMs in Schwäbische Alb (South-West), Hainich-Dün (Central) and Schorfheide-Chorin (North-East) (see following pages). Given are the R^2 values for endogenous variables, i.e. the historic (mediator$_h$) and the change (mediator$_\Delta$) of a mediator variable and the soil microbial response variable (MO variable).

Region	**MO variable**	**mediator**	**R^2 mediator$_h$**	**R^2 mediator$_\Delta$**	**R^2 MO variable**
South-West	Cmic	CWM leaf P	0.52	0.01	0.12
South-West	Cmic	CWM MycInt	0.08	0.09	0.15
South-West	Cmic	Plant biomass	NA	0.03	0.21
South-West	Cmic	Lignin content	NA	0.01	0.07
South-West	Cmic	pH	0.01	0.00	0.14
South-West	Nmic	CWM leaf P	0.52	0.01	0.14
South-West	Nmic	CWM MycInt	0.08	0.09	0.17
South-West	Nmic	Plant biomass	NA	0.03	0.21
South-West	Nmic	Lignin content	NA	0.01	0.08
South-West	Nmic	pH	0.01	0.00	0.17
South-West	Cmic:Nmic ratio	CWM leaf P	0.52	0.01	0.06
South-West	Cmic:Nmic ratio	CWM MycInt	0.08	0.09	0.08
South-West	Cmic:Nmic ratio	Plant biomass	NA	0.03	0.09
South-West	Cmic:Nmic ratio	Lignin content	NA	0.01	0.04
South-West	Cmic:Nmic ratio	pH	0.01	0.00	0.12
South-West	Pmic	CWM leaf P	0.55	0.03	0.24
South-West	Pmic	CWM MycInt	0.06	0.07	0.25
South-West	Pmic	Plant biomass	NA	0.07	0.26
South-West	Pmic	Lignin content	NA	0.04	0.21
South-West	Pmic	pH	0.04	0.01	0.25
South-West	beta-glucosidase	CWM leaf P	0.52	0.01	0.12
South-West	beta-glucosidase	CWM MycInt	0.08	0.09	0.13
South-West	beta-glucosidase	Plant biomass	NA	0.03	0.17
South-West	beta-glucosidase	Lignin content	NA	0.01	0.12
South-West	beta-glucosidase	pH	0.01	0.00	0.27
South-West	beta-xylosidase	CWM leaf P	0.52	0.01	0.28
South-West	beta-xylosidase	CWM MycInt	0.08	0.09	0.12
South-West	beta-xylosidase	Plant biomass	NA	0.03	0.12
South-West	beta-xylosidase	Lignin content	NA	0.01	0.11
South-West	beta-xylosidase	pH	0.01	0.00	0.32
South-West	chitinase	CWM leaf P	0.52	0.01	0.28
South-West	chitinase	CWM MycInt	0.08	0.09	0.12
South-West	chitinase	Plant biomass	NA	0.03	0.12
South-West	chitinase	Lignin content	NA	0.01	0.11
South-West	chitinase	pH	0.01	0.00	0.32
South-West	urease	CWM leaf P	0.52	0.01	0.18
South-West	urease	CWM MycInt	0.08	0.09	0.17
South-West	urease	Plant biomass	NA	0.03	0.04
South-West	urease	Lignin content	NA	0.01	0.05
South-West	urease	pH	0.01	0.00	0.04
South-West	DEA	CWM leaf P	0.52	0.01	0.35
South-West	DEA	CWM MycInt	0.08	0.09	0.24
South-West	DEA	Plant biomass	NA	0.03	0.22
South-West	DEA	Lignin content	NA	0.01	0.22
South-West	DEA	pH	0.01	0.00	0.29
South-West	phosphatase	CWM leaf P	0.52	0.01	0.06
South-West	phosphatase	CWM MycInt	0.08	0.09	0.08
South-West	phosphatase	Plant biomass	NA	0.03	0.03
South-West	phosphatase	Lignin content	NA	0.01	0.14
South-West	phosphatase	pH	0.01	0.00	0.63
South-West	bacteria	CWM leaf P	0.52	0.01	0.06
South-West	bacteria	CWM MycInt	0.08	0.09	0.08
South-West	bacteria	Plant biomass	NA	0.03	0.03
South-West	bacteria	Lignin content	NA	0.01	0.04
South-West	bacteria	pH	0.01	0.00	0.16
South-West	fungi:bacteria ratio	CWM leaf P	0.52	0.01	0.23
South-West	fungi:bacteria ratio	CWM MycInt	0.08	0.09	0.14
South-West	fungi:bacteria ratio	Plant biomass	NA	0.03	0.11
South-West	fungi:bacteria ratio	Lignin content	NA	0.01	0.11
South-West	fungi:bacteria ratio	pH	0.01	0.00	0.19
South-West	fungi	CWM leaf P	0.52	0.01	0.12
South-West	fungi	CWM MycInt	0.08	0.09	0.14
South-West	fungi	Plant biomass	NA	0.03	0.08
South-West	fungi	Lignin content	NA	0.01	0.09
South-West	fungi	pH	0.01	0.00	0.07
South-West	ergosterol	CWM leaf P	0.52	0.01	0.26
South-West	ergosterol	CWM MycInt	0.08	0.09	0.26
South-West	ergosterol	Plant biomass	NA	0.03	0.18
South-West	ergosterol	Lignin content	NA	0.01	0.22
South-West	ergosterol	pH	0.01	0.00	0.17

Region	MO variable	mediator	R^2 mediator$_h$	R^2 mediator$_\Delta$	R^2 MO variable
Central	Cmic	CWM leaf P	0.41	0.00	0.09
Central	Cmic	CWM MycInt	0.02	0.00	0.13
Central	Cmic	Plant biomass	NA	0.02	0.10
Central	Cmic	Lignin content	NA	0.01	0.08
Central	Cmic	pH	0.00	0.02	0.11
Central	Nmic	CWM leaf P	0.41	0.00	0.22
Central	Nmic	CWM MycInt	0.02	0.00	0.22
Central	Nmic	Plant biomass	NA	0.02	0.21
Central	Nmic	Lignin content	NA	0.01	0.22
Central	Nmic	pH	0.00	0.02	0.21
Central	Cmic:Nmic ratio	CWM leaf P	0.41	0.00	0.11
Central	Cmic:Nmic ratio	CWM MycInt	0.02	0.00	0.10
Central	Cmic:Nmic ratio	Plant biomass	NA	0.02	0.13
Central	Cmic:Nmic ratio	Lignin content	NA	0.01	0.11
Central	Cmic:Nmic ratio	pH	0.00	0.02	0.34
Central	Pmic	CWM leaf P	0.43	0.01	0.10
Central	Pmic	CWM MycInt	0.02	0.00	0.02
Central	Pmic	Plant biomass	NA	0.02	0.04
Central	Pmic	Lignin content	NA	0.02	0.01
Central	Pmic	pH	0.00	0.02	0.08
Central	beta-glucosidase	CWM leaf P	0.41	0.00	0.40
Central	beta-glucosidase	CWM MycInt	0.02	0.00	0.15
Central	beta-glucosidase	Plant biomass	NA	0.02	0.16
Central	beta-glucosidase	Lignin content	NA	0.01	0.11
Central	beta-glucosidase	pH	0.00	0.02	0.10
Central	beta-xylosidase	CWM leaf P	0.35	0.00	0.24
Central	beta-xylosidase	CWM MycInt	0.01	0.00	0.14
Central	beta-xylosidase	Plant biomass	NA	0.01	0.19
Central	beta-xylosidase	Lignin content	NA	0.01	0.19
Central	beta-xylosidase	pH	0.00	0.02	0.18
Central	chitinase	CWM leaf P	0.41	0.00	0.27
Central	chitinase	CWM MycInt	0.02	0.00	0.13
Central	chitinase	Plant biomass	NA	0.02	0.16
Central	chitinase	Lignin content	NA	0.01	0.20
Central	chitinase	pH	0.00	0.02	0.14
Central	urease	CWM leaf P	0.42	0.00	0.26
Central	urease	CWM MycInt	0.02	0.01	0.16
Central	urease	Plant biomass	NA	0.00	0.11
Central	urease	Lignin content	NA	0.02	0.25
Central	urease	pH	0.01	0.02	0.12
Central	DEA	CWM leaf P	0.41	0.00	0.10
Central	DEA	CWM MycInt	0.02	0.00	0.08
Central	DEA	Plant biomass	NA	0.02	0.29
Central	DEA	Lignin content	NA	0.01	0.09
Central	DEA	pH	0.00	0.02	0.10
Central	phosphatase	CWM leaf P	0.41	0.00	0.16
Central	phosphatase	CWM MycInt	0.02	0.00	0.11
Central	phosphatase	Plant biomass	NA	0.02	0.15
Central	phosphatase	Lignin content	NA	0.01	0.13
Central	phosphatase	pH	0.00	0.02	0.15
Central	bacteria	CWM leaf P	0.41	0.00	0.05
Central	bacteria	CWM MycInt	0.02	0.00	0.23
Central	bacteria	Plant biomass	NA	0.02	0.21
Central	bacteria	Lignin content	NA	0.01	0.06
Central	bacteria	pH	0.00	0.02	0.11
Central	fungi:bacteria ratio	CWM leaf P	0.41	0.00	0.29
Central	fungi:bacteria ratio	CWM MycInt	0.02	0.00	0.31
Central	fungi:bacteria ratio	Plant biomass	NA	0.02	0.31
Central	fungi:bacteria ratio	Lignin content	NA	0.01	0.31
Central	fungi:bacteria ratio	pH	0.00	0.02	0.31
Central	fungi	CWM leaf P	0.41	0.00	0.14
Central	fungi	CWM MycInt	0.02	0.00	0.22
Central	fungi	Plant biomass	NA	0.02	0.19
Central	fungi	Lignin content	NA	0.01	0.15
Central	fungi	pH	0.00	0.02	0.22
Central	ergosterol	CWM leaf P	0.41	0.01	0.08
Central	ergosterol	CWM MycInt	0.02	0.00	0.16
Central	ergosterol	Plant biomass	NA	0.02	0.07
Central	ergosterol	Lignin content	NA	0.02	0.14
Central	ergosterol	pH	0.00	0.04	0.13

Region	MO variable	mediator	R^2 mediator$_h$	R^2 mediator$_\Delta$	R^2 MO variable
North-East	Cmic	CWM leaf P	0.00	0.06	0.01
North-East	Cmic	CWM MycInt	0.06	0.02	0.23
North-East	Cmic	Plant biomass	NA	0.06	0.19
North-East	Cmic	Lignin content	NA	0.07	0.01
North-East	Cmic	pH	0.00	0.00	0.06
North-East	Nmic	CWM leaf P	0.00	0.06	0.02
North-East	Nmic	CWM MycInt	0.06	0.02	0.03
North-East	Nmic	Plant biomass	NA	0.06	0.13
North-East	Nmic	Lignin content	NA	0.07	0.01
North-East	Nmic	pH	0.00	0.00	0.08
North-East	Cmic:Nmic ratio	CWM leaf P	0.00	0.06	0.13
North-East	Cmic:Nmic ratio	CWM MycInt	0.06	0.02	0.11
North-East	Cmic:Nmic ratio	Plant biomass	NA	0.06	0.15
North-East	Cmic:Nmic ratio	Lignin content	NA	0.07	0.09
North-East	Cmic:Nmic ratio	pH	0.00	0.00	0.34
North-East	Pmic	CWM leaf P	0.00	0.08	0.15
North-East	Pmic	CWM MycInt	0.10	0.01	0.32
North-East	Pmic	Plant biomass	NA	0.04	0.07
North-East	Pmic	Lignin content	NA	0.09	0.11
North-East	Pmic	pH	0.00	0.00	0.17
North-East	beta-glucosidase	CWM leaf P	0.00	0.06	0.05
North-East	beta-glucosidase	CWM MycInt	0.06	0.02	0.08
North-East	beta-glucosidase	Plant biomass	NA	0.06	0.05
North-East	beta-glucosidase	Lignin content	NA	0.07	0.05
North-East	beta-glucosidase	pH	0.00	0.00	0.28
North-East	beta-xylosidase	CWM leaf P	0.00	0.06	0.06
North-East	beta-xylosidase	CWM MycInt	0.06	0.02	0.15
North-East	beta-xylosidase	Plant biomass	NA	0.06	0.06
North-East	beta-xylosidase	Lignin content	NA	0.07	0.06
North-East	beta-xylosidase	pH	0.00	0.00	0.22
North-East	chitinase	CWM leaf P	0.00	0.06	0.17
North-East	chitinase	CWM MycInt	0.06	0.02	0.08
North-East	chitinase	Plant biomass	NA	0.06	0.08
North-East	chitinase	Lignin content	NA	0.07	0.08
North-East	chitinase	pH	0.00	0.00	0.18
North-East	urease	CWM leaf P	0.00	0.06	0.04
North-East	urease	CWM MycInt	0.06	0.02	0.07
North-East	urease	Plant Biomass	NA	0.06	0.02
North-East	urease	Lignin content	NA	0.07	0.02
North-East	urease	pH	0.00	0.00	0.50
North-East	DEA	CWM leaf P	0.00	0.06	0.15
North-East	DEA	CWM MycInt	0.06	0.02	0.31
North-East	DEA	Plant biomass	NA	0.06	0.01
North-East	DEA	Lignin content	NA	0.07	0.01
North-East	DEA	pH	0.00	0.00	0.52
North-East	phosphatase	CWM leaf P	0.00	0.06	0.25
North-East	phosphatase	CWM MycInt	0.06	0.02	0.19
North-East	phosphatase	Plant biomass	NA	0.06	0.13
North-East	phosphatase	Lignin content	NA	0.07	0.13
North-East	phosphatase	pH	0.00	0.00	0.25
North-East	bacteria	CWM leaf P	0.00	0.06	0.13
North-East	bacteria	CWM MycInt	0.06	0.02	0.31
North-East	bacteria	Plant biomass	NA	0.06	0.11
North-East	bacteria	Lignin content	NA	0.07	0.06
North-East	bacteria	pH	0.00	0.00	0.06
North-East	fungi:bacteria ratio	CWM leaf P	0.00	0.06	0.21
North-East	fungi:bacteria ratio	CWM MycInt	0.06	0.02	0.08
North-East	fungi:bacteria ratio	Plant biomass	NA	0.06	0.04
North-East	fungi:bacteria ratio	Lignin content	NA	0.07	0.05
North-East	fungi:bacteria ratio	pH	0.00	0.00	0.09
North-East	fungi	CWM leaf P	0.00	0.06	0.10
North-East	fungi	CWM MycInt	0.06	0.02	0.32
North-East	fungi	Plant biomass	NA	0.06	0.10
North-East	fungi	Lignin content	NA	0.07	0.10
North-East	fungi	pH	0.00	0.00	0.10
North-East	ergosterol	CWM leaf P	0.00	0.06	0.17
North-East	ergosterol	CWM MycInt	0.06	0.02	0.14
North-East	ergosterol	Plant biomass	NA	0.06	0.23
North-East	ergosterol	Lignin content	NA	0.07	0.15
North-East	ergosterol	pH	0.00	0.00	0.28

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