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CICLO XXVII

EVALUATION, MAINTENANCE AND IMPROVEMENT OF BIODIVERSITY FOR ENVIRONMENTAL PROTECTION AND CROP NUTRITIONAL PROPERTIES

Direttore della Scuola: Ch.mo Prof. Giuseppe Zanotti

Coordinatore d'indirizzo: Ch.ma Prof.ssa Fiorella Lo Schiavo

Supervisore: Ch.mo Prof. Andrea Squartini

Co-supervisore: Ch.mo Prof. Maurizio Guido Paoletti

Dottoranda: Silvia Fusaro

<<Parliamo sempre di capitale economico e non ci interessa il capitale naturale.
Le decisioni sono prese dando priorità all'economia rispetto alla natura.
Come se le leggi dell'economia fossero più forti delle leggi della natura.>>

Ferdinando Boero (2014)

<<Soil is not a machine, it is a living being of astonishing, and still largely unexplored, complexity>>

Tiziano Gomiero (2013)

<<Knowing your planet is a step towards protecting it>>

Jacques Yves Cousteau

2015
International Year of Soils

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List of Abbreviations

ES = Ecosystem Services
OM = Organic Matter

Arable = arable land use
SemN = semi-natural land use
Urb = urban land use

A.R.I.S.A. =Automated Ribosomal Intergenic Spacer Analyses

EU =Effort Unit
AD= Activity Days
DA_{10} = Activity Density

FDA = Fluorescein Diacetate
F = Fluorescein

SIR = Substrate Induced Respiration

QBS-ar = Soil Biological Quality Index based on arthropods
QBS-e = Soil Biological Quality Index based on earthworms

E.I. =Entomophily Index

TAC = Total Antioxidant Capacity
FRAP = Ferric Reducing Antioxidant Power
d.m. = dry matter
d.w. = dry weight

NMDS = Non-metric multidimensional scaling
PCA = Principal Components Analysis

D.I. = Diversity Indexes
S = Taxa diversity index
H = Shannon diversity index
1-D = Simpson diversity index
D = Dominance diversity index
e^H/S = Evenness diversity index
J = Equitability diversity index

AryS = Arylsulfatase activity
Gluc = β–glucosidase activity
Leu = Leucine-aminopeptidase activity
Ester = Acetate-Esterase activity
AcP = Acid Phosphomonoesterase
Piro = Pyrophosphate–phosphodiesterase activity
AlkP = Alkaline phosphomonoesterase activity

b.c. = biological control
DBM = DiamondBack Moth (*P. xylostella*)
IGP = IntraGuild Predation

Abstract

Biodiversity is expected to be an assurance for agroecosystem resilience because it seems fundamental to preserve basic ecosystem services (ES). To examine in depth these topics, the present research aims: a) to evaluate, in real farms, the environmental sustainability by measuring the efficiency of some key ES in agroecosystems with different management; b) to search for relationships among biodiversity groups and ES and c) to explore the existence of correlations between different bioindication methodologies. The basic hypothesis is that a high efficiency of the ES can improve the environmental sustainability of agroecosystems.

ES were studied by using several bioindicators associated to the functional biodiversity, which guarantees these useful services to crops. The chosen bioindicators, representing the principal trophic levels, were appropriate tools to investigate the complexity of food web in the crop field. The chosen bioindicators providing basic ES were: 1. *Earthworms*, soil structure drivers, responsible for air and water circulation and drainage, for organic matter (OM) decomposition and for cast enriching activity; 2. *Mesofauna* (including mites and springtails), which comprises mainly detritivores and small preys and predators; 3. Soil *bacteria* and *fungi*, promoters of OM decomposition, nutrient cycles, soil enzymatic activities and improvement of soil-root-water relationships; 4. Key *Predators* (including *carabids*) and *parasitoids*, natural control agents for crop pest outbreaks; 5. *Crop Weeds* and *field margin vegetation*, important reporters of soil conditions, can act as shelters for overwintering, provide alternative food sources for useful fauna and can attract pollinators in the field area. The research was carried out during 2012-2013 in five organic-biodynamic and five conventional horticultural fields in the Venice and Treviso provinces.

The methodologies adopted to sample biodiversity of these bioindicators were: 30x30x20cm soil core hand sorting with irritant mustard powder water suspension for earthworms; Berlese-Tullgren extractor for mesofauna; Automated Ribosomal Intergenic Spacer Analysis and 16S and ITS sequencing performed in a 454 system (Roche) for overall communities of soil bacteria and fungi, PCR and qRT-PCR with specific primers for Arbuscular Mycorrhizal Fungi (AMF); Visual control on the aboveground part of crop for phytophagous agent and predator communities; Indoor breeding for parasitoid communities; Random nested data collection for weed communities.

After sampling with the aim to know the biodiversity guilds, other innovative techniques were exploited to measure environmental quality. Regarding the component of soil mesofauna, the QBS-ar index was applied to assess the status of soil alteration but not performable by a taxonomically inexperienced operator. In order to analyse earthworms, the new QBS-e index based on earthworm ecological categories, similar to QBS-ar but easier to use also by non-experts, was successfully applied. To measure microbiological activity and biomass, soil respiration rate assay, Fluorescein Diacetate hydrolysis test, dsDNA quantification together with key soil enzymatic activities were carried out along with probes with Fertimeters[1], simple devices made of silk and cotton yarns working as reporters of organic matter

[1] International patent PCT N. WO2012 140523 A1, Squartini, Concheri, Tiozzo, Padova University

degradation. In order to assess the natural pest control, besides the quantification of predator presence in the field, the parasitization and hyperparasitization percentages regarding one of the most problematic cabbage pest (*Plutella xylostella)* were calculated. To quantify the extent of pollinator and useful fauna attraction of weed communities, an Entomophily Index (E.I.) was adopted that takes into account the presence and abundance of insect-pollinated species.

Some conclusive remarks were:

1. Taxa composition of a bioindicator group does not always change according to different agroecosystem managements. There seem to be more sensitive bioindicators to management practices, such as predators and parasitoids (belonging to higher trophic levels), than others, such as phytophagous agents and weeds.

2. Biodiversity, simply described with classical diversity indexes found in literature, seemed not to be associated to the ES efficiency, probably because the link has to be searched in the complexity of interactions among all biodiversity groups.

3. Agroecosystems managed in an organic-biodynamic way demonstrated to have more efficient ES (almost all among the ones measured) both in the aboveground and in the epigeal sectors and therefore this management system can be defined as more sustainable from environmental point of view.

4. Finally a great quantity of correlations emerged between all analysed indicators (biotic and functional): these could be very useful to better planning future programs of monitoring of agroecosystem conditions.

Riassunto

Valutazione, mantenimento e miglioramento della Biodiversità per la protezione dell'ambiente e per le proprietà nutrizionali della coltura

La biodiversità è ritenuta essere una sorta di garanzia per la resilienza dell'agroecosistema in quanto sembra fondamentale per preservare basilari servizi ecosistemici (SE). Al fine di approfondire queste tematiche, questo lavoro si propone di: a) valutare, in aziende reali, la sostenibilità ambientale misurando l'efficienza di alcuni SE chiave in agroecosistemi a differente gestione; b) cercare relazioni fra i gruppi di biodiversità studiati e i SE e c) esplorare l'esistenza di correlazioni fra le differenti metodologie di analisi considerate. L'ipotesi di base è che una elevata efficienza dei SE può migliorare la sostenibilità ambientale dell'agroecosistema.

I SE sono stati studiati utilizzando numerosi bioindicatori associati alla biodiversità funzionale, che è in grado di garantire alla coltura questi utili servizi. I bioindicatori scelti, appartenenti ai principali livelli trofici, sono stati strumenti appropriati per indagare la complessità della rete trofica nel campo coltivato. I bioindicatori scelti, che provvedono a SE fondamentali, sono stati: 1. *Lombrichi*, promotori della struttura del suolo, fra i maggiori responsabili della circolazione di aria e acqua e del drenaggio, della decomposizione della sostanza organica e della attività di arricchimento del suolo in nutrienti dovuta agli escrementi; 2. *Mesofauna* (come acari e collemboli), che comprende principalmente detritivori e piccole prede e predatori; 3. *Batteri* e *funghi* del suolo, promotori della degradazione della sostanza organica, dei cicli biogeochimici dei nutrienti, delle attività enzimatiche del suolo e del miglioramento delle relazioni suolo-radici-acqua; 4. *Predatori* (compresi i *carabidi*) e *parassitoidi*, agenti di controllo naturale delle pullulazioni di fitofagi; 5. *Malerbe del campo coltivato* e *Piante spontanee di margine*, importanti reporter delle condizioni del suolo, che possono fungere da rifugi per lo svernamento, possono fornire fonti alternative di cibo per la fauna utile e inoltre possono attrarre impollinatori nell'area del campo. La ricerca è stata sviluppata negli anni 2012-2013 in cinque campi biologici-biodinamici e cinque campi convenzionali coltivati ad orticole siti nelle province di Venezia e Treviso.

Le metodologie per campionare la biodiversità di questi bioindicatori sono state le seguenti: hand sorting su una zolla di 30x30x20cm con precedente versamento di sospensione acquosa di polvere di senape, che funge da irritante per i lombrichi (in particolare per i profondi scavatori); l'estrazione con l'apparato Berlese-Tullgren per la mesofauna; la tecnica Automated Ribosomal Intergenic Spacer Analysis e il sequenziamento del gene 16S e ITS eseguito con il sistema 454 (Roche) per lo studio completo delle comunità di batteri e funghi del suolo, la tecnica PCR e real time-PCR con primer specifici per i funghi micorrizici (AMF); il controllo visivo sulla parte epigea della pianta coltivata per l'indagine della presenza di fitofagi e predatori; il successivo allevamento in laboratorio per indagare le comunità di parassitoidi; la raccolta raggruppata e casuale di dati sulle specie e le relative abbondanze di piante erbacee spontanee per esaminarne le comunità nell'area del campo e del margine erboso di capezzagna.

Dopo aver campionato con lo scopo di conoscere i principali gruppi di biodiversità, si è proceduto applicando delle tecniche innovative e speditive utili per misurare la qualità dell'agroecosistema.

Considerando la componente della mesofauna del suolo, è stato applicato l'indice QBS-ar per valutare lo stato di alterazione del suolo ma non applicabile da un operatore non esperto in tassonomia. Al fine di analizzare la comunità di lombrichi, è stato applicato il nuovo indice QBS-e basato sulle loro categorie ecologiche, simile al QBS-ar ma più facile da usare anche da non esperti. Per misurare l'attività e la biomassa microbica, il test di valutazione del tasso di respirazione del suolo, il test di idrolisi della fluoresceina diacetato, la quantificazione del dsDNA unitamente a saggi sulle attività di enzimi chiave del suolo sono stati condotti insieme al test con il fertimetro[2], un semplice strumento costituito da fili di seta e cotone che fungono da reporter della degradazione della sostanza organica. Al fine di valutare il controllo biologico naturale dei parassiti delle colture, oltre alla quantificazione dei predatori presenti sul campo, sono state calcolate anche le percentuali di parassitizzazione e iperparassitizzazione relative ad uno fra i più problematici parassiti del cavolfiore (*Plutella xylostella*). Per quantificare l'entità dell'attrazione di impollinatori e fauna utile svolta dalla comunità delle piante erbacee spontanee, un indice di entomofilia (E.I.), che prende in considerazione la presenza e l'abbondanza di specie entomofile, è stato applicato.

Alcune considerazioni conclusive sono state:

1. La composizione in taxa di un gruppo di bioindicatori non sempre cambia in base a differenti gestioni dell'agroecosistema. Sembrano esserci bioindicatori più sensibili alle pratiche di gestione, come ad esempio i predatori e i parassitoidi (appartenenti a livelli trofici superiori), rispetto ad altri, come fitofagi e malerbe.

2. Gli agroecosistemi a gestione biologico-biodinamica hanno dimostrato di avere SE più efficienti (quasi tutti fra quelli misurati) sia nel settore ipogeo che in quello epigeo e perciò questo tipo di gestione si può definire più sostenibile dal punto di vista ambientale.

3. La biodiversità, descritta semplicemente con i classici indici di biodiversità che si trovano in letteratura, non sembra essere associata all'efficienza dei SE, probabilmente perché il collegamento fra questi due fattori deve essere cercato nella complessità delle interazioni fra tutti i gruppi di biodiversità considerati.

4. Infine, una grande quantità di correlazioni fra tutti gli indicatori analizzati (biotici e funzionali) è emersa: tali correlazioni potrebbero essere molto utili per pianificare meglio futuri programmi di monitoraggio delle condizioni degli agroecosistemi.

[2] Brevetto internazionale PCT N. WO2012 140523 A1, Squartini, Concheri, Tiozzo, Università di Padova

INTRODUCTION

Agroecosystem

Agroecosystems are ecological systems or communities of plants and animals interacting with their physical and chemical environments that have been modified by humans and so they are intensively managed for the purpose of producing food, feed, fibres, fuel and other products suitable for human consumption and which support many human activities (Smith et al., 2000; Altieri, 2002).

On the European Community scale, agricultural areas are more significant (44%) than protected areas, which represent less than 5% (Clergue et al., 2005). In Italy 2010 ISTAT census declared 12.9 millions of cultivated hectares that correspond to 42% of the total national area[3]. From an ecological point of view it is an environment artificially simplified in comparison with the original natural one, but it still maintains a pool of wild organisms and natural processes, because it usually contains parcels of unmanaged or lightly managed areas, such as woodlots, fencerows, riparian areas, wild margins (fig. 1) that can act both as refuges for beneficial biodiversity for crop production (Letourneau, 1997; Landis et al., 2000) as well as reservoirs of insect pests, weed seeds and sources of plant pathogens (Smith et al., 2000).

Agroecosystems may be subjected to different management by the farmer, which can be defined as a set of mechanical practices for soil tillage and use of substances that allow and improve crop growth.

[3] Data available on ISTAT web service "Annuario statistico italiano 2014" on the website: http://www.istat.it/it/files/2014/11/Pillole-ASI-_2014.pdf

Fig. 1: A horticultural agroecosystem characterized by polyculture, studied in this research. In the background a semi-natural habitat is visible: a hedgerow (Ph. S. Fusaro).

Conventional management

The traditional or *conventional* farming system implies a more intensive crop production: since World War II agriculture has become more specialized and dependent on off-farm inputs and has substantially increased per acre yield (Pesek et al., 1989). Several practices help to obtain increased yields. First of all the use of heavy machineries to speed the time for soil tillage and to optimize the human manpower and of invasive practices such as ploughing, which is an inversion tillage technique that can be up to 30-40 cm deep (Giardini, 2003). Soil fertilization is obtained with the use of synthetic chemical and mineral fertilizers, mainly based on principal plant nutrients, such as nitrogen, phosphorus and potassium [N:P:K]. Weed control is obtained with chemical herbicides, often barely selective (Pimentel et al., 2005). Pest control is mainly practiced with pesticides, also only partially selective (Pimentel, 2005). If there are crop rotations, these are less regular and shorter. In general this type of agriculture favours monoculture or the cultivation of a wider area with the same crop variety, in order to facilitate mechanical practices. Resuming, conventional agriculture tends to maximize the production by mechanizing as much as possible all stages of processing and considering of minor interest the marginal semi-natural non-productive environments of the farm (Pimentel et al., 2005; Gomiero et al., 2011).

Organic management

Organic farming system is regulated by international and national institutions (Alimentarius, 2004; Regulation (EC), 2007). Its origins are within the years 1920-1930 in Northern Europe (mostly Germany and UK) but it is now widely spread all over the world (Lotter, 2003; Gomiero et al., 2011). Organic agriculture has been defined as "a *production system that sustains the health of soils, ecosystems and people. It relies on ecological processes, biodiversity and cycles adapted to local conditions, rather than the use of inputs with adverse effects. It combines tradition, innovation and science to benefit the shared environment and promote fair relationships and a good quality of life for all involved*" (IFOAM, 2010).

In Italy there are more than 1.3 million hectares cultivated with the organic method, which correspond to 10.2% of the total national cultivated area[4], while in Veneto region there are 17920 hectares[5] cultivated with organic method, which correspond to 2.2% of the total regional cultivated area[6]. SINAB in its annual report about the organic farming system has counted an increase of 12.8% of cultivated surface with the organic method in respect with 2013 (De Matthaeis et al., 2014). Organic agriculture is subjected to Regulation (EC) no. 834/2007 of 28th June 2007 and in Italy it is under the control of an authority certified by the Ministry of Agriculture and Forestry. It provides a less intensive tillage trying to avoid or minimize too invasive practices, like ploughing. Soil fertilization is practiced without the use of synthetic chemical fertilizers and natural soil fertility is improved by the use of green manure, that is a crop not finalized to production and that, at the end of its growing cycle, is buried and incorporated into the soil, by intercropping, polyculture, cover crops and mulching and crop rotation over time on the same plot in order to reduce the soil tiredness (Lotter, 2003; Regulation (EC), 2007; Gomiero, 2013). Pest control is obtained avoiding chemical pesticides in favour of biological pest control or the use of more natural substances (mainly extracted from plants) and allowed by law (Regulation (EC), 2007). Weed control is managed by appropriate rotation, seeding timing, mulching, flaming, stale seedbed (Gomiero, 2013). Organic farming system aims to achieve a better balance between supply and demand of agricultural products, environmental protection and conservation of rural areas (Lotter, 2003; Regulation (EC), 2007) then also pursuing the maintenance and protection of natural and semi-natural marginal areas of the farm but important from the ecological point of view. It is a production system aimed at producing food with minimal harm to ecosystems, animals or humans (Seufert et al., 2012).

Biodynamic management

There is another farming system, the so called *biodynamic* agriculture, which is based on the teachings of the anthroposophic school developed by the philosopher Rudolf Steiner in 1924 (Steiner, 1958). It is subjected to Regulation (EC) no. 834/2007 of 28th June 2007 (Regulation (EC), 2007), the same

[4] Data available on SINAB web site: Bio in cifre 2014 (http://www.sinab.it/sites/default/files/share/bio%20in%20cifre%202014_3.pdf)
[5] Data available on VenetoAgricoltura web site (http://www.venetoagricoltura.org/basic.php?ID=431)
[6] Data available on "Rapporto di analisi per Priorità 4 e 5 delPSR Veneto 2014-2020" (http://piave.veneto.it/resource/resolver?resourceId=2ba4e74d-a41e-4111-bf29-932e08466f6e/Analisi%20di%20Contesto%20e%20SWOT_Priorit%C3%A0%204%20e%205_PSR%20Veneto%202014-2020)

for organic agriculture and furthermore currently the institution prepared to biodynamic certification of a farm is Demeter International (Demeter): so all biodynamic certified farms must have the certification according to Regulation (EC) 2007 plus the Demeter one. It endorses some principles of organic farming, but the basic concept is to consider soil and life developed on it as a unique system; the farm must be a complete reality and that is self-supporting on the basis of various plant and animal products, respecting seasonal, lunar and cosmic equilibriums. Biodynamic management is a unique organic farming system that, within soil organic matter management practices and as an alternative to mineral fertilization and crop rotation, aims at improving the chemical, physical and biological properties of cultivated soils upon application of organic materials (Spaccini et al., 2012). In order to maintain and improve soil fertility it uses two biodynamic field spray preparations based on manure and quartz powder in homeopathic dilution (500 and 501 preparations). Other six preparations are those based on macerated officinal herbs that are used as additives for the compost heap (preparations n° from 502 to 507).

Despite criticism has often arisen regarding the scientific nature and the reliability of this farming system, stating that Steiner's teachings are so obscure and dogmatic as not to contribute to the realization of a sustainable and alternative agriculture (Kirchmann, 1994), conversely some scientific studies have underlined the differences between this type of farming system and organic and conventional ones in terms of agronomic and ecological performances (Mader et al., 2002). Moreover more recent researches have claimed that by analysing the 500 preparation (called also “horn manure”), the key element in biodynamic agriculture, this seems to be enriched of biolabile components and potentially conducive to plant growth stimulation (Spaccini et al., 2012) and also it appears to have a role in the potential of bioactivity for fertility, nutrient cycling and as a soil bio-stimulant (Giannattasio et al., 2013).

Environmental sustainability in the agroecosystem

Our global food production system faces the unprecedented challenge of feeding a rapidly increasing world population while simultaneously reducing its environmental footprint (Godfray et al., 2010; Bennett et al., 2014). In fact another big concern is the degradation of soil resources, which is also closely associated with the loss of soil quality by climate changes, wildfires, erosion, salinization and agricultural–industrial pollution problems (Karaca et al., 2011). The most likely scenario is that more food will need to be produced from the same amount of (or even less) land. This challenge requires changes in the way food is produced, stored, processed, distributed, and accessed that are as radical as those that occurred during the 18th- and 19th-century Industrial and Agricultural Revolutions and the 20th-century Green Revolution. Increases in production will have an important part to play, but they will be constrained as never before by the finite resources provided by Earth’s lands, oceans, and atmosphere (Godfray et al., 2010; Seufert et al., 2012). Another important factor that has to be considered is the waste of perishable products. In this respect, a study made at Wageningen University found that in Europe the food waste amounts to 50% for potatoes and other root crops, 45% for fruit and vegetables and 33% for grains (Smit et al., 2012). Surely also the reduction of these wastes would help to solve the problem of feeding an increasing world population.

Here the concept of sustainability is inserted: it implies the use of resources at rates that do not exceed the capacity of Earth to replace them. In fact environmental sustainability signifies maintaining the productivity and potential of an ecosystem used by humans with time: it seeks to improve human welfare by protecting the sources of raw materials used for human needs, and interest ensuring that the sinks for human wastes are not exceeded, in order to prevent harm to humans. Humanity must learn to live within the limitations of the biophysical environment. In other words, environmental sustainability signifies that natural capital must be maintained, both as a provider of inputs of sources and as a sink for wastes. This requires that the scale of the human economic subsystem be held to within the biophysical limits of the overall ecosystem on which it depends. On the sink side, this translates into holding waste emissions within the assimilative capacity of the environment without impairing it. On the source side, harvest rates of renewables must be kept within regeneration rates (Paoletti, 1999b). Human intervention in the landscape almost always has a strong impact on resources, which become depleted or degraded in their potentialities and are soon substituted with artificial ones that are more energy intensive (for example organic compounds in agroecosystems substituted by chemical fertilizers and pesticides) (Paoletti, 1999b). By definition, dependency on non-renewable inputs is unsustainable, even if in the short term it is necessary as part of a trajectory toward sustainability (Godfray et al., 2010). Pursuing the perspective of sustainability, the best yields that can be obtained locally with the reduction of external inputs, an improved management of species and depend on the capacity of farmers to access and use, among other things, seeds, water, nutrients, pest management, soils, biodiversity, and knowledge (Paoletti, 1999b; Godfray et al., 2010). So as defined by the United State Department of Agriculture in the 1990 Farm Bill "*Sustainable agriculture must over the long term, satisfy human needs, enhance environmental quality and natural resource base, make the most efficient use of non-renewable resources and integrate natural biological processes, sustain economic viability and enhance quality of life*" (USDA, 1990). Sustainable agricultural management practices are crucial in the production of food and human nutrition (Niemi et al., 2008) and should aim at preserving the natural resources, such as soil and water, relying on minimum artificial inputs from outside the farm system, being economically and socially viable (Gomiero, 2013).

In order to evaluate sustainability of agricultural practices, assessment of soil health using various indicators of soil quality is needed (Doran and Zeiss, 2000). Soil quality is the concept that has been developed to evaluate the factors effecting soil functionality and it is mainly concerned with sustainable use of soil resources in terms of enhanced agricultural productivity, environmental quality and human health (Karaca et al., 2011). The biological component of the soil system has a high dependence on the chemical and physical soil components and hence tends to be a sensitive indicator to disturbance or degradation processes (Slavich, 2001). Ecosystemic processes of the soil, but also those regarding the whole agroecosystem can be characterised in terms of their *resistance* to change by an imposed disturbance and their *resilience*, or potential to recover following disturbance/degradation (Pimm, 1984). These concepts are valid for assessing the sustainability of agricultural production systems (Herrick, 2000).

Biodiversity and ecosystem services in agroecosystems

Without biodiversity, life on earth would be impossible (Paoletti, 1999b). Biodiversity, a more and more considered concept in land management, can be defined at different levels or scales: it is the variety of life, including variation among genes, species and functional traits. It is the diversity considered at scale of different habitats in the landscape; the diversity at scale of different species present in a habitat and the diversity at genetic scale within a species. The concept of biodiversity implies that any environment is rich in different organisms and can be read as a system in which species circulate and interact. Structure, scale, and features of the landscape also enter into the definition of biodiversity (Paoletti, 1999b; Cardinale et al., 2012). Biodiversity is responsible for the provision of many ecosystem services; human well-being is based on these services and consequently on biodiversity (Blouin et al., 2013). We must avoid the temptation to further sacrifice Earth's already hugely depleted biodiversity for easy gains in food production, not only because biodiversity provides many of the public goods on which mankind relies but also because we do not have the right to deprive future generations of its economic and cultural benefits (Godfray et al., 2010). Whilst there appears to be general agreement that biodiversity confers stability/resilience, the potential value of biodiversity measurements as indicators of soil health requires more research (Pankhurst, 2002). There is the need to identify the relationships that exist between ecological entities and ecosystem functions or services, and to propose different technical approaches to manipulate the former, with the aim of reaching management objectives (Blouin et al., 2013). The argument for the importance of biodiversity in directing environmental policy presupposes that animals, plants, microorganisms and their complex interactions respond to human landscape management and impacts in different ways, with some organisms responding more quickly and definitively than others (Paoletti, 1999b).

Ecosystem services (ES) are the benefits provided by ecosystems to humankind as well as to other species (Howarth and Ramakrrshna, 2005). To achieve environmental sustainability, we must grow food in a manner that protects, uses and regenerates ecosystem services (for instance favours natural pest control over the use of synthetic pesticides), rather than replacing them (Bennett et al., 2014). Replacing ecosystem services often has unintended, negative consequences, such as lethal or sub-lethal effects of pesticides on humans, beneficial insects and wildlife (Henry et al., 2012; Ponisio et al., 2014). Understanding the relationships between biodiversity and ecosystem functioning is of great theoretical interest for the comprehension of the processes structuring communities and of practical importance to predict the effect of human-induced biodiversity loss. Several experiments have demonstrated that a range of ecosystem functions depend on biodiversity (usually species richness) (Loreau et al., 2002; Allan et al., 2013). Considering the role of agriculture in the preservation of biodiversity appears to be a key issue: to improve biodiversity conservation on the large scale, knowledge and creation of conservation tools are necessary not only in protected and restricted areas but also, and above all, in agricultural areas (Clergue et al., 2005).

A clear consequence of the link biodiversity-ES is represented by the insurance hypothesis (Yachi and Loreau, 1999). It predicts, for instance, that a high diversity of natural enemies ensures the functioning of biological control because the larger number of species provides a greater guarantee that some species will maintain functioning if others fail in situations of environmental fluctuations (Yachi and Loreau, 1999).

In order to have a complete picture of an agroecosystem it is better to proceed with the study of biodiversity composition that is linked to ES efficiency, which in turn, if higher, it corresponds to an improved environmental sustainability. Inventory and monitoring are necessary tools for the achievement of an adequate level of knowledge regarding the soil biodiversity status and for detection of biodiversity hot spots as well as areas where current levels of biodiversity are under threat of decline, as agroecosystems are. Generally, an inventory of biodiversity is an estimation of taxonomic diversity at one/several site(s) at a given time, while monitoring is achieved by estimating diversity at the same site, at more than one time, so as to allow inferences concerning change to be drawn (Gardi et al., 2009).

Although Cardinale et al. (2012) made a distinction between ES, described as above, and ecosystem functions defined as ecological processes that control the fluxes of energy, nutrients and organic matter through an environment, in this study all of them will be considered together for practice.

Functional agrobiodiversity

Another important concept considered in the present work is functional biodiversity (Moonen and Barberi, 2008; ELN-FAB, 2012; Barberi, 2013). This concept is raising in importance with several initiatives across Europe (Bianchi et al., 2013). Peeters et al. (2004) individuated three types of agrobiodiversity, clearly related to the main agroecosystem function, which is crop production. These are:

- Agrobiodiversity *sensu stricto*, which is the diversity of organisms directly useful for production, such as crops;
- Para-agrobiodiversity, also defined as "functional biodiversity", which is the one indirectly beneficial for production, for example useful predator fauna, soil microorganisms, etc.;
- Extra-agricultural biodiversity, which is present in an agroecosystem but unrelated to production process.

The European Learning Network on Functional AgroBiodiversity defined functional agrobiodiversity as "*those elements of biodiversity on the scale of agricultural fields or landscapes, which provide ES that support sustainable agricultural production and can also deliver benefits to the regional and global environment and the public at large*" (ELN-FAB, 2012).

To complete the picture with also the neutral and negative functions Moonen and Barberi (2008) defined functional biodiversity as "*that part of the total biodiversity composed of clusters of elements providing the same ecosystem service, which is driven by within-cluster diversity*". Therefore in this work functional biodiversity is referred to the amount of living organisms belonging to key trophic groups that, with their ecological-ethological-physiological activities, carry out ES fundamental to crop growth.

Bioindicators for agrobiodiversity

Since Slavich (2001) asserted that there is a need for measurable indicators to evaluate the sustainability of resource use by particular management systems, it can be profitable to use bioindicators. A bioindicator can be loosely defined as a species or a species assemblage with precise ecological requirements reflecting the abiotic or biotic state of the environment, which by its presence provides the operator with important information about the environmental conditions in which it lives and so it is particularly well-matched to specific features of the landscape, reacts to impacts and changes on a habitat, community or ecosystems, or indicates the diversity of other species (Paoletti et al., 1991; Paoletti and Bressan, 1996; van Straalen, 1997; McGeoch, 1998). More in detail and pointing out some advantages of their use, Landres, et al. (1988) specify that an indicator species is an organism whose characteristics such as presence or absence, population density, dispersion, reproductive success are used as an index of attributes too difficult, inconvenient, or expensive to measure for other species or environmental conditions of interest. It has to be assumed that changes in landscape management influence the biota, and that certain transient or permanent signs remain inside the system of biological communities (Paoletti et al., 1992; Paoletti, 1999b).

One of the primary goals of research on bioindicators is to identify species or other taxonomic units that would reliably indicate disturbances in the environment and reflect the responses of other species or the overall biodiversity (Rainio and Niemela, 2003). For example speaking about soil quality, since soil organisms are intimately involved in soil functioning, they also provide an integrated measure of soil health, an aspect that cannot be obtained with chemical/physical measures alone (Paoletti et al., 1991; Pankhurst, 2002). In fact soil organisms meet most of the criteria for useful indicators of soil quality, such as:

- to respond sensitively to land management practices and climate;
- a good correlation with beneficial soil and ecosystem functions including water storage, decomposition and nutrient cycling, detoxification of toxicants and suppression of noxious and pathogenic organisms;
- to illustrate the chain of cause and effect that links land management decisions to ultimate productivity and health of plants and animals;
- to be comprehensible and useful to land managers, who are the ultimate stewards of soil health;
- to be easy and inexpensive to measure, even if the need for knowledge of taxonomy complicates the measurement of soil organisms (Paoletti et al., 1991; Doran and Zeiss, 2000).

Generally according to Dale et al. (2008) the criteria to choose a good ecological indicator are:

(1) ease in measuring,

(2) sensitivity to system stresses,

(3) responsiveness to stress,

(4) anticipation of change in the ecological system,

(5) predictivity of changes,

(6) being integrative,

(7) ability to respond to natural disturbances, anthropogenic stresses and changes over time,

(8) variability with response,

(9) possibility to be measured in relation to spatial and temporal change.

Although larger, feathered, furry or colourful animals like birds, mammals and butterflies are easier to see and of greater interest to the public, media and scientists, the small, inconspicuous invertebrates such as insects, mites and nematodes can offer a database of millions of species, thereby offering a more abundant sophisticated tool to assess the environment (Paoletti et al., 1991; Paoletti and Bressan, 1996; van Straalen, 1997; Erwin, 1997; Paoletti, 1999b; Gerlach et al., 2013). Usually the aim of bioindicator-based studies is to use the living components of the environment under study (especially those with the highest diversity, the invertebrates), as the key to assess the transformations and effects, and, in the case of landscape reclamation, to monitor the remediation process in different parts of the landscape over time (Paoletti, 1999b).

Several authors tried to classify bioindicators. McGeoch (1998) divided them into three classes: (a) environmental, (b) ecological and (c) biodiversity indicators, while Lindenmayer et al. (2000) divided them into seven groups, however the basic difference is that environmental and ecological indicators are used to detect changes in the environment, while biodiversity indicators reflect the diversity of the overall biota.

But why is it recommended to use bioindicators? One of the most important advantages is their cost-effectiveness: in fact by using bioindicators it is possible to assess the impact of human activities on the biota, instead of examining the entire biota (Rainio and Niemela, 2003). There are, however, some problems related to use of bioindicators. A difficult issue is the generalisation of results, for example, how well does one species or a species group represent the remaining biota? (Landres et al., 1988). Also for this reason the use of a single taxon representative of the general biodiversity state is now surpassed and the interaction of information derived by the study of many bioindicators is becoming more and more used (Paoletti et al., 1991; Paoletti et al., 2010; McMahon et al., 2012; Gerlach et al., 2013). In this respect in this study it has been chosen to analyse the presence and the abundance of multiple bioindicators in the same environment and their links with ES in the belowground and epigeal sectors. After the research phase, the next step would be to involve land-users into the practical use of soil health bioindicators and into adopting a more holistic management system approach to food and fibres production (Pankhurst, 2002).

Soil microbiology

The biological activity in soil is largely concentrated in the topsoil, the depth of which may vary from few to 30 cm. These biological components consist mainly of soil organisms, especially microorganisms. Despite of their small volume in soil, microorganisms are key players in a number of important biochemical processes as the cycles of bio-elements (carbon, nitrogen, phosphorous and sulphur), the energy transfers in soil ecosystem and the decomposition of organic residues. Thereby they affect nutrient and carbon cycling on a global scale (Pankhurst et al., 1997; Karaca et al., 2011). Microorganisms possess the ability to give an integrated measure of soil health, an aspect that cannot be obtained with physical/chemical measures. They respond quickly to changes; hence they rapidly adapt to environmental conditions and thus they can be used for soil health assessment, and changes in microbial populations as well as changes in microbial activities may therefore function as an excellent indicator of change in soil health (Pankhurst et al., 1995). The diversity is fundamental: in fact different microbes perform different functions in ecosystems, contributing to decomposition, by associating with different plant species and facilitating plant productivity by supplying different limiting nutrients (van der Heijden et al., 2008). Basic source of soil microbial activities is soil organic matter (OM) and, depending on the land use and other soil characteristics, microorganisms are in a continuous labour to govern soil OM and, in most cases like stress conditions caused by adverse anthropogenic effects, this can be rapidly reflected either to the microbial diversity level or to biologically active soil OM components such as microbial biomass, enzymes and other ephemeral organic compounds like proteins and carbohydrates (Karaca et al., 2011).

Bacteria

Bacteria are the main component of soil biota: in fact typically there are between 10^6 and 10^9 bacteria per gram of soil (Stirling, 2001). Bacteria are among the main responsible biota for OM decomposition, represented by important biochemical reactions (ammonification, nitrification, denitrification) that occur in soil and which involve the cycle of the nutrients; in this way OM is again readily available to plants. In particular, biological fixation of nitrogen occurs predominantly but not exclusively in symbiotic associations between plant roots and bacteria. The symbiotic bacterial genera most commonly involved are *Rhizobium* and *Bradyrhizobium,* which specifically infect leguminous plant roots. Moreover among the free-living bacteria, *Azotobacter, Azospirillum* and *Bacillus* may also contribute relatively small amounts of nitrogen to soils (Stirling, 2001). However among the multitude of soil bacteria there are some that cause harmful diseases in plants: to cite some examples *Erwinia*, which originates brown rot and *Agrobacterium*, which causes bacterial gall[7]. Bacteria play an important role in soil because their diverse metabolic capabilities enable them to exploit many sources of energy and carbon in soil. They are the principal agents for the global cycling of inorganic compounds such as nitrogen, sulphur and phosphorus (Stirling, 2001). In the following table the main bacterial functions into the soil are summarized.

[7] Data from Fitodifesa: http://www.fitodifesa.it/microorganismi/115-batteri.html

Soil bacterial functions	Decomposition of organic residues with release of nutrients
	Formation of beneficial soil humus by decomposing organic residues and through synthesis of new compounds
	Release of plant nutrients from insoluble inorganic forms
	Transformation of atmospheric N_2 to plant available N
	Improvement of soil aggregation, aeration, and water infiltration
	Antagonistic action against insects, plant pathogens, and weeds (biological control)

Tab. I: Principal bacterial functions into the soil (Kennedy, 1999).

A considerable number of studies deals with the community of soil bacteria or, generally, the overall soil microbial activity or biomass as bioindicators of soil conditions (Kennedy, 1999; van Bruggen and Semenov, 2000; Fliessbach and Mader, 2000; Adam and Duncan, 2001; Emmerling et al., 2001; Pankhurst et al., 2001; Schloter et al., 2003; Bending et al., 2004; Marinari et al., 2006; Franklin and Mills, 2009; Santos et al., 2012; Shi et al., 2013; Bardhan et al., 2013). In particular about the importance of studying soil microbial community, Bending et al. (2004) stressed that microbial parameters are more effective and consistent indicators of management practices that induce changes to soil quality than biochemical parameters and that a variety of biochemical and microbial analyses should be used when considering the impact of management on soil quality.

Fungi

About 70% of soil microbial biomass is contributed by fungi, whose numbers vary typically from 10^4 to 10^6 per gram of soil. Fungi may be free-living or have a mutually beneficial or parasitic relationship with plant roots. They exploit a diversity of substrates because of their filamentous nature and are decomposers of large molecules such as cellulose and lignin produced by plants (Stirling, 2001). Soil fungi are highly mobile organisms thanks to the spore stage in their life cycle and they are responsible for many ecological processes such as OM decomposition, pathogenicity to some species (especially with very humid climate), such as *Pythium, Phytophtora, Rhizoctonia, Armillaria, Plasmodiophora, Spongospora, Pennicillium*[8], but they are also responsible for important mutualistic interactions with the plant roots, called mycorrhizae.

Mycorrhizae are divided into three morphologically distinct groups, depending on whether or not there is fungal penetration of the root cells:

[8] Data from Fitodifesa: http://www.fitodifesa.it/funghi-patogeni/104-funghi-radicali.html

(1) endomycorrhizae, when the fungus penetrates in the root cells (intracellular interaction);
(2) ectomycorrhizae, when the fungus does not penetrate in the root cells (extracellular interaction);
(3) ectendomycorrhizae, when there is the combination of the two previous ones.

The most widespread plant root symbiosis is represented by arbuscular endomycorrhiza and is formed by more than 80% of plant families. All the fungi involved (AMF) belong to the Glomeromycota phylum and some known genera are *Glomus*, *Acaulospora*, *Gigaspora*, *Entrophospora*, *Sclerocystis, Scutellospora* (Gianinazzi et al., 2006). In tab. II the main effects of AMF into the soil ecosystem are summarized.

Effects of mycorrhizal symbiosis on plant and microbial communities	N and P mobilization from organic polymers (OM decomposition)
	Aid to plant host in the uptake of relatively immobile nutrients such as P, Zn, NH_4^+, Cu
	Release of nutrients from mineral particles or rock surface (weathering)
	Effects on C cycling
	Mediations of plant responses to stress factors and reduce damage (such as drought, soil acidification, toxic metals, plant pathogens- like *Fusarium*, *Pythium*, *Phytophthora*)
	Connection of the plant hosts to the heterogeneously distributed nutrients necessary for their growth
	Increase in the nutrient absorptive surface area of the host plant root system
	Supply by external mycelium to the plant host with an extensive supplementary pathway for absorbing water
	Provision of a larger surface area for interaction with other microorganisms
	Contribution to soil aggregate formation and soil stability at both micro- and macro- levels by enmeshing mineral and organic debris in a network of external hyphae

Tab. II: Main effects of the symbiosis between AMF and plant roots (from Stirling, 2001; Gianinazzi et al., 2006; Finlay, 2008).

Starting from the point that plants often grow badly in soils where AMF have been eliminated (Gianinazzi et al., 2006) one can notice that by acting as agents of nutrient transport, AMF form a vital link between plants and soil and therefore represent an important bioindicator of soil fertility (Stirling, 2001; Finlay, 2008). According to several studies fungi in general or AMF in particular are considered bioindicators of soil conditions (Pankhurst et al., 1995; Schloter et al., 2003; Andreson and Cairney, 2004; Gianinazzi et al., 2006; Finlay, 2008).

Soil enzymes

Mostly microorganisms and as well as plants and animals produce soil enzymes. Although certain soil enzymes are associated with viable cells, others remain catalytic in cell debris, in soil solution, or complexed with clay or organic colloids (Alkorta et al., 2003). In fact a greater production of organic colloids and aggregation should help to stabilize and to protect complexed enzymes in the soil matrix (Alkorta et al., 2003; Das and Varma, 2011; Nannipieri et al., 2011).

Soil enzymes are continuously playing an important role in maintaining ecology, physical and chemical properties, fertility and health of the soil system: in fact they catalyse several vital reactions necessary for life processes of micro-organisms and the stabilization of soil structure, they play key biochemical functions in the overall process of OM decomposition and nutrient cycles (Karaca et al., 2011; Das and Varma, 2011). In detail they are key elements in soil functioning due to:

(1) their role in decomposition of organic inputs,

(2) transformation of soil OM,

(3) releasing nutrients in available form to plants,

(4) participating in N_2 fixation,

(5) detoxification of xenobiotics (unnatural compounds such as pesticides, industrial wastes) and

(6) participating in nitrification and denitrification processes (Dick, 1997).

Hence they play an important role in agriculture and crop production. Often soil enzymatic activities are used as a useful tool for measuring soil biochemical quality as parameters (Doran and Zeiss, 2000), because they have been suggested as sensitive indicators due to the fact that they measure principal microbial reactions involving nutrient cycles in soil, they may easily respond to changes in soil by natural or anthropogenic factors and they can be easily measured (Das and Varma, 2011; Karaca et al., 2011).

Speaking about their role in agroecology, many studies showed that agricultural practices such as crop rotation, mulching, tillage, application of fertilizers, pesticides might have different effects on both soil enzymes and microbial activities and so soil enzymes can be indicators of agricultural practices but also more generally they can help to discriminate different farming systems (Alkorta et al., 2003; Fliessbach et al., 2007; Mina et al., 2008; Karaca et al., 2011; Das and Varma, 2011; Nannipieri et al., 2011). Moreover another useful application of monitoring soil enzymatic activities is the measurement of perturbations, such as for example may be an alternative way of monitoring overall effects of the introduced Genetically Modified Microorganisms on the ecosystem in a more sensitive and comprehensive way (Naseby and Lynch, 1997).

In detail tab. III shows the links between each enzymatic activity studied in this work and the corresponding ES driven by that soil enzyme.

Soil enzymes (indicators)	Organic substrate	End product	Information about soil ES
Arylsulfatase (AryS)	Sulfate esters	Inorganic sulfate (SO_4)	S-cycling (limiting nutrient); disease suppression by applying organic amendments
β- glucosidase (Gluc)	Carbon compounds (cellulose)	Glucose	C-cycling; different tillage systems; soil pH
Acid phophomonoesterase (AcP)	Organic phosphoric compounds (nucleic acids)	Inorganic phosphate (PO_4)	P-cycling; fertilization system (manure); soil fertility
Pyrophosphate-phosphodiesterase (Piro)	Organic phosphoric compounds (nucleic acids)	Inorganic phosphate (PO_4)	P-cycling; fertilization system (manure); soil fertility
Alkaline phosphomonoesterase (AlkP)	Organic phosphoric compounds (nucleic acids)	Inorganic phosphate (PO_4)	P-cycling; fertilization system (manure); soil fertility
Leucine aminopeptidase (Leu)	Peptides	Amino acids	N-cycling; proteic metabolism; N mineralization
Acetate- esterase (Ester)	Acetic esters	Alcohol, acetate	Global enzymatic activity; aromatic molecules, polyesters (PBS) and pollutants degradation

Tab. III: Summary of the activity (substrate, end product) and the utility for ES functionality indication for each enzyme considered in this work (elaborated from Sakai et al., 2002; Alkorta et al., 2003; Makoi et al., 2008; Karaca et al., 2011; Das and Varma, 2011; Nannipieri et al., 2011).

By studying the activity of these seven soil enzymes it is possible to have an overview concerning the C, P, N, S macronutrients cycling and for this reason they can be considered key soil enzymes.

Soil mesofauna

Soil mesofauna is the set of soil invertebrates, which size is comprised between 0,2 and 4mm such as for example mites, springtails, psocoptera, miriapoda, pseudoscorpionida, ants and many juvenile forms of soil insects (fig. 2) (Bachelier, 1986).

Fig. 2: Examples of edaphic mesofauna
(http://www.agencia.cnptia.embrapa.br/gestor/sistema_plantio_direto/arvore/CONT000fwuzxobq02wyiv807fiqu95qsd16v.html).

Population densities vary from 10 to 10^7 per square meter of soil and they are generally highest in the first 5 cm of topsoil and decline with increasing depth (Stirling, 2001). They are a heterogeneous group with a wide range of feeding habits, but collectively they play a role in:

(1) regulating microbial populations,
(2) disseminating microbial propagules,
(3) degrading OM,
(4) accelerating decomposition of plant residues by fragmenting large pieces of OM,
(5) reworking the faeces of larger fauna,
(6) acting their function of biological control of small plant parasites,
(7) sustaining trophic web (in fact they can be numerous preys) (Stirling, 2001; Renker et al., 2005).

Living at different depths into the soil, they present a range of several morphological features resulting from adaptations to edaphic life as reduction or loss of body pigmentation, streamlined body form, with reduced and more compact appendages (hairs, antennae, legs), reduction or loss of flying, jumping or running adaptations (with consequent decrease of dispersal ability), anophthalmia or reduction of the visual apparatus, reduced water-retention capacity (thinner cuticle, lack of hydrophobic compounds on the outer surface) (Parisi, 1974).

They are considered bioindicators of soil conditions (Paoletti et al., 1991), in particular there are studies concerning the role in biological control and bioindication of mesostigmatic mites (Koehler, 1997,1999; Salmane, 2000; Beaulieu and Weeks, 2007), of oribatid mites (Paoletti et al., 1995; Behan-

Pelletier, 1999; Ruf and Beck, 2005; Paoletti et al., 2007) and mites in general (Gulvik, 2007), but also there are researches focused on the role of springtails in bioindication (Paoletti et al., 1995; Rusek, 1998; Greenslade, 2007; Paul et al., 2011). Apart studies concerning the role of one single mesofaunal group in bioindication, there are also studies about cumulative indexes that take into account the presence in a target habitat of different organisms and with different edaphic adaptations, such as QBS-ar index (Parisi, 2001), which is based on the concept: the higher soil quality, the higher will be the number of microarthropod groups well adapted to soil habitats, separated according to the biological form (Parisi et al., 2005) or mites/springtails ratio (Bachelier, 1986) according to it in conditions of soil equilibrium, the quantity of mites is higher than the one of springtails and it tends to decrease in favour of springtails with the increase of soil degradation.

Earthworms

Earthworms belong to macrofauna (which size ranges from 4mm to 80mm) but some individuals can belong also to megafauna (>80mm) (Bachelier, 1986). These Annelida Oligochaeta are considered soil engineers as they are able to modify soil structure and features with their etho-physiological action (Blouin et al., 2013) (fig. 3).

Fig. 3: (a) Adult of *Allolobophora caliginosa*, one of the most abundant endogeic species found in the agroecosystems studied in this work, with two cocoons resulted from its reproduction. Several burrows are visible made by etho-physiological activity of earthworms; (b) Adult of *Octodrilus complanatus*, anecic species sampled with mustard powder suspension; (c) Adult of *Allolobophora chlorotica*, endogeic species; (d) Adult of *Lumbricus terrestris*, anecic species (Ph. S. Fusaro).

It is possible to recognise three types of effects of earthworm activity on soil (Lee, 1985; Dell'Agnola and Nardi, 1987; Pérès et al., 1998; Paoletti, 1999a; Stirling, 2001; Blouin et al., 2013), which are:

- the physical effects, which result from excavation of burrows and production of casts (fig. 3). Burrows provide a pathway for the movement of surface water and large particles from the surface to deeper layers and ready access for plant roots to penetrate the soil. Moreover they have influence on soil porosity through the production of macroporosity (mainly burrows or aestivation chambers), mesoporosity and microporosity (mainly casts), practically on water infiltration and aeration deep into the soil. They can therefore improve the conditions of anoxia and allow the correct action of aerobic bacteria. They also may influence solute leaching through soil and hence the capacity of soil to function as an environmental buffer. Casts consist of mixed inorganic and organic materials from the soil that are voided after passing through their intestine; they contribute to pedogenesis, soil profile development and structure.

- the chemical effects, which consist in chemical weathering produced by earthworms, microorganisms stimulated in their gut or by a collective action of both organisms, with the result of OM decomposition taking partially decomposed plant litter from the soil surface and producing OM humified soil horizon. In this case they are responsible of the humification rate. In detail after digestion, some organic compounds are released into the soil as small organic compounds or mineral nutrients: in fact their casts enrich the soil of macronutrients (especially N) and then make it better for the growth of plants.

- the biological effects, which consist mainly in interactions (symbioses) with soil microorganisms (bacteria and fungi) by ingesting them together with litter and contributing to their dispersal. Moreover their activity results in an increase in the surface area of organic substrates available for microbial activity.

Another important feature of earthworm community of an environment is the distinction in different ecological categories supported by literature (Bouché, 1972; Sims and Gerard, 1985; Lee, 1985; Edwards, 1998; Paoletti, 1999a; Paoletti et al., 2013):

- Epigeic, dorsally pigmented, living in the litter or in A01 horizon of soil profile, with scarce digging capacity (i.e. *Lumbricus castaneus*);
- Endogeic, usually but not always less pigmented, living between A02 and A1 horizons, able to dig mainly horizontal burrows (i.e. *Allolobophora caliginosa* -fig. 3(a));
- Anecic or deep burrowers, even large size, can reach A2 and B soil horizons, able to dig vertical burrows up to a few meters in depth, but often rise to the surface to feed on litter (i.e. *Octodrilus complanatus*- fig.3(b));
- Coprophagic, living in manure or compost and closely associated with it (i.e. *Eisenia foetida*);
- Hydrophilic, living in soils with high groundwater (i.e. *Eiseniella tetraedra*).

Many studies considered earthworms as bioindicators of soil state and fertility (Paoletti et al., 1991; Pfiffner and Mader, 1997; Paoletti, 1999a; Kingston, 2001; Lavelle et al., 2007; Peigné et al., 2009; Paoletti

et al., 2013). Not only from environmental point of view earthworms are important in agroecosystem, but also for their implication in crop production. In fact van Groeningen et al. (2014) with a meta-analysis demonstrated that earthworm presence significantly increases crop yield by +25%, aboveground biomass by +23%, belowground biomass by +20% and total biomass by +21%.

Natural control agents of crop pests

The damage caused by phytophagous insects (crop pests) in agriculture is one of the most important problems for crop production. Despite intensive use of pesticides, (Pimentel, 1997) estimated potential crop losses during pre-harvest due to insects (13%), diseases (12%) and weeds (12%) in the United States, whereas worldwide the crop losses due to insects reaches 15% or more. Most benefits of pesticides are based on the direct crop returns. Although pesticides are generally profitable in agriculture, their use does not always decrease crop losses and moreover they cause estimated environmental and societal damages for an amount of $10 billion just in the United States (Pimentel, 2005). For this reason natural control of crop pests is a flourishing branch of agroecology and represents a key ES necessary to have a sustainable crop production system (Bianchi et al., 2006; Losey and Vaughan, 2006). Natural enemies such as predators, parasitoids and pathogens play a central role in limiting damage from native and exotic pests (Losey and Vaughan, 2006). Conservative estimates suggest that the economic value provided by wild insect natural enemies controlling pests attacking crop plants is about $4.5 billion per year only in the United States (Losey and Vaughan, 2006).

Carabids

Among coleoptera, Carabidae family consists of 40.000 known species worldwide, of which 12.000 are known for Italy (Lovei and Sunderland, 1996; Brandmayr et al., 2005). Carabid beetles are epigeal geophylous insects whose spatial distribution and morpho-ecological adaptation (for example wing morphology, diet and body dimension) are strongly influenced by the physical (such as humidity, temperature) and the chemical (such as pH, heavy metal concentration) soil parameters. For this reason, these insects are considered good indicators of the effects of environmental changes like soil warming, management, pollution etc. on soils and humus forms (Lovei and Sunderland, 1996; Gobbi, 2000).

Fig. 4: Adult female of *Carabus coriaceus* an example of carabid species with big body dimension (30-40mm length), sampled with pitfall traps during this work (Ph. S. Fusaro).

Concerning their trophic strategies, carabids can be divided in:

- olfactory-tactile predators, with medium or less developed compound eyes, generally nocturnal locomotory activity, very variable prey choice (generalist), widespread mainly in semi-natural habitats (i.e. genus *Carabus* -fig. 4);

- visual predators, with enlarged compound eyes that cover the anterior-superior head surface, typically daytime locomotory activity, they can be generalist but also specialist, common in environments with bare soils or poor herbaceous vegetation (i.e. *Asaphidion*, *Cicindela*, *Notiophilus*);

- spermophagous, with enlarged based and bluff mandibles, normal size eyes, locomotory activity during day or night, still regularly present predatory behaviour (zoospermophagous i.e. *Amara*, *Harpalus*) or completely absent (exclusive spermophagous i.e. *Ophonus*), common in habitats like grassland or meadows (Lovei and Sunderland, 1996; Brandmayr et al., 2005).

If they are generalist predators (polyphagous), the most common ones as well as the larvae of most species (Lovei and Sunderland, 1996; Kromp, 1999), they can help to take under control crop pest outbreaks (mainly aphids, dipterans, lepidopterans, slugs), but in general their major beneficial role is to prolong the period between pest outbreaks and so they can have an important role in natural pest control ES in

agroecosystems (Thiele, 1977; Lovei and Sunderland, 1996; Kromp, 1999; Holland and Luff, 2000; Guseva and Koval, 2013).

Another important role they exert in agroecosystem is the potential as biological weed control due to spermophagous feeding habits of certain species such as *Harpalus* and *Amara* (Kromp, 1999).

Usually carabid trophic preferences can be utilized as biological parameter to evaluate anthropic impact on habitat. Along an "increasing trophic opportunism" the most sensible elements are the specialist predators, then the generalist predators, then exclusive spermophagous and finally the most adaptable zoospermophagous, which are able to eat both various preys both cultivated plants or weeds (Thiele, 1977; Brandmayr et al., 2005).

More in general, carabids are considered useful bioindicators because of some advantages, such as easy and cheap sampling by the use of pitfall traps (see in materials and methods), species assemblages, species richness, adaptive parameters of species, like flying ability, body dimension and diet, but most of the researches have been done in environments such as grasslands, cereal fields, boreal and temperate forests (Luff, 1996; Rainio and Niemela, 2003). In agroecosystems carabids have been used as bioindicators of environmental quality and sustainability of management practices (Kromp, 1999; Doring and Kromp, 2003; Gobbi and Fontaneto, 2005) and in particular they were used as bioindicators also in horticultural crops (Lupi et al., 2007). Moreover using carabids as environmental conservation bioindicators, it is possible to distinguish for carabids a "potential community" typical of theoretically undisturbed conditions, from a "real community" due to impact of human activities; between these two situations then it is possible to identify several alteration and substitution stages whit respect to original community (Brandmayr et al., 2005).

Other generalist and specialist predators

Not only carabids can act as predators in agroecosystems. There is a plethora of other arthropods enumerated among predators and therefore being part of beneficial fauna. Spiders, harvestmen, rove beetles, ladybirds, hoverflies, lacewings, minute pirate bugs, damsel bugs are among the most common predators that can be found in cultivated environments.

They can be specialist or generalist, according to the feeding habit of a usual type of prey or many types. Ladybirds (Coleoptera: Coccinellidae), hoverflies (Diptera: Syrphidae) larvae or lacewing (Neuroptera: Chrysopidae) larvae are examples of predators specialized in feeding of aphids (Sommaggio, 1999; Burgio et al., 2006; Gardiner et al., 2009), while spiders (Araneae), harvestmen (Opiliones) or rove beetles (Coleoptera: Staphylinidae) are not selective predators (Sunderland, 1975; Sunderland et al., 1987; Nyffeler and Symondson, 2001; Maloney et al., 2003). To be more precise in many arthropod species, there is a switch between predatory and plant-feeding habits at different life stages: for example hoverflies and lacewings have predaceous larvae and plant-feeding adults (fig. 7) (Alomar, 2007). Indeed there is another term to indicate consumption of materials at another trophic level within the same developmental stage: this is facultative; therefore in a continuum of feeding habits can be recognised phytozoophagy or

zoophytophagy. The mainly contribution of facultative predators to biological control of crop pests is prevention rather than eradication of pest outbreaks (Alomar, 2007).

Often the presence of predators in general was studied in agroecological researches, because they can contribute to prevent crop pest outbreaks (Landis et al., 2000; Guseva and Koval, 2013) and in some studies just one group was considered like bioindicator, for example hoverflies (Sommaggio, 1999; Burgio and Sommaggio, 2007; Bokina, 2012), rove beetles (Bohac, 1999; Guseva and Koval, 2013), spiders (Isaia et al., 2006; Chatterjee et al., 2009) (fig. 5), while in some other ones more predator groups were considered together (Burgio et al., 2006; Gardiner et al., 2009; Schellhorn et al., 2014).

Fig. 5: Two examples of generalist predators found during the fieldwork: (left) a spider (*Argiope bruennichi*) on its web with the stabilimentum in the cropfield while preying an adult of cabbage butterfly (*Pieris* sp.); (right) a rove beetle (*Paederus fuscipes*) with a prey in its mandibles (Ph. S. Fusaro).

Parasitoids and hyperparasitoids

Parasitoids are insects mainly belonging to the orders of Hymenoptera and Diptera, which, during their life cycle need to develop exploiting the body of a host species, killing it. They are second level consumers as well as predators. There are two principal types of parasitization (Van den Bosch et al., 1982; Godfray, 1994):

- ectophagy, in which parasitoids develop outside the host body that is paralyzed from toxins injected by female while egg laying;
- endophagy, in which parasitoids develop inside the host body, eluding its immune defences (fig. 6).

As regard trophic specialization, a parasitoid can be monophagous (specialist adapted to a life stage of one host species), oligophagous or polyphagous (generalist). Moreover concerning host exploitation strategies there can be:

- superparasitism, a condition in which several larvae (more than one) of the same species of parasitoid develop simultaneously on the same host individual (gregarious parasitoids) and can be an example of intraspecific competition (fig. 6) and
- multiple parasitism, a condition in which parasitoids of different species attack a single host and can be described as an interspecific competition event (Mills, 1994).

A natural parasitoid community consists of an assemblage or complex of primary parasitoid species that exploits the population of a host species in a given locality (Mills, 1994). Since it is frequent that in agroecosystems the target host is a crop pest, parasitoids are considered a group of natural enemies and play a very important role in regulating pest populations (Landis et al., 2000; Buchori et al., 2008; Gardiner et al., 2009; Macfadyen et al., 2011).

Fig. 6: Above: (left) *Autographa gamma* adult; (right) *A. gamma* caterpillar, a polyphagous common crop pest. Below: (left) *A. gamma* caterpillar on which the first stage of parasitization is visible; (middle) first evidences of puparia of diptera parasitoid *Voria ruralis* (Tachinidae); (right) open puparia after *Voria ruralis* hatching. This is an example of endophagy and superparasitism (Ph. S. Fusaro).

Besides parasitoid Hymenoptera were considered also bioindicators to assess the wider biodiversity of arthropod populations in agroecosystems (Anderson et al., 2011), but also to assess agroecosystem management sustainability (Macfadyen et al., 2009; Macfadyen et al., 2011; McMahon et al., 2012) and landscape structure complexity (Marino and Landis, 1996; Thies et al., 2005; Tscharntke et al., 2007; Schellhorn et al., 2014).

Hyperparasitoids or secondary parasitoids are insects considered third level consumers. They develop at the expense of a primary parasitoid, so they may have a considerable influence on the "top-down" control of crop pest populations by parasitoids (Sullivan and Volkl, 1999). They were included in several researches focused on pest control ES efficiency (Lohaus et al., 2013; Nofemela, 2013; Harvey et al., 2014).

Wild plants and weeds

An appropriate non-crop vegetation management in the agroecosystem can moderate soil degradation by reducing water evaporation, preventing soil erosion and regulating soil nutrient content (Akobundu, 1992). Moreover wild plants can provide information about soil conditions as well as climate changes (Peters et al., 2014). In fact wild plants and weeds are considered bioindicators of soil conditions due to their ecological requirements: plant species can be stenoecious/euryecious (if they can live only in a restricted range or wide range of conditions respectively), ruderal, endemic. For example the local weed complex can be affected by soil chemical composition, mainly the available amount of K, N, P, as well as by soil pH (Altieri and Letourneau, 1982; Ducerf, 2007), but also they can be bioindicators of soil management practices, as for example the use of herbicides that can cause a shift in weed communities, selecting for resistant biotypes or soil disturbance due to mechanical practices (ploughing, mowing, rotary tillage, soil compaction) (Altieri and Letourneau, 1982; Ducerf, 2007; Benvenuti, 2007; Gago et al., 2007; Nascimbene et al., 2013). Besides weed species diversity was considered a bioindicator influenced by landscape complexity as well as farming system (Roschewitz et al., 2005; Nascimbene et al., 2012).

Non-crop plants as support for useful biodiversity

Since as a result of frequent and intense disturbance regimes many agroecosystems, especially the annual ones, are recognized as particularly difficult environments for natural enemies (affected seriously in abundance and efficiency), the goal of farm habitat management is to create a suitable ecological infrastructure within the agricultural landscape to provide resources such as food (pollen and nectar) for adult natural enemies, alternative preys or hosts, shelter from adverse conditions, nesting and overwintering sites (Altieri and Letourneau, 1982; Landis et al., 2000). Moreover as regarding the facultative predators, many of them require foods that are often not available in crops and therefore consumption of plant foods may provide essential nutrients for their diet or are a substitute resource when prey are scarce and thus play a critical role in maintaining predators (Alomar, 2007).

Wild plants and weeds (non-crop plants) are a fundamental part of these ecological infrastructures (Altieri and Letourneau, 1982; Nentwig, 1998). Several studies focused on the important influence of non-crop plant diversity on the maintenance and improvement of useful biodiversity (pollinators and natural enemies–fig. 7) in agroecosystems (Nentwig, 1998; Vattala et al., 2006; Burgio et al., 2007; Bianchi and Wackers, 2008; Batary et al., 2013; Fabian et al., 2013; Lysenkov, 2014).

Fig. 7: Example of attraction for useful fauna due to wild flowers (*Sonchus* sp.). (Left) *Episyrphus balteatus*, a common hoverfly while eating pollen source from a wildflower grown next to the crop field. (Right) Larva of hoverfly while preying an aphid in the cropfield (Ph. S. Fusaro).

GENERAL AIM AND OBJECTIVES

The general aim of this research is to evaluate and compare the environmental sustainability of agroecosystems with different management practices, by using bioindicators belonging to key trophic levels of agroecosystem food web and which are the main groups of functional biodiversity, and functional indicators. The main hypothesis is:

Environmental sustainability of the farming system will be improved,

if ecosystem services will be more efficient.

Some key ES have been selected such as OM degradation and decomposition, soil respiration, soil enzymatic activities, soil nutrients recycling, air and water circulation into the soil, improvement of root-soil-water relationships, soil microbial activity, soil structure conservation in the belowground sector and biological control of crop pests, attraction of pollinators in the cropfield area, sources of shelters and alternative food for useful fauna in the epigeal sector (fig. 8).

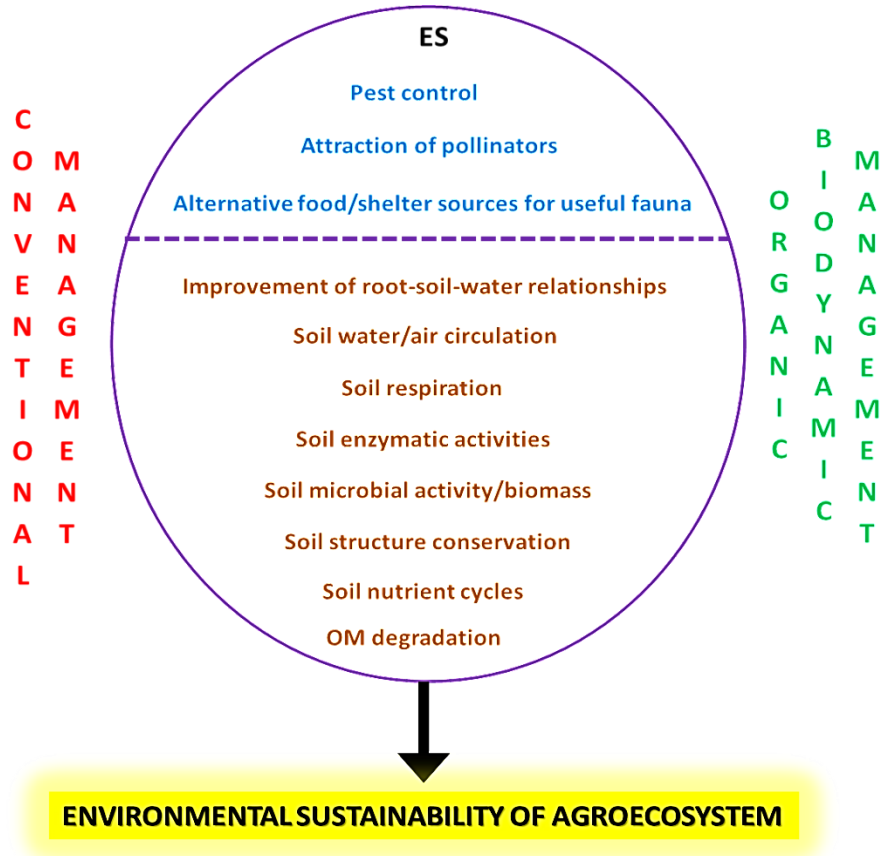


Fig. 8: Scheme of the research general aim. ES: ecosystem services; OM: Organic Matter. Brown: ES that take place in the belowground sector; Blue: ES that take place in the epigeal sector.

To study the efficiency of these ES, the diversity of groups of organisms mainly responsible of them has been considered. The choice of using several bioindicators, providing the basic ES listed above, as tools of analysis is in line with the need to optimize economic resources and time. Moreover, to date there are few studies using such a large number of bioindicators simultaneously to evaluate ES efficiency in agroecosystems.

In detail, the specific objectives are to answer the following questions:

(1) Can different agroecosystem managements (organic/conventional) change taxa composition of the different bioindicator groups in horticultural crops?

(2) Is a higher biodiversity always linked to higher efficiency of ecosystem services in the agroecosystem?

(3) Which ecosystem services are more efficient in each of the two agroecosystem management types (organic vs. conventional)?

(4) Are there correlations between different functional indicators? Are some indicators more informative and representative of the overall on-going phenomena? Can we choose one single indicator and spare monitoring analysis costs?

STUDY CASES AND METHODS OF SAMPLING AND ANALYSES

Crops under analysis

In Europe, Italy is the leading country for the production of vegetables, representing 22% of the total production (FAOSTAT, 2012). Horticultural fields are generally less extensive than cereal ones: the area occupied for horticultural crops is seven times less than the one occupied for cereal crops (ISTAT, 2011). In the Veneto region horticultural agroecosystems cover 33400 ha (1.8%) of the total regional surface[9] and they are sites of production of more typical crop species or varieties (Elia and Santamaria, 2013). In addition horticulture usually requires more manpower and therefore a greater investment of people and resources to obtain a higher valuable quality product but in smaller quantities (Cisilino and Madau, 2008; FAOSTAT, 2014). Since horticultural vegetables are often strictly linked to a particular region, concerning global food security, Godfray et al. (2010) underlined how, in order to increase the global efficiency of food production it is also important to allow regional specialization in the production of the locally most appropriate foods. In the present research two Italian typical crops were chosen.

Cichorium intybus

Treviso red chicory (fig.10) is a typical chicory of the Veneto Region (North-Eastern Italy) that in the recent years has been gaining increasing commercial interest (Nicoletto and Pimpini, 2010). In tab. IV some of its features are summarized.

Botanical name	*Cichorium intybus* L., group *rubifolium*
Common name	Treviso red chicory
Family	Asteracea (Compositae)
Life cycle	Biennial (wild plant)- Annual (commercial plant)
Sowing	Early summer

[9] Data from ISTAT webservice elaborated by VenetoAgricoltura available on website: http://www.venetoagricoltura.it/basic.php?ID=3743

Harvest	From autumn to late winter (according to the variety)
Raunkiaer life form	Hemicryptophyte
Pollination	Entomophilous
Floral formulae	K 0, C (5), A(5), G 2 inferior
Inflorescence	Flower head (light blue)
Fruit	Achene
Agronomical requirements	N: low need; P: medium need; K: high need
Edible parts	Leaves

Tab. IV: Botanical, agronomical and commercial features of Treviso red chicory (Pignatti, 1982; Accorsi et al., 2011).

Two varieties of Treviso red chicory can be recognised:

- late variety[10], characterized by deep and bright red colour leaf sheets, as well as white elongated prime rib, regular, uniform and with good compactness shoots; leaves lockouts, enveloping that tend to close the clump in the apical part; clump together with a portion of the taproot perfectly prepared and of length proportional to the size of the head, however not more than 6 cm.
- early variety[11], characterized by massive, elongated, tightly closed head, accompanied by modest portion of the root; deep red and wider leaf sheets, with a broader white prime rib and white thinner secondary ribs.

As concerns its origin, it is probable that all the varieties in commerce derive from Treviso red chicory late variety, as in the scheme of Nicoletto (2010) (fig.9).

[10] Data from Consorzio Tutela Radicchio rosso di Treviso: http://www.radicchioditreviso.it/cms/index.php?option=com_content&view=article&id=12&Itemid=22
[11] Data from Consorzio Tutela Radicchio rosso di Treviso: http://www.radicchioditreviso.it/cms/index.php?option=com_content&view=article&id=15&Itemid=21

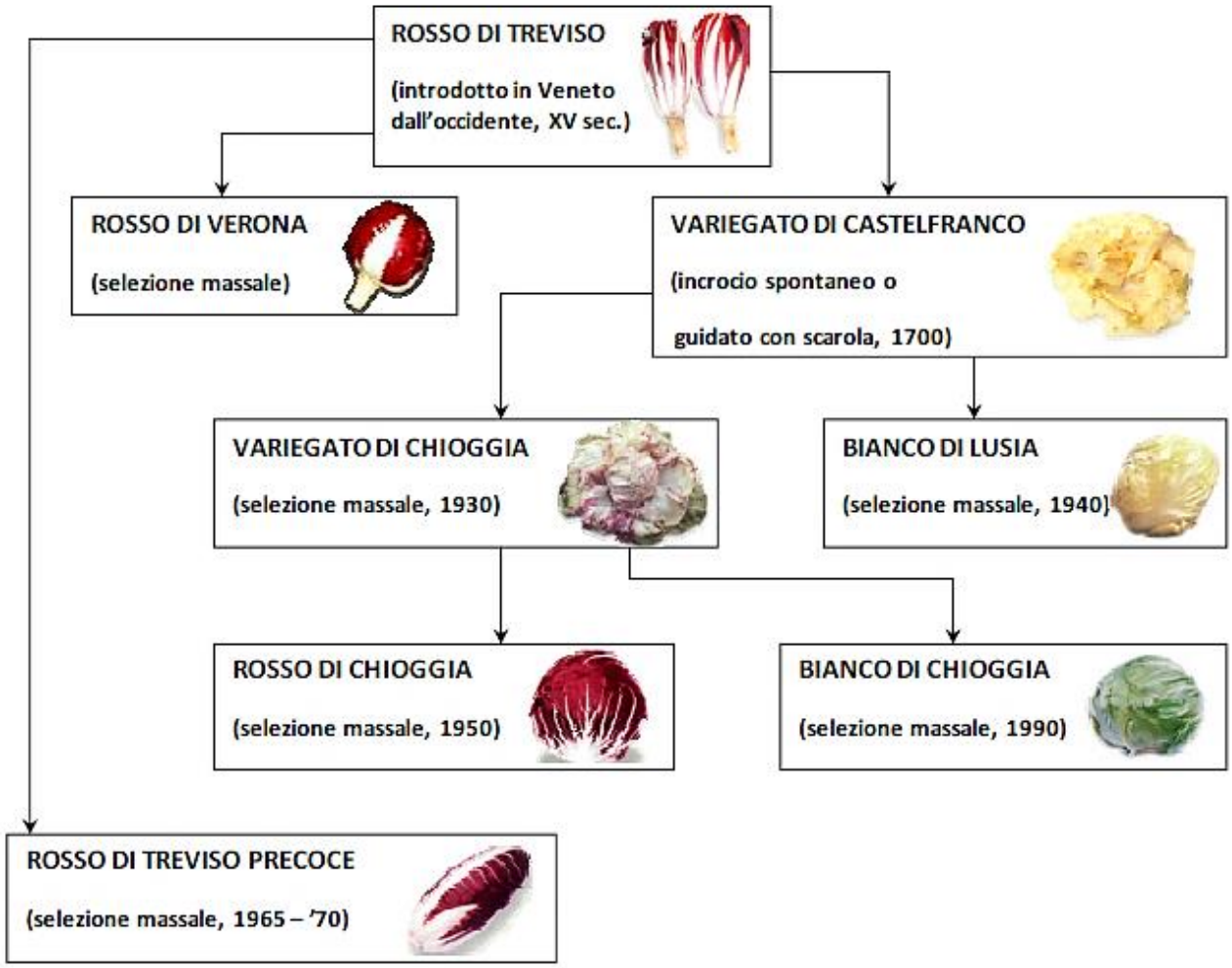


Fig. 9: Varieties of *Cichorium intybus* and their origins, from Nicoletto (2010): the first one on the top (late variety) and the last one on the bottom (early variety) were chosen for this research.

In this research Treviso red chicories belonging to late and early varieties were chosen (fig. 9).

Brassica oleracea

White cabbage (fig. 10) is widespread worldwide. All varieties of the species *Brassica oleracea* originated in Europe and Asia. In tab. V some of its features are summarized.

Botanical name	*Brassica oleracea* L. var. *botrytis*
Common name	White cabbage, cauliflower
Family	Brassicaceae (Cruciferae)
Life cycle	Biennial (wild plant)- Annual (commercial plant)
Sowing	Early summer

Harvest	From autumn to late winter (according to the variety)
Raunkiaer life form	Hemicryptophyte
Pollination	Entomophilous
Floral formulae	K 2+2, C 4, A 2+4, G (2) inferior
Inflorescence	Corymb (yellow flowers)
Fruit	Siliqua
Agronomical requirements	N: high need; P: high need; K: medium need; It likes S and Ca
Edible part	Corymb

Tab. V: Botanical, agronomical and commercial features of white cabbage (Pignatti, 1982; Accorsi et al., 2011).

After the rosette stage (a circular arrangement of leaves, with all the leaves at a similar height), new leaves develop with shorter petioles and the leaves begin to cup inward to envelop the head. Head is white, round, compact or slightly flattened. Leaf texture is from smooth to crinkled and leaf colour is light green, with thick prime rib (Delahaut and Newenhouse, 1997).

Depending on climate required for the corymb formation, it is possible to distinguish early cultivars, which do not require a period of low temperature (vernalization), and late cultivars, which require a chilling period of variable duration (20-40 days), as a function of relative precocity. In any case, in all cultivars, both early and late, the induction of corymb formation is only after the plants have reached a certain stage of the vegetative phase, which is identifiable with a number of leaves, which is different in function of the relative precocity of the cultivar. There are three main cultivars, according to the development period:

- early cabbages, which can develop in 60-100 days;
- medium cabbages, which can develop in 110-140 days;
- late cabbages, which can develop in 150-230 days (Santamaria and Serio, 2009).

In this research cabbages were chosen belonging to Naruto variety, which is a medium cultivar (110-120 days).

Fig. 10: Treviso red chicory (left) and white cabbage (right): the crops chosen for this research (Ph. S. Fusaro).

Study sites

Ten study sites were considered in this research, everyone belonging to different farm located in the Venetian plain in the provinces of Venice and Treviso, North-Eastern Italy. These farms are specialized in horticultural crops production since years and the studied fields have been cultivated since at least the late 90s (tab. VI).

Conventional and organic-biodynamic fields, producing the same type of crop, were compared and in the same area, in order to reduce the climatic condition and landscape structure differences. The fields chosen in pairs were from 250m to 6,5km far from each other (fig.11). By interviewing the farmers information was collected concerning the agronomical history of the examined fields and the management practices adopted during the sampling period (2012-2013).

Farm (code)	Sampling Year	Management	Agronomical history	Position
Madre Terra (**BiMt**)	2012-2013	Organic	Horticulture with crop rotation- certified since 2000	Santa Maria di Sala (VE)
Biogatta (**BiBg**)	2012-2013	Organic	Horticulture with rotation- certified since 2000	Zelarino (VE)

Cà Manuela (**BiCm**)	2012-2013	Organic	Horticulture with crop rotation- certified since 2007	Asseggiano (VE)
San Michele (**BdTm**)	2012-2013	Biodynamic	Horticulture with crop rotation - Certified since 1992	Breda di Piave (TV)
Tre Marie sul Piave (**BdTmp**)	2012	Biodynamic	Horticulture with crop rotation- certified since 2007	Maserada di Piave (TV)
Mandato (**CoMa**)	2012-2013	Conventional	Horticulture with crop rotation since 1982	Ballò di Mirano (VE)
Mion (**CoMi**)	2012	Conventional	Horticulture with crop rotation since 1989	Mirano (VE)
Zabeo (**CoZa**)	2013	Conventional	Horticulture with crop rotation since 1925	Zigaraga - Salzano (VE)
Zorzetto (**CoZo**)	2012-2013	Conventional	Horticulture with crop rotation since 1987	Villetta prima - Salzano (VE)
Uliana (**CoTmp**)	2012	Conventional	Arable crops (soy- wheat) with rotation since at least late 90s	Maserada di Piave (TV)
Uliana (**IncTmp**)	2013	Untilled		
Case Nuove (**CoTm**)	2012	Conventional	Arable crops (corn) since 1992	Breda di Piave (TV)

Tab. VI: List of sampled fields with codes used in the text from now on.

Details on all management practices are listed in the tabb. LV and LVI (in the appendix) and information on pesticide treatments are summarized in tab. LVII (in the appendix).

Meteorological characterization of study sites

During the sampling period (2012-2013) meteorological data were collected from three different ARPAV weather stations[12] located nearby the study areas (fig.11):

- Breda di Piave (TV) weather station;
- Favaro Veneto (VE) weather station;
- Mira (VE) weather station.

In particular, when available, data of total precipitation (mm), mean temperature (°C) at soil surface and mean temperature (°C) at 2 m a.s.l. were collected for each day (fig.12).

[12] Data available on ARPAV website: http://www.arpa.veneto.it/bollettini/meteo60gg/Mappa_TEMP.htm

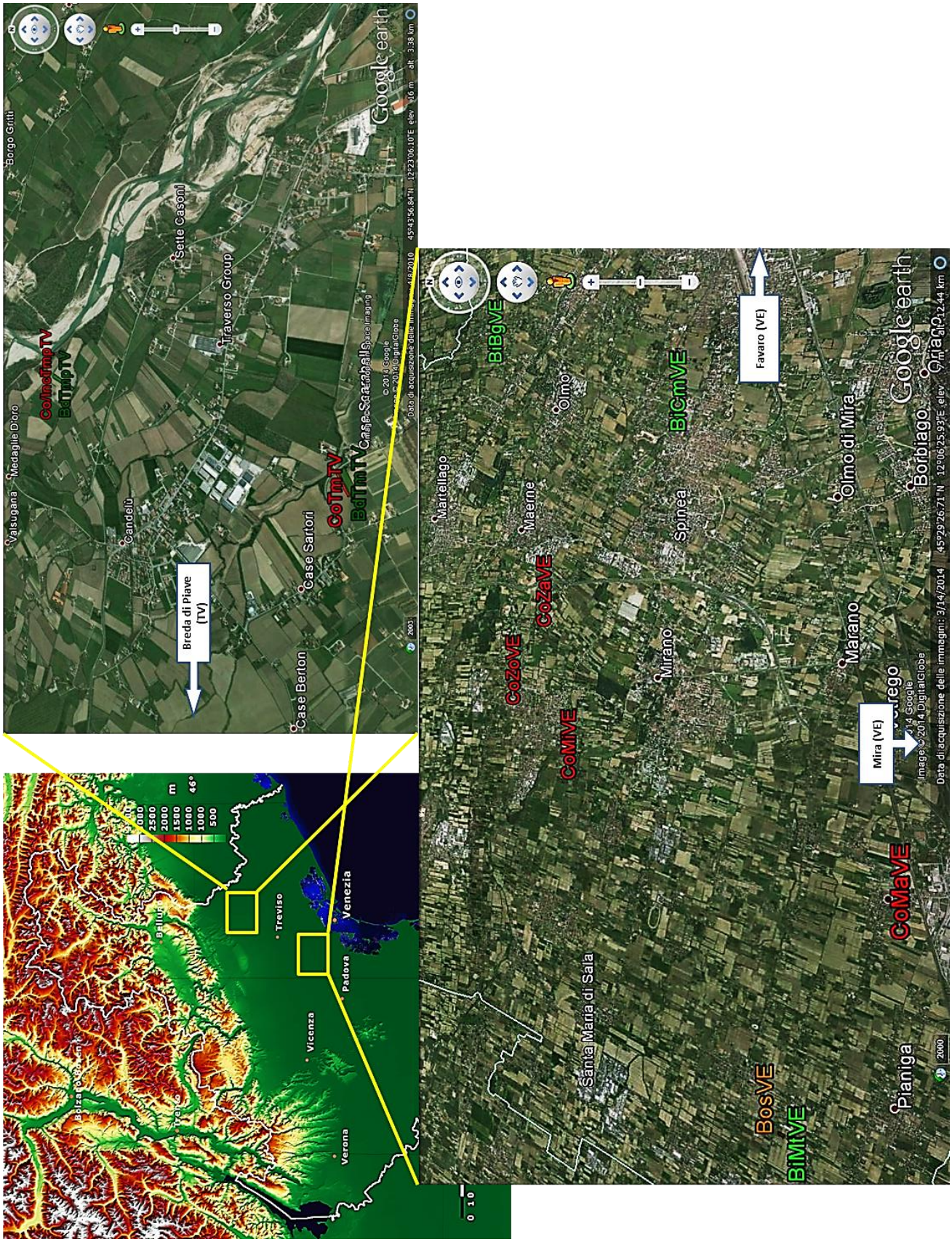
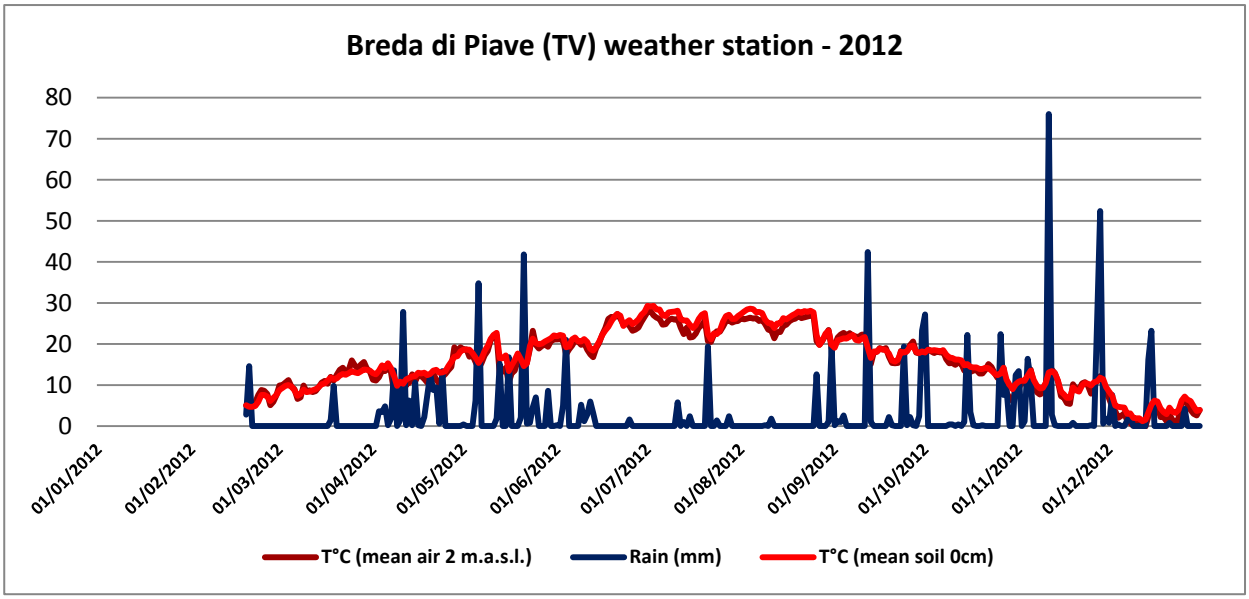
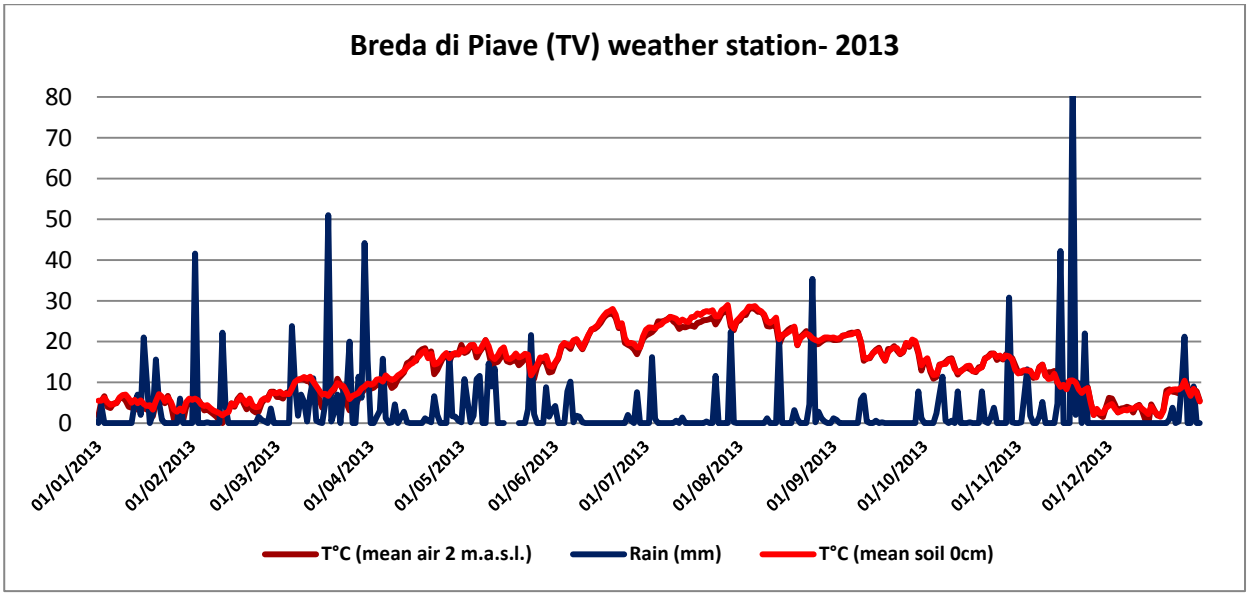


Fig. 11: Map with the position of farms object of this study. Image elaborated from Google Earth. Below: detail of field position in the Venice province. Right: detail of field position in the Treviso province. Red: conventional fields; light green: organic fields; dark green: biodynamic fields; brown: semi-natural environment; white rectangular: position of weather stations.

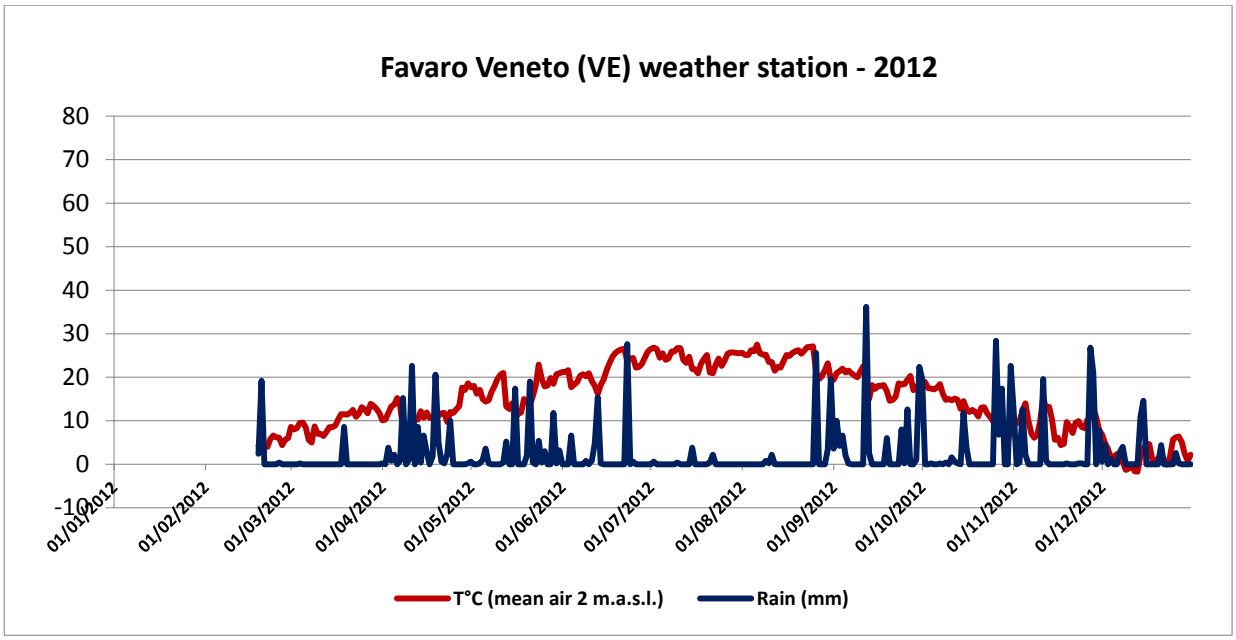
The following charts show the detailed weather data collected during the fieldwork period.



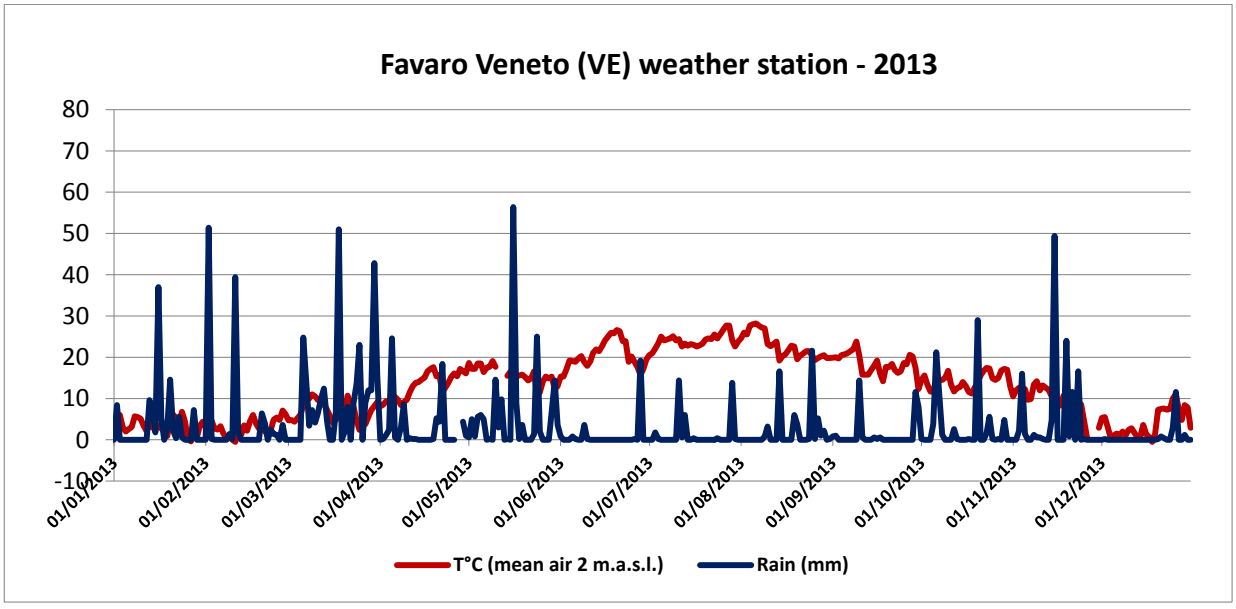
a)



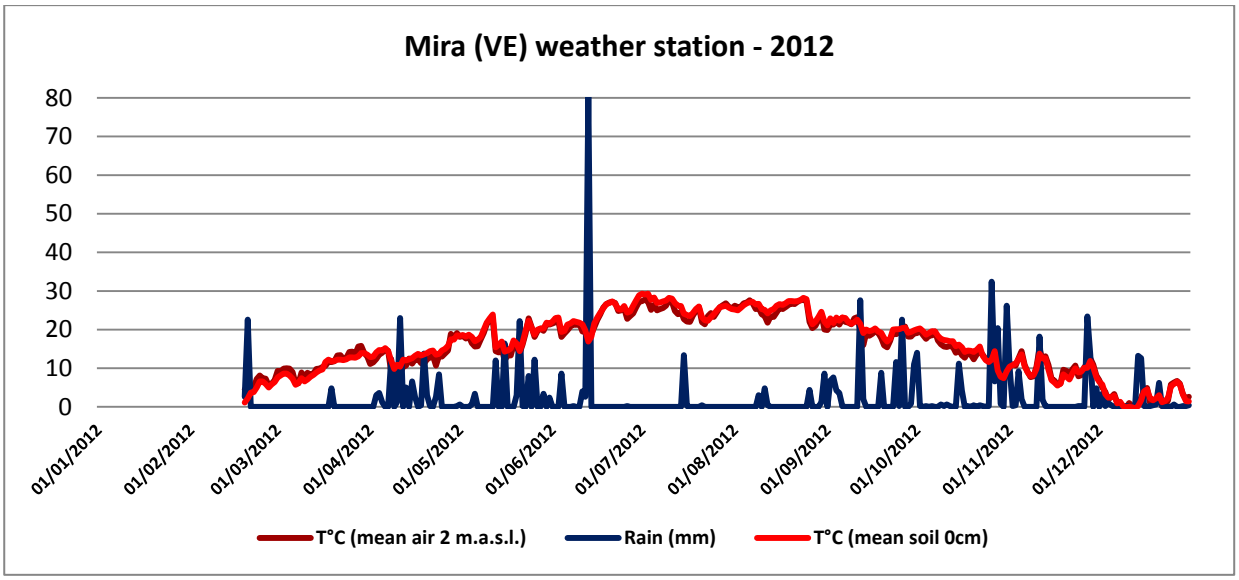
b)


Favaro Veneto (VE) weather station - 2012
80
70
60
50
40
30
20
10
0
-10
01/01/2012
01/02/2012
01/03/2012
01/04/2012
01/05/2012
01/06/2012
01/07/2012
01/08/2012
01/09/2012
01/10/2012
01/11/2012
01/12/2012
T°C (mean air 2 m.a.s.l.)
Rain (mm)

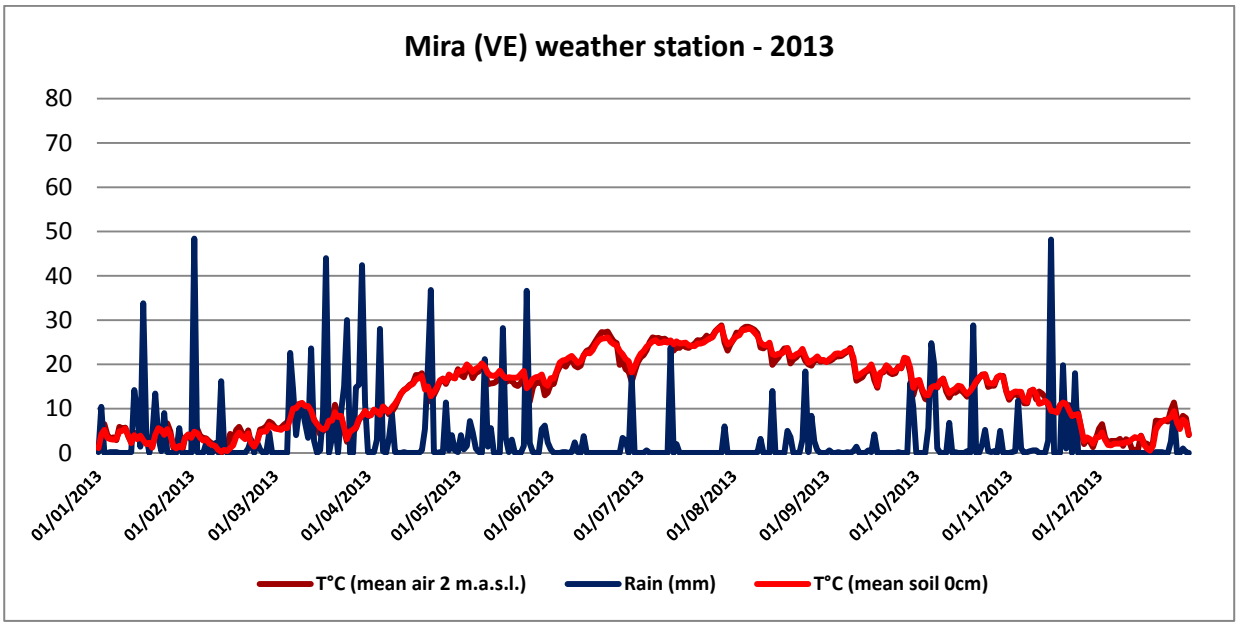
c)


Favaro Veneto (VE) weather station - 2013
80
70
60
50
40
30
20
10
0
-10
01/01/2013
01/02/2013
01/03/2013
01/04/2013
01/05/2013
01/06/2013
01/07/2013
01/08/2013
01/09/2013
01/10/2013
01/11/2013
01/12/2013
T°C (mean air 2 m.a.s.l.)
Rain (mm)

d)



e)



f)

Fig. 12: Meteorological data taken from Breda di Piave (TV) (a, b), Favaro Veneto (VE) (c, d) and Mira (VE) (e, f) weather stations. Data collected from ARPAV webservice.

Landscape structure analysis around studied fields

In literature there are many evidences concerning the importance of landscape structure for agrobiodiversity study (Marino and Landis, 1996; Roschewitz et al., 2005; Tscharntke et al., 2012). For this reasons, in order to contextualize the studied fields, also the area around the fields was examined by observing aerial photographs (Marino and Landis, 1996) on Google Earth and during the fieldwork activities.

Three landscape categories were recognised:

- arable land use (Arable), such as cultivated fields, orchards;
- semi-natural land use (SemN), such as woodlots, hedgerows, natural waterways, untilled areas;
- urban land use (Urb), such as houses, towns, cities, streets, industries.

In fig.13 there are some examples of the three categories of land use considered, by observing aerial photographs in Google Earth.

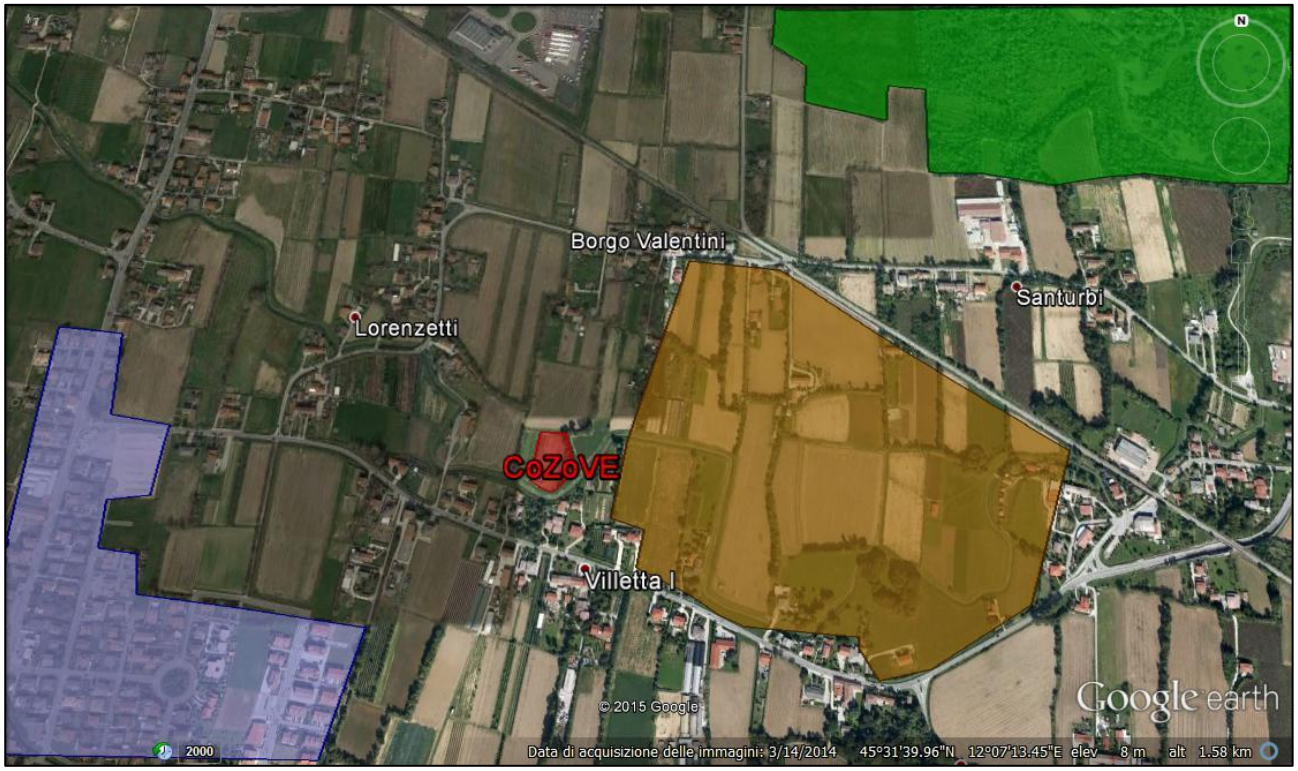


Fig. 13: Aerial photograph elaborated from Google Earth concerning the surroundings of CoZoVE field, with the highlighting of examples of the three considered land use categories: arable (brown); semi-natural (green); urban (violet).

The aim was to quantify in percentage the arable, semi-natural and urban areas within concentric areas of 150m, 300m, 500m, 750m and 1000m radius from the centre of each field (Roschewitz et al., 2005). In fig.14 there is an example of landscape structure analysis of BiBg field.

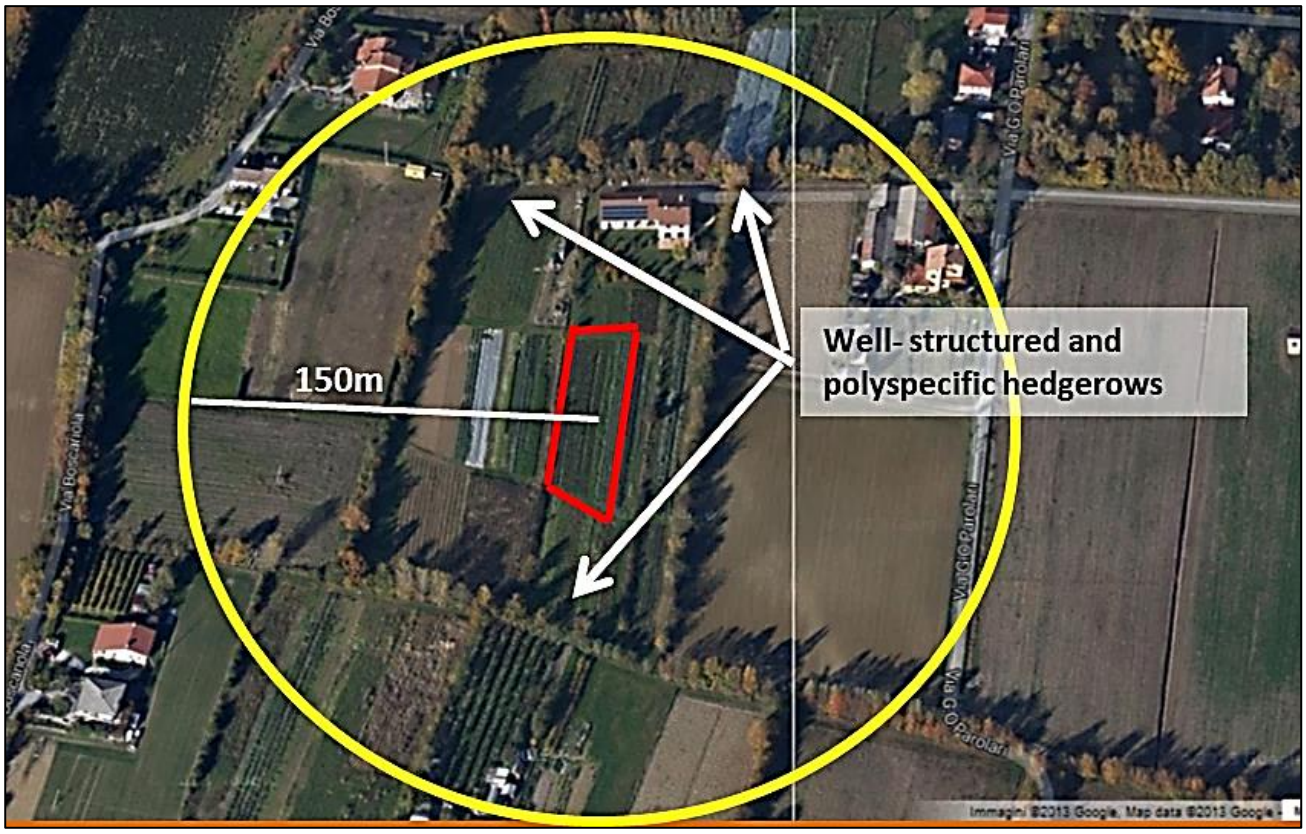


Fig. 14: Example of landscape analysis within a 150m radius concentric area from the centre of BiBg field. Image elaborated from Google Earth.

Methodologies of sampling and analyses

A.R.I.S.A.

One of the most powerful ways to explore microbial diversity in nature is to analyse DNA sequences that encode target genes, such as the bacterial 16S rRNA and the fungal 18S rRNA molecules. These genes are present in all life forms, they have well defined regions for taxonomic classification that are not subject to horizontal transfer and they are essential only as a structural transcript forming parts of the ribosome for translating genes into functional proteins. Since certain structural features of the 16S rRNA and 18S rRNA molecules must be preserved for their function, it follows that 16S–23S rRNA and 18S-28S rRNA intergenic spacer region sequences are highly conserved in given regions and heterogeneous in others, and for this reason useful to distinguish taxa down to the species level (Vancov, 2001; Fisher and Triplett, 1999; Kirk et al., 2004). In 1999 an automated method of ribosomal spacer analysis (A.R.I.S.A.) was developed for the rapid assessing of microbial diversity and community composition. After soil DNA extraction, PCR amplification of the 16S–23S intergenic spacer region in the bacterial rRNA operon is executed using a fluorescent-labelled specific primer pair. ARISA-PCR fragments can range in size from 400 to 1200 bp and

they are separated and measured by using an automated electrophoresis system (Fisher and Triplett, 1999). The same technique can be applied to survey overall soil fungal community, by performing PCR amplification of the 18S-28S intergenic spacer region in the rRNA operon using another fluorescent-labelled specific primer pair (Andreson and Cairney, 2004). The A.R.I.S.A. output is an electropherogram: a fingerprint profile of peaks, the size of which is estimated by comparison to fragments in the internal size standard. The software also calculates the fluorescence contained in each peak, which is proportional to the quantity of DNA of the fragment. So the relative amount of each fragment in the PCR product is estimated as the ratio between the fluorescence (peak area) of the fragment of interest and the total fluorescence of all fragments in the profile (Fisher and Triplett, 1999). This technique was successfully applied in several types of environmental samples coming from freshwater (Fisher and Triplett, 1999), grassland soil (Kennedy et al., 2005), agroecosystem and semi-natural soils (Ranjard et al., 2001; Stevanato et al., 2014).

In particular in this work the DNA from 500mg soil sample was extracted with Genomic DNA from Soil commercial kit (Macherey Nagel firm). The extraction protocol included a mechanical lysis with ceramic marbles for the breaking of soil grains and for cell lysis of bacteria, spores and fungal cells. The lysate obtained was filtered through a column (NucleoSpin Inhibitor Removal Column) for the removal of the inhibitors of the enzymatic reactions eventually contained in the sample. The DNA isolation was carried out into the elution system silicon columns after adding a binding buffer to the lysate that improved the interaction of the DNA with the silicon membrane of the column. The quality and the quantity of DNA extracted from the samples were verified with absorbance: on average 1.2 ug of total DNA were extracted with an $A_{260/280}$ mean ratio of 1.6. Then A.R.I.S.A. was used for the genetic characterization of bacterial and fungal communities. In particular two different pairs of primers were used:

· the SD-Bact-1522-b-S-20 and LD-Bact-132-a-A-18 (Ranjard et al., 2001) primers allowed to amplify specifically the bacterial intergenic spacer region genes between sub-units 16S rRNA and 23S rRNA;

· the ITS1 and ITS2 (White et al., 1990) primers allowed to amplify specifically the fungal intergenic spacer region genes between sub-units 18S rRNA and 28S rRNA.

This analysis was done at Piattaforma Genomica Laboratory (Parco Tecnologico Padano, Lodi, Italy).

All the procedure is summarized in fig.15.

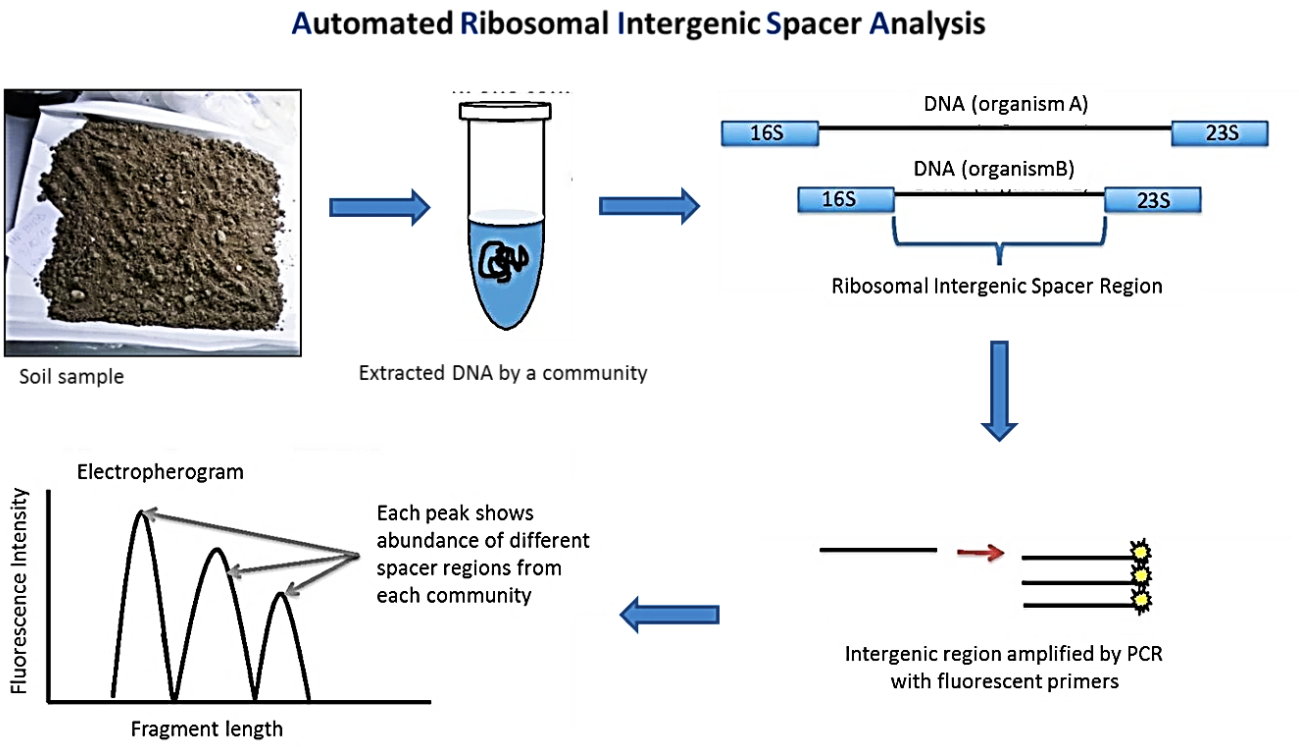


Fig. 15: A.R.I.S.A. technique used to explore microbial communities, here in particular the 16S-23S spacer region useful for soil bacterial community fingerprint is shown (modified by Ilyanassa, 2012).

Data analysis was performed by Gene Mapper software (4.0 version).

A.R.I.S.A. application may face on a disadvantage: overlapping intergenic spacer size classes among unrelated organisms taking part of the profile can lead to the underestimation of the community diversity[13], but Fisher and Triplett (1999), assuming that biases remain constant between samples, suggested that by counting the total number of fragments in a fingerprint profile, this technique can be used to estimate the relative diversity among sampled sites.

In this study soil samples of all fields were analysed with three replicates each.

DNA Sequencing

Since a less expensive technique as A.R.I.S.A. may underestimate diversity and moreover it does not provide direct phylogenetic information on particular fragments in the fingerprint profile (Fisher and

[13] That is because unrelated microorganisms may possess intergenic spacer regions of identical length and so be represented in the A.R.I.S.A. profile by a single peak.

Triplett, 1999), also a much more detailed but more expensive technique was applied to explore overall soil bacterial and fungal communities.

In detail 16S rRNA gene amplicon sequencing was performed to explore bacterial communities and ITS (Internal Transcribed Spacer) amplicon sequencing to explore fungal communities, by using Roche 454 Genome Sequencer (Roche Diagnostics Corp., Branford, CT, USA) that is a PCR-based Next Generation Sequencing (NGS) technology (Shokralla et al., 2012; Fierer et al., 2012; Mouhmadou et al., 2013; Kohout et al., 2014). This technology has been chosen because it is among the most appropriate to analyse environmental samples, such as soil DNA extracts containing DNA from thousands of individuals for ecological applications (Fierer et al., 2012). In particular 454 sequencer uses real-time sequencing-by-synthesis pyrosequencing technology, in which each nucleotide incorporated by DNA polymerase results in the release of a pyrophosphate molecule that starts a series of reactions to produce light by luciferase: the light quantity is proportional to the number of incorporated nucleotides (Margulies et al., 2005).

Among the main advantages in using Roche 454 technology are its long read length and the relatively short run time and moreover it is a good choice for applications involving non-model organisms (Shokralla et al., 2012; Kohout et al., 2014). It is an amplicon sequencing because it can analyse pools of PCR-amplified molecules (Shokralla et al., 2012).

In particular the procedure consisted in soil DNA extraction from 0.25g using MoBio Powersoil DNA isolation kit (MoBio Laboratories, Carlsbad, CA, USA) as recommended by the manufacturer; then PCR was performed to amplify the region of interest and in particular the variable regions V1, V2 and part of V3 from 16S gene for bacteria (Nacke et al., 2011) or the variable regions ITS1 and ITS2 from ITS gene for fungi (Kohout et al., 2014), by using specific primers with a unique sample-specific identifier (the "barcode" sequence incorporated in the complete forward primer sequence), which allows to sort the reads into sample libraries via detection of the appropriate barcode. These steps were performed by the Department of Genomics and Biology of Fruit Crops at the IASMA Research and Innovation Centre (Fondazione Edmund Mach, San Michele all'Adige, Italy) using the primer pair 27F (5'- AGAGTTTGATCMTGGCTCAG – 3')/ 533R (5' – TTACCGCGGCTGCTGGCAC – 3') for 16S rRNA gene amplification, and ITS1F (5' – CTTGGTCATTTAGAGGAAGTAA – 3')/ ITS2R (5' – GCTGCGTTCTTCATCGATGC – 3') for ITS gene amplification. The generated raw sequences were processed using the analysis software QUIIME[14] and screened by various quality filters to remove poor-quality sequences (quality filtering phase) (Shokralla et al., 2012). A subsampling was performed, which consists in sorting at random the same number of sequences from all the samples, in order to make a normalization and to analyse the same number of sequences for each sample.

Although NGS technology allows to explore in detail the overall bacterial and fungal communities from a phylogenetic point of view, conceptually to define a microbial species remains a non-solved problem. The definition of bacterial species is however a temptative concept, since the classical species definition cannot be applied to prokaryotes or asexual organisms (Godfray and Lawton, 2001). Moreover the genetic plasticity of bacteria, allowing DNA transfer through plasmids, bacteriophages and transposons, complicates the concept of species by violating its boundaries. Different problems apply to fungi: fungal

[14] This software can be found in this webpage: http://qiime.org/index.html

taxonomy often encounters limits in identifying below-ground vegetative structures (Kirk et al., 2004). For these reasons, the most detailed taxonomic level aimed at in the present analysis was prudentially set as the Genus.

In this study soil samples of all fields were analysed with one replicate each.

dsDNA content analysis

After nucleic acids extraction, this analysis aims to quantify soil double-stranded DNA (dsDNA) content. It involves a fluorescent nucleic acid stain, the PicoGreen®(Life Technologies, Grand Island, NY, USA), which binds specifically to double-stranded DNA and then the fluorescence emitted by the DNA-PicoGreen complex is detected by a spectrofluorimeter (Sandaa et al., 1998). Among the advantages in using the PicoGreen® reagent have to be cited the increase of its fluorescence emission of about 200 times (Sandaa et al., 1998), due to its high sensitivity which allows the extract to be diluted to avoid quenching of fluorescence by humic substances (Howeler et al., 2003) and moreover it is a relatively low-cost method suited to high throughput (Cowie et al., 2013; Fornasier et al., 2014).

In this work the new method for DNA extraction developed by Fornasier et al. (2014) was adopted: DNA was extracted with pH 8 sodium phosphate buffer using bead beating. In detail, the technique proceeds with a mechanical lysis that disrupts soil aggregates, microbial biofilm and cell walls, then a chemical lysis using a non-ionic detergent applied to the soil suspension (Martin-Laurent et al., 2001). Differentially from other methods, which provides for subsequent DNA purification, the method of Fornasier et al. (2014) implies that crude (not purified) DNA-extracts are immediately quantified for dsDNA. After the fluorometric quantification, the comparison with the reference curve previously made with standard DNA diluted solutions at known concentrations makes possible to calculate the exact DNA concentration in each sample.

In ecological applications, dsDNA quantification assay is a method of quantifying soil microbial biomass and can be used as a parameter (indicator) for measuring soil quality (Doran and Zeiss, 2000; Fornasier et al., 2014). Blagodatsky et al. (2005) highlighted that soil microbial biomass and activity are key factors controlling C-turnover in soil and respectively acceleration/mitigation of the resultant CO_2 flux from soil to atmosphere in response to proposed increase of C input to soil in elevated CO_2 world. Some other applications in literature were, for example, to allow the differentiation of soils according to their microbial communities and the monitoring of differences in the microbial communities in a soil in response to a stress (Martin-Laurent et al., 2001); a robust alternative to chloroform fumigation and extraction-labile carbon when quantifying microbial biomass in agricultural soils under the same climatic conditions. Moreover, in general terms, it offers the possibility of analysing each kingdom separately and it allows the evaluation of agricultural management effects on microbial community structure (Gangneux et al., 2011).

In this research six soil samples (from three organic and three conventional fields) were analysed with ten replicates each.

Fertimeter[15]

A fertimeter is a simple device using silk and cotton textile yarns, useful to measure microbiological activity and consequently OM degradation within the first 15 cm of soil depth (soil A horizon). Each fertimeter consists by a silk (animal protein) and a cotton (cellulose) textile yarn 15 cm long (fig.16 a). It is buried into the soil for exactly seven days (fig.16 c) and then gently extracted from the soil and air-dried. Then each yarn is subject to traction after being tied to a dynamometer (IMAD ZP, ELIS Electronic Instruments and Systems, Rome, Italy), which measures the peak force required to break it by applying progressive tractional force (fig.16 d). The more force is necessary to break the yarn, the smaller was the degradation of that yarn caused by microorganisms' activities. In particular the extent of degradation of these yarns, compared to that of unburied controls, is taken as an index of the cellulolytic (on cotton) and proteolytic (on silk) attitudes of the soil microbial populations (Stevanato et al., 2014).

Fig. 16: Phase of construction of fertimers (a), treatment with N and P solutions in the laboratory (b), exposition time (c), breakage test with the dynamometer (d) (Ph. S. Fusaro).

[15] International patent PCT N. WO2012 140523 A1, Squartini, Concheri, Tiozzo, University of Padova

In one sampling point there are three single fertimeters (fig.16 c):

1. the control one, without any treatment;
2. the nitrogen (N) one, with yarns pre-treated with NH_4NO_3 (3 g/l) solution;
3. the phosphorus (P) one, with yarns pre-treated with Na_2HPO_4 (6 g/l) + KH_2PO_4 (3 g/l) solution (fig.16 b).

The difference between the degradation percentage of the control and the pre-treated fertimeter, can detect any deficiencies in macronutrient N and P and therefore to give the operator information about some possible soil fertility problems. Moreover Stevanato et al. (2014) have demonstrated a link between fertimeter and crop productivity: in particular a higher productivity in vineyards is correlated with a higher degradation level of yarns, hence the fertimeter can be considered as a practical and inexpensive index of soil microbial activity as well as a valuable predictive tool for plant performance and soil fertility. From literature the importance of a tool to measure OM, and in particular cellulose, degradation also emerges, since cellulose is the main structural component of higher plant cell walls and represents approximately 35–50% of plant dry weight (Ransom-Jones et al., 2012). Those authors stressed that the photosynthesis process creates extensive amounts of plant biomass (cellulose), which must be degraded by cellulolytic microorganisms that are present in the soil (Ransom-Jones et al., 2012).

In this research four samplings were made: in each field for each sampling, three sets of yarns (control, N-treated, P-treated) per fibre (cotton and silk) were buried.

FDA hydrolysis test

Soil microbial activity expressed as Fluorescein Diacetate (FDA) hydrolysis was determined following the method of Schnurer and Rosswall (1982). This method is widely accepted as an accurate and simple one for measuring total microbial activity in a range of environmental samples, including soils.

FDA is a general substrate for several hydrolytic enzymes including esterases, lipases and certain proteases. From a biochemical point of view, colourless FDA is hydrolysed by both free and membrane bound enzymes, releasing a coloured end product fluorescein (F) which can be measured by spectrophotometry (Adam and Duncan, 2001).

In detail, the assay consisted of suspending 1.0 g soil in 20 ml phosphate buffer (pH 7.6), shaking for 15 min, and adding 100 µl FDA (4.8 mM). The mixture was placed on a rotary shaker at 100 rpm and after incubated at 30◦C for 105 min. The assay was terminated by extraction with acetone (10 ml) followed by filtration by using filter paper (Whatman n. 2). The optical density of each filtrated sample was measured at 490 nm and the total amount of formed product was calculated based on a regression equation generated from standards of known concentrations. A representation of the chemical reaction is shown in fig.17.

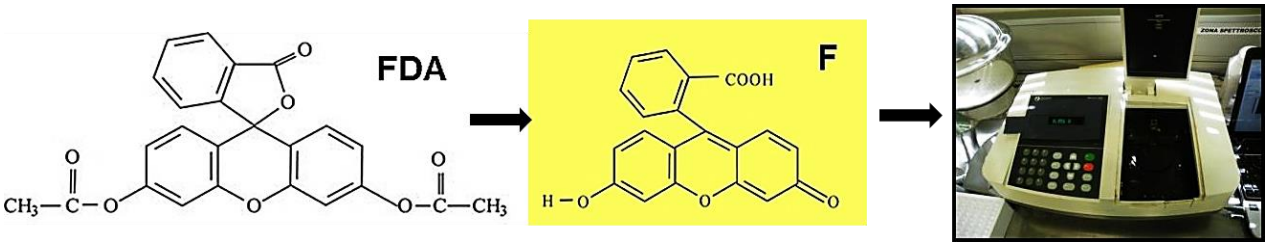


Fig. 17: Reaction of hydrolysis of Fluorescein Diacetate (colourless FDA) to Fluorescein (yellow F), then read with spectrophotometer.

The enzymes responsible for FDA hydrolysis are plentiful in the soil environment. Non-specific esterases, proteases and lipases, which have been demonstrated to hydrolyse FDA, are involved in the decomposition of many types of tissues. The ability to hydrolyse FDA thus seems widespread, especially among the major decomposers, bacteria and fungi (Schnurer and Rosswall, 1982; Alkorta et al., 2003). Generally more than 90% of the energy flow in a soil system passes through microbial decomposers, therefore an assay that measures microbial decomposer activity will provide a good estimate of total microbial activity (Adam and Duncan, 2001).

Other ecological applications of FDA hydrolysis test concerned cultivated soils (Schnurer and Rosswall, 1982; Pankhurst et al., 2004) and as a soil quality indicator in different pasture systems in respect with the native forest soil (da Costa and de Godoi, 2002).

In this research eight soil samples (from four organic-biodynamic and four conventional fields) were analysed with three replicates each.

Soil respiration tests

This simple method is based on the Substrate-Induced Respiration (S.I.R.) technique, which has the aim to quantify the respiration efficiency of soil microorganisms. In particular it is a quantitative estimate of CO_2 product by OM oxidation process made by microbial community. S.I.R. is also a physiological method for measurement of the soil microbial biomass (Anderson and Joergensen, 1997; Stenstrom et al., 1998). This method is significantly correlated with Fumigation-Extraction (F.E.) method, which utilizes $CHCl_3$ to kill the overall soil microflora in order to determine microbial biomass C, but S.I.R. method has one advantage: the relationships of S.I.R. (CO_2 quantification) with environmental conditions are clearer than those of F.E. (CO_2 quantification) (Anderson and Joergensen, 1997).

The new method, applied in this study, uses the pH variation to measure the respiration rate, because the soil respiration reaction occurs in a closed environment and so the liberation of protons (H^+) can modify pH (fig.18). Practically a solution of 5ml of agarose plus Carlo Erba colouring is prepared at the

bottom of tube, then a small piece of cotton is put as spacer and holder in order to sustain the unsieved air-dried soil sample (3g) and to prevent the contact between soil and agarose solution. After that the tube is accurately closed.

Three different tests were performed:

1. dry basal respiration test, with just soil sample;
2. re-wetted respiration test, by adding 100µl of demineralised water;
3. S.I.R. test, by adding 100µl of glucose solution (at concentration of 18mg/100µl) (fig.18).

For each test there was also the control, without soil.

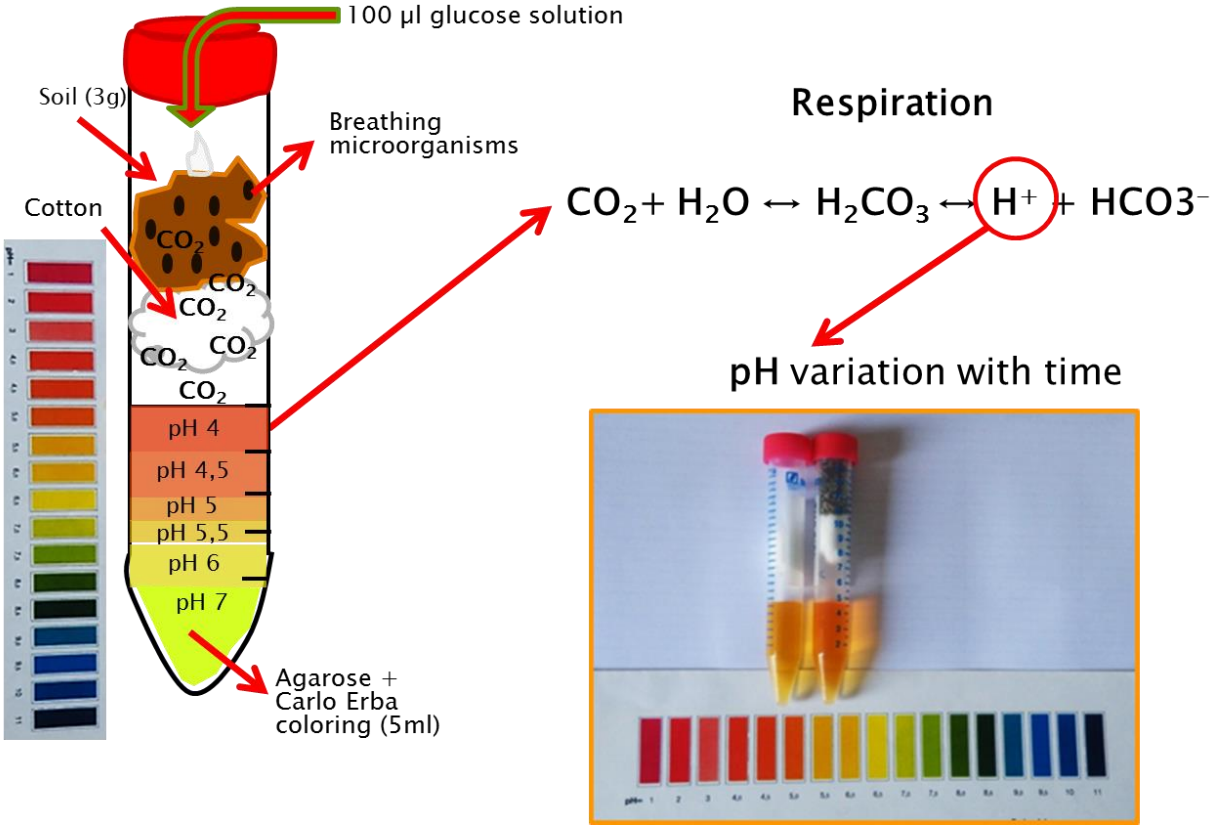


Fig. 18: The new S.I.R. method based on pH variation with time.

Since soil samples were previously accurately air-dried and all samples were analysed for at least 520 hours, the conditions were such that the occurrence of any fermentation reaction could be excluded.

Each soil sample was analysed with two replicates for each of the three tests.

PCR for AMF DNA fragment amplification experiment

The polymerase chain reaction (PCR) is a technique that aims the amplification of a single or a few copies of a specific portion of DNA generating up to millions of copies. By using specific primers it is possible to amplify only a particular DNA fragment. In this work the specific primers that have been used to detect the presence of Arbuscular Mycorrhizal Fungi (AMF) were AMV4.5NF (5' – AAGCTCGTAGTTGAATTTCG -3') and AMDGR (5' – CCCAACTATCCCTATTAATCAT – 3') (Sato et al., 2005). The PCR reactions were performed in the PCR system I-Cycler (BIO-RAD, Cressier, Switzerland). GoTaq DNA polymerase (Promega, Madison, WI, USA) was the enzyme used in the PCR amplification and in particular the 25 µl reaction mixture was the following:

5X PCR reaction buffer	5 µl
BSA (Bovine Serum Albumin) (3%)	0,5 µl
dNTPs mix (200 µM)	0,5 µl
Primer Fw (10 µM)	1 µl
Primer Rw (10 µM)	1 µl
Template DNA	1 µl
GoTaq (5 U/µl)	0,1 µl
MilliQ water	up to 25 µl

GoTaq reaction buffer contained 7.5mM Magnesium.

The thermal cycling program was the following:

Phase	**Temperature**	**Time**	**Cycle N°**
Initial denaturation	95°C	10 min	1x
Denaturation	95°C	30 sec	35x
Annealing	51°C	30 sec	
Extension	72°C	1 min	
Final extension	72°C	10 min	1x
Cooling	4-15°C		

After PCR, horizontal gel electrophoresis was performed on 1 % agarose gels (GellyPhor, EuroClone), based on the length of the DNA fragments that had to be separated. DNA samples were electrophoresed in 0.5X TBE buffer. EuroSafe Nucleic Acid Staining Solution (EuroClone, Pero, Milano, Italy), added directly to the gel before the pouring (0.5µl EuroSafe solution in 100µl gel), was used to stain gels. After the

electrophoresis, which was run at 100V, gels were visualized with GENi device (Syngene, Cambridge, England, UK). 5x TBE buffer composition was the following:

Tris HCl 54g/l

Boric acid 27.5 g/l

NaEDTA 4.65 g/l

Three samplings were made to collect soil samples from all fields, one in spring, one in summer and one in autumn, therefore the presence of AMF was detected in three seasons along the year.

Quantitative Real Time PCR for AMF quantification in soil samples

Quantitative Real Time PCR (qRT-PCR) technique was applied in order to quantify the amount of functional genes of Arbuscular Mycorrhizal Fungi in soil samples. The assay was carried out with Power SYBR® Green PCR Master Mix (Applied Biosystems) in the Quantstudio 12K Flex Real Time PCR system using 384 well plates (Applied Biosystems). The 10µl reaction mixture was the following:

	Volume	Final concentration
BSA (3%)	0,07 µl	0,2 mg/ml
DMSO	0,25 µl	2,50%
Template DNA	1 µl	
Primer Fw (AMV4.5NF)(10 µM)	0,5 µl	0,4 µM
Primer Rw (AMDGR)(10 µM)	0,5 µl	0,4 µM
Power SybrGreen	5 µl	
MilliQ water	up to 10 µl (2,68)	

DNA extracted from soil was used not diluted (TQ).

The thermal cycling conditions were the following:

Phase	Temperature	Time	Cycle N°
Initial denaturation	50°C	2 min	1x
Enzyme activation	95°C	15 min	1x
Denaturation	95°C	15 sec	40x
Annealing	51°C	20 sec	
Extension and	72°C	40 sec	

fluorescence detection

The quantification of the gene copy number was obtained with the standard curve method. With this method a standard curve is created using known amounts of plasmids containing the specific portion of DNA to be amplified, and subsequently the Ct values obtained for the unknown samples are interpolated in the standard curve and a gene copy number value is extrapolated. The amplification reaction was concluded with the melt-curve stage, to confirm the specificity of the reaction.

For this qRT-PCR the same soil samples of the previous PCR experiment were analysed.

Soil enzymatic activities assay

The activities of the following key enzymes (tab. III) were determined in soil samples:

- arylsulfatase (AryS),
- β-glucosidase (Gluc),
- acid phosphomonoesterase (AcP),
- pyrophosphate-phosphodiesterase (Piro),
- alkaline phosphomonoesterase (AlkP),
- leucine aminopeptidase (Leu) and
- acetate-esterase (Ester).

First of all an extraction-desorption procedure was applied by adding a solution containing bovine serum albumin (BSA-4%) and Triton X-100 to Tris buffer as described in Fornasier and Margon (2007), because it increases the enzyme extraction yield of 2-8 times and moreover the use of nondenaturing detergent extractants (as Triton X-100) improves the separation of enzymes from humic substances (Fornasier and Margon, 2007; Fornasier et al., 2011). Subsequently, just after extraction, a fluorescence assay was performed using soil extracts on microplates and fluorescent substrates (in particular 4-Methyl-umbelliferyl substrates) in order to determine enzymatic activities (Cowie et al., 2013; Stevanato et al., 2014). To perform this analysis also OM and calcium content was useful to determine: the former was determined for loss of ignition (LOI) at 550°C and the latter was determined for LOI at 850°C. These analyses were performed at the Centro di Ricerca per lo Studio delle relazioni fra Pianta e Suolo (CRA-RPS), Gorizia.

As regards the importance of studying soil enzymatic activities, Karaca et al. (2011) reviewed soil enzymatic activity under various soil management systems and described enzymatic activity as a good indicator of agricultural practices, or a measure for detecting the effect of soil management on carbon cycling.

In this research six soil samples (from three organic and three conventional fields) were analysed with ten replicates each.

Berlese-Tullgren extractor for mesofauna sampling

Berlese-Tullgren extractor is a typical method that aims to extract mesofauna from standard soil samples. It is constituted by funnels, one for each soil sample, and the mesofauna organisms fall down in the collection glass filled with a salt water solution. Mesofauna organisms, typically edaphic, fall down driven by a light and heat gradient.

In detail in this work a modified extractor was used, as described in Paoletti and coworkers (1991): a simplified system of 84 plastic canisters, one for each soil sample, is composed by a steel tank which supports a refrigeration system of running water on the bottom, and a cover, equipped with an electric resistance to heat the air (fig.21 a). Moreover in this apparatus the gradient of temperature can be regulated between 30°-50°C on the top and 10°-28°C on the bottom. The extraction phase lasts 10 days. This modified extractor allows to extract mesofauna from many (84) soil samples simultaneously, so to speed up this phase.

In this research three samplings of soil samples of all studied fields were made with eight replicates each. Each replicate was composed by three soil cores extracted with an appropriate corer within the first 10 cm of soil. Each core was 2,5 cm in diameter and 4 cm in length.

After the extraction phase the organisms were determined by using an optical microscope (RZ 3699 lens, MA 748 ocular, RZP Stand, Meiji Techno Japan).

QBS-ar index

The Soil Biological Quality (QBS) Index is a method proposed with the aim to evaluate the biological quality of soil based on the biological forms of sampled edaphic microarthropods. It consists in the attribution of a numeric value to each sampled biological form so as to calculate an index, which characterizes the soil environment object of study (Parisi, 2001). This index is based on the idea that the more a species is adapted to the edaphic conditions, the more the conditions of that soil are better and stable. Among the advantages, there is the overcoming of the difficulties in taxonomic expertise at species level for mesofauna.

To better define the edaphic conditions, it is possible to say that during the evolution period and adaptation to hypogeal life, the euedaphic biological forms have accumulated characteristics such as reduction or loss of pigmentation and visual apparatus, streamlined body form, with reduced and more compact appendages (hairs, antennae, legs); reduction or loss of flying, jumping or running adaptations; reduced water-retention capacity—i.e. thinner cuticle, lack of hydrophobic compounds on the outer surface (Parisi, 1974). In the QBS-ar methodology a score is assigned to each microarthropod taxon, the EMI score (EcoMorphological Index- tab. VII) based on its edaphic adaptations.

Taxa	EMI scores
Protura	20
Diplura	20
Collembola	1-20
Microcoryphia	10
Zygentomata	10
Dermaptera	1
Orthoptera	1-20
Embioptera	10
Blattaria	5
Psocoptera	1
Hemiptera	1-10
Tysanoptera	1
Coleoptera	1-20
Hymenoptera	1-5
Diptera (larvae)	10
Other Olometabola (larvae)	10
(adults)	1
Pseudoscorpionida	20
Palpigrada	20
Opiliones	10
Araneae	1-5
Acaridida	20
Isopoda	10
Diplopoda	10-20
Pauropoda	20
Symphyla	20
Chilopoda	10-20

Tab. VII: EcoMorphological (EMI) scores attributed to each microarthropod taxon (Parisi, 2001). EMI score ranges from 1 (=minimal adaptation to edaphic conditions) to 20 (=maximal adaptation to edaphic conditions).

The overall QBS-ar value for a studied site is calculated with the formula:

$$QBS\text{-}ar = \Sigma \text{ EMI scores}$$

It is not necessary to determine population density of each taxon. The higher is the soil quality, the higher will be the number of microarthropod groups well adapted to the soil habitat and also QBS-ar value will be higher (Blasi et al., 2012).

For each field and each sampling was calculated the QBS-ar index value.

Hand sorting for earthworm sampling

Hand sorting is the classical active collection of earthworms from standard soil volumes (Raw, 1960; Paoletti et al., 1991; Valckx et al., 2011). In detail this technique consists in extracting a soil bulk (30x30x20cm) with a spade fork (fig.21 b). Afterwards the manual examination of bulk soil takes place for 15 minutes upon a white cloth and each earthworm is picked up. In order to collect also the anecic species (deep burrowers), an effective advice is the previously use of an irritant solution/suspension (Bouché, 1972; Lee, 1985). The mustard powder acts as an expellant for earthworms and it is a natural substance without toxic or dangerous consequences for the operator and for the environment (Chan and Munro, 2001; Pelosi et al., 2009; Valckx et al., 2011) and for these reasons it was adopted in this work.

Two samplings per year (in 2012 and 2013) were made, one in spring and the other in autumn, which are the best periods to collect earthworms because of the good soil moisture. During each sampling in each field, 7 random hand sorting points were analysed. The water suspension of mustard powder (*Sinapis alba*, Ai Preti grocery, Padova) with concentration 25 g/l previously prepared, was spread upon the 30x30cm soil surface before hand-sorting.

The collected specimens were determined at species level by using an optical microscope (RZ 3699 lens, MA 748 ocular, RZP Stand, Meiji Techno Japan). The interactive LOMBRI software (Paoletti and Gradenigo, 1996) was the key tool for species determination, but also Sims and Gerard (1985) and Bouché (1972).

QBS-e index

Based on the QBS-ar index (Parisi, 2001), our research group proposed a new index for assessing the sustainability of agroecosystem soil management practices based on earthworms (Paoletti et al., 2013). Given the importance of earthworms as bioindicators of soil management sustainable practices, the standard and quantitative method of sampling (hand sorting), the interactive tool for Italian species identification (LOMBRI software Paoletti and Gradenigo, 1996), we proposed this simple method designed for the farmer and the operator with limited expertise on species taxonomy, who can monitor in autonomy the status of the agroecosystem soil. This method is based on the attribution of an ecological category to each sampled earthworm among five categories: endogeic, epigeic, anecic, coprophagic, hydrophilic established on the ecology, ethology and anatomic characteristics of each living specimen, and the age recognition between juvenile and adult (without or with clitellum- fig.3). Then to each ecological category and age we established a EcoMorphological score (EMI) (tab.VIII), with the higher scores to adult anecic individuals which have a lower reproductive rate, are bigger than the others, so they can have their influence in a more remarkable soil part and can reach higher soil depth digging their tunnels, therefore they have a more important eco-physiological action into the soil. The lowest EMI score values, instead, were attributed to hydrophilic species because their life conditions (high level of groundwater) scarcely fit together with good conditions for agriculture (water stagnation in the field that originates soil anoxia).

Ecological category	Age	EMI score
Hydrophilic (IDR)	Juvenile (J)	1
Hydrophilic (IDR)	Adult (Ad)	1
Coprophagic (COP)	Juvenile (J)	2
Coprophagic (COP)	Adult (Ad)	2
Epigeic (EPI)	Juvenile (J)	2,5
Endogeic (END)	Juvenile (J)	2,5
Epigeic (EPI)	Adult (Ad)	3
Endogeic (END)	Adult (Ad)	3,2
Anecic (ANE)	Juvenile (J)	10
Anecic (ANE)	Adult (Ad)	14,4

Tab. VIII: EcoMorphological (EMI) scores attributed to each ecological category and age (Paoletti et al., 2013).

Subsequently, the following formula has to be applied to calculate the index value:

QBS-e = (IDR J,Ad score * N) + (COP J, Ad score * N) + (EPI J score * N)

+ (END J score * N) + (EPI Ad score * N) + (END Ad score * N)

+ (ANE J score * N) + (ANE Ad score * N)

where N = n° individuals/m^2, therefore to apply this index it is important to determine the population density of each ecological category in order to compare data.

To conclude the evaluation it is necessary to refer the QBS-e calculated value to a Quality Class, according to the tab.IX.

QBS-e value	Quality Class (agroecosystem, semi-natural environment)
QBS-e > 1000	Excellent - 4
600 < QBS-e < 1000	Good - 3
300 < QBS-e < 600	Decent - 2
100 < QBS-e < 300	Sufficient - 1
0 < QBS-e < 100	Poor - 0

Tab. IX: Quality classes based on calculated value of QBS-e index (Paoletti et al., 2013).

For each field object of study and for each sampling, the QBS-e index value was calculated.

Pitfall trap for carabid sampling

Carabid beetles were collected using pitfall traps (Luff, 1975; Thiele, 1977; Paoletti et al., 1991; Lovei and Sunderland, 1996; Kromp, 1999; Brandmayr et al., 2005). Pitfall trapping is the most frequently used, inexpensive and easy to use field method for studying carabids and it is suitable for studying several population parameters and community measurements such as species presence (Lovei and Sunderland, 1996; Kromp, 1999; Menalled et al., 1999). Each trap was composed of a 750ml plastic glass (95 mm mouth diameter, 120 mm deep) let into the ground up to the rim (used to maintain the hole open) and a 500ml plastic glass (95 mm mouth diameter, 90 mm deep) contained inside the former (that is picked up every time one needs to empty the trap) (fig. 21 c), in order to catch every insect passing by.

In detail in this research, seven samplings were made along two years (2012-2013) with seven pitfall traps (replicates) each. The traps were placed in random position within the field between a plant and the other of the crop along the row, in order to disturb as little as possible the management practices, with a minimum distance of 9-10m between the traps. Each trap was half filled with a water and salt saturated solution and with a drop of liquid soap, which acts as surfactant, and it was covered with a low-standing plastic roof 12 x 12 cm in size to prevent excess leaf litter, rain water and vertebrate animals from falling into the trap. The traps acted just in a passive way because the preserving fluid put inside the trap was without bait and therefore not attractive. During 2012 four samplings were made from March to November and during 2013 three sampling were made from August to November. Beetles were stored in 80% alcohol and identified using an optical microscope (RZ 3699 lens, MA 748 ocular, RZP Stand, Meiji Techno Japan) and the identification keys (Magistretti, 1965; Trautner and Geigenmueller, 1987; Facchini, 2001) as well as the websites Carabidae (2014) and Iconographie des Coleopteres Carabidae d'Alsace (Schott, 2014). Moreover Marco Uliana (entomologist at Venice Natural Hystory Museum, Italy) was the expert consulted for a help in the identification of the most uncertain specimens.

Since the number of animals trapped depends on the size of population present in the habitat but also on the animals' activity (Heydemann, 1953), for each sampling and each species the Activity Density (DA_{10}) was calculated in order to standardize the data, with the following formula:

$$DA_{10} = \left(\frac{n^{\circ}\ individuals}{\sum EU}\right) * 10$$

where EU (Effort Unit) = (Days of trap activity * n° traps), which provides a good estimate of the role of a species in an ecosystem, not only depending on its frequency and abundance but also on its mobility. In fact activity density offers a mechanical method of documenting in any habitat species that escape simple catching, gives an idea of the order of magnitude of their frequency and allows an exact analysis of daily and annual rhythms in activity (Thiele, 1977).

Visual control for pest control quantification

In order to quantify the natural pest control ES, the visual control technique was adopted. In detail during the vegetative period of the crop in each year three samplings were made (tab. X). In each field, six sampling points were randomly chosen for each sampling time. In each sampling point four crop plants were visually checked from the ground up to the top of the plant on each leaf and inflorescence, searching for every invertebrate eating plant parts and predators.

Crop	Year	Transplanting period	Visual Control Sampling periods
Cichorium intybus	2012	16-31/7	1) 30/8 – 14/9
			2) 24/9 – 8/10
			3) 17/10- 6/11
Brassica oleracea	2013	9-21/7	1) 5/8 – 7/8
			2) 26/8 – 29/8
			3) 9/10- 17/10

Tab. X: Examined crops and visual control sampling periods (from Fusaro et al, in prep).

Each phytophagous agent (mainly lepidopteran caterpillars) was picked up in order to breed it.

Insect indoor breeding

Each collected lepidopteran larva and pupa was reared until hutching, to record possible parasitoid emergence (Marino and Landis, 1996). After collection, larvae and pupae were isolated in small plastic boxes (4 cm diameter; 5 cm height -fig. 21 d) and kept in laboratory at room temperature until the emergence of either adult or parasitoids. Larvae were fed with crop plant leaves collected from the original sites. The most spread crop pest, and therefore the most present in the breeding, was *Plutella xylostella* (fig. 19).

The percentages of emergence (% E), mortality (% M), parasitization (% P) and hyperparasitization (% IP) were calculated using the following formulae:

$$\% E = \left(\frac{(A+P)}{N}\right) * 100 \qquad \% M = \left(\frac{D}{N}\right) * 100$$

$$\% P = \left(\frac{P}{(A+P)}\right) * 100 \qquad \% IP = \left(\frac{IP}{(A+P)}\right) * 100$$

where,

A = number of adults emerged from reared pupae and larvae,

P = number of parasitized larvae and pupae,

N = total number of larvae and pupae reared,

D = number of dead insects,

IP = number of hyperparasitized larvae.

Larvae and pupae that died before completing their development were not considered in the parasitization and hyperparasitization percentages.

Fig. 19: (a) *Plutella xylostella* larva feeding on cabbage leaf; (b) *P. xylostella* while hatching from cocoon of pupa in the field; (c) Two individuals of *P. xylostella* during the indoor breeding: (above) an healthy pupa in its cocoon, (below) a parasitized larva, while larva of parasitoid is emerging from host body; (d) *P. xylostella* adult in the field (Ph. S. Fusaro).

Hatched parasitoids were determined by specialized entomologists: Daniele Sommaggio (Padova University), Pascal Rousse (Museum of Iziko, South Africa), Christer Hansson (Lund University, Sweden), Claire Villamant (Museum of Paris, France), Pierfilippo Cerretti (Sapienza University, Roma).

Moreover for each sampling point, a visual quantification of crop plant damage was evaluated. Three damage classes were previously established:

- 1-10% damaged leaf surface,
- 11-50% damaged leaf surface and
- >50% damaged leaf surface.

Fig. 20: Example of cabbage leaf damage caused by butterfly caterpillars (strip feeders) (Ph. S. Fusaro).

According to Root (1973) it was possible to distinguish the damage caused by “strip feeders” which chew leaves (mainly due to butterfly caterpillars- fig.20) and “pit feeders” which rasp small pits or holes from the leaf surfaces (mainly due to adult flea beetles *Phyllotreta* sp.). In 2012 the damage on red chicory was not quantifiable.

Fig. 21: Sampling methodologies applied in this research: (a) Berlese –Tullgren extractor modified as described in Paoletti et al. (1991), with detail of one canister, for soil mesofauna extraction; (b) Hand sorting for earthworm sampling; (c) Phase of installation of one pitfall trap in the field, for carabids collection; (d) Indoor breeding for crop pests sampled in the field with the visual control technique (Ph. S. Fusaro).

Floristic survey with random plots

In order to properly sample the spontaneous vegetal part of biodiversity in these agroecosystems, census and estimate of abundance of each herbaceous species were sampled as in Nascimbene et al. (2013) both in the field margins and within the area of cropfield. Having preliminarily observed the habitats of field margins present in each farm, it was decided to sample the same habitat present in every farm: the grassy strip margin useful to the passage of agricultural vehicles along the sides of the field (fig. 22). The plant species composition, which is found in this zone, is affected by the treatments carried out in the adjacent field, by the heaviness of agricultural vehicles and the frequency of their transits, which consequently cause soil compaction.

Fig. 22: Grassy field margin, an example of sampled habitat within the farm (left); Floristic survey: estimate of the abundance of different herbaceous species within a standard area of 1x1m (right) (Ph. S. Fusaro).

For a quantitative survey, ten sampling points (1X1m- fig.22) were randomly selected in the grassy margins and ten sampling points (1X1m) within the cropfield area. For each point all herbaceous species were listed and their abundance in relation to the total coverage was estimated in percentage, with a resolution of 5%. If a plant species was present with just one individual, its abundance percentage was considered 1%. Plant species were determined with the aid of identification guides (Pignatti, 1982; Aeschimann et al., 2004; Schauer and Caspari, 2005).

Indicator plants method

To have more information than the simple plant species list about the meaning of every species in terms of pedological indications, the classification of ecological attributes method proposed by Gérard Ducerf was applied (Ducerf, 2007). It consists in the attribution to each plant species of a pedological value based on the conditions of seed dormancy of that species, which indicate changes in the secondary habitat. Ducerf established the following three categories (tab.XI):

Pedological category	Bioindication features
EQU	Favourable plant bioindicator: it indicates that the soil is in a state of equilibrium
REV	Reversible plant bioindicator: it indicates that equilibrium is broken but it is possible to invert the tendency, if there will be a change in management practices
IRR	Irreversible plant bioindicator: it indicates dangerous soil disequilibrium, the ruin of the soil is near or has passed the threshold of no return

Tab. XI: Bioindication categories attributed to plant species according to Ducerf (2007).

The following scheme represents the relationships among the three above mentioned categories of pedological bioindication.

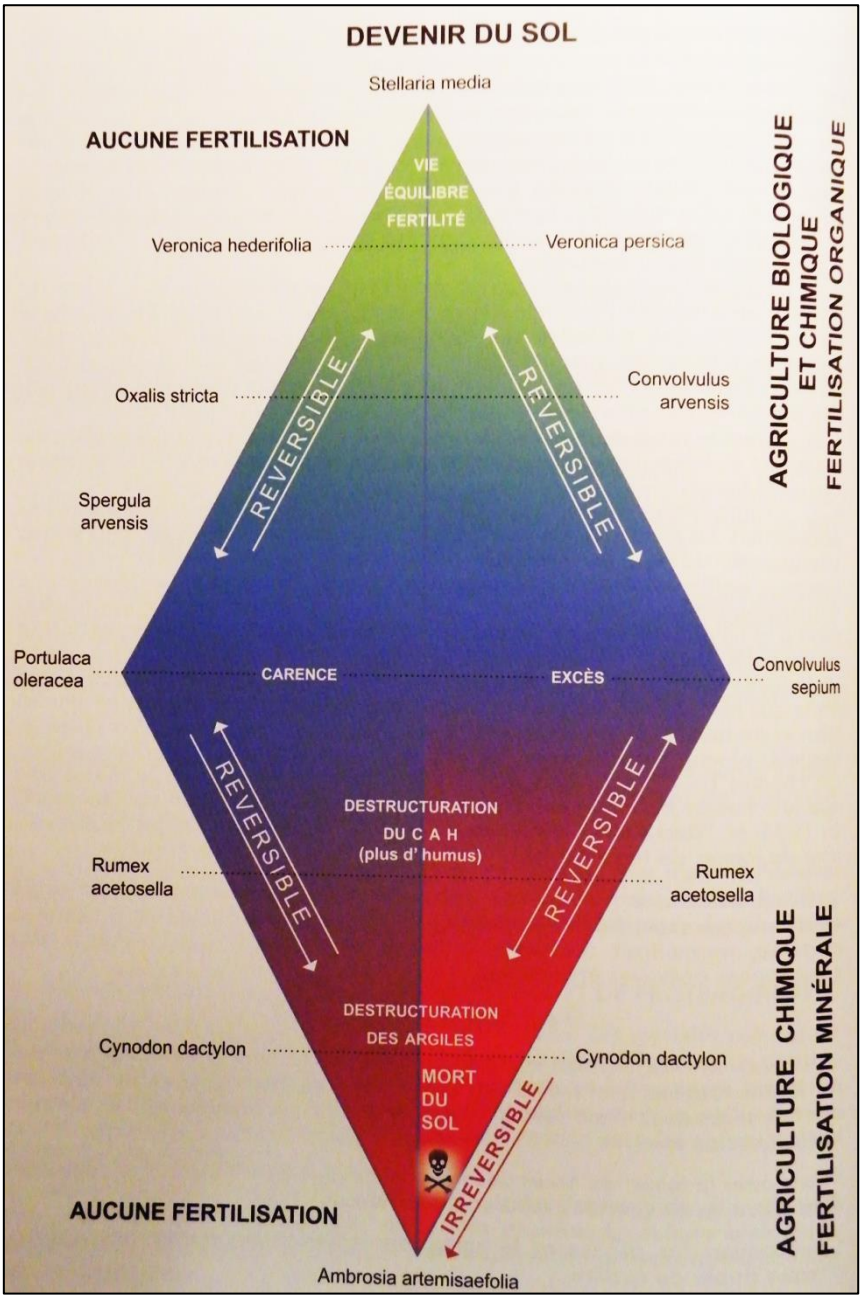


Fig. 23: Scheme with the values of pedological indication attributed to different spontaneous plants, from Ducerf (2007).

A Fidelity value (Fd*i*) was calculated for species *i* present or just in one management or just in one habitat, with the following formula:

$$Fd_i = \frac{n°\ fields\ with\ species_i}{total\ n°\ fields\ of\ the\ same\ management}$$

Fd*i* can range from 0 (no one field of that management with species *i*) to 1 (all fields of that management have species *i*).

An Incidence value (IV*i*) was calculated for species *i* for both the two managements (organic-biodynamic and conventional) and for both habitats (margin and cropfield):

$$IV_i = distr\ coeff_i * cover\ sum\%_i$$

where,

Distr coeff *i* = n° fields with species *i*/total n° fields

Cover sum%*i* = sum of the cover in % of species *i* in that habitat

Subsequently, in order to calculate an overall IV for each of the three bioindication categories (EQU-REV-IRR) for each habitat (margin and cropfield), the Incidence values of all species belonging to that category present in that habitat were summed.

Entomophily Index

Since in literature some researches demonstrated that there is a relationship between the richness and the cover of insect-pollinated plants and agroecosystem management (Batary et al., 2013), in this study an Entomophily Index (E.I.) was calculated for each analysed field, both for crop field area and grassy margin area, in order to take into account the improvement of pollination ES through the supply of alternative sources of pollen and nectar to pollinators like bees, bumblebees, hoverflies and others.

The E.I. formula was the following:

$$E.I. = \frac{n°ent\ sp * \sum(poll\ score * cover\%)}{10}$$

where,

N° ent sp = total number of insect-pollinated plants in that field habitat (crop field or grassy margin);

Poll score = score attributed to each plant species based on its pollination strategy:

1: if it is insect-pollinated (entomophilous)

0.5: if it has a mixed pollination strategy (for example entomophilous but also auto-pollinated, or entomophilous but also anemophilous);

Cover% = sum of the total cover of that species in percentage for that habitat.

The higher is the E.I. value, the higher is the potential of attraction of that area for pollinators and useful fauna.

Soil physical-chemical analyses

The soil sampling to perform physical-chemical analyses was done in the following way: to have a complete picture of each field, six subsamples were taken in homogeneous conditions in the central area of the field (where there was no stagnant water and avoiding marginal areas) by using a corer (6cm diameter, 12cm depth), after having freed the soil from herbaceous vegetation. Then these subsamples were mixed homogenously and 1.5kg of the mixture was used for the laboratory analyses, after air-drying upon absorbent paper for one week. These analyses were performed in the soil analyses laboratory (Concheri, Stellin, DAFNAE, Legnaro, Italy).

Texture analysis

In order to determine soil texture hydrometric method was adopted. 50g of soil sample previously sieved to 2 mm in diameter was poured into a blender with the addition of 100 ml $(NaPO_3)_6$ (Sodium Hexametaphosphate or Calgon-5%) solution, to facilitate the dispersion of the particles, and 250 ml of deionized water. After 10 minutes in the mechanical blender, the sample was transferred in a cylinder for particle size and filled up to final volume (for very sandy soils up to 1205 ml, or up to 1130 ml) with washing of the blender water. The cylinder was closed with the cap and capsized at least twenty times to mix the solution. To separate the different size fractions it is necessary to fix the sedimentation time, which is influenced by temperature, depth and real density of particles and it is obtained from the Stokes law. The Bouyoucos's densimeter was immersed (fig.24), after 4 minutes for the sand complete precipitation the density was read, caused by the sum of the components of silt and clay. If foam tended to form on the surface a few drops of ethanol were added to dissolve it. After two hours, the time necessary for silt complete precipitation (fig.24), the second reading of the density was performed, caused by the clay component that had remained in suspension in the liquid medium. With a thermometer it is necessary to measure the environmental temperature, since temperature influences the sedimentation time: when the solution temperature was different from 20°C the value 0.36 was added (> 20°C) or removed (< 20°C) to the hydrometer readings for each degree of difference.

The percentages of the components present in the soil sample were determined with the following formulae:

% Clay = [read after 2 hours – control + temperature correction factor] x 2

% Silt = [read after 4 minutes - reading after 2 hours + temperature correction factor] x 2

% Sand = [100 - % clay - % sand]

Having the sand, silt and clay percentages obtained from analytical determination, it is possible to know the texture class of the analysed soil sample by using the USDA "textural triangle" (fig.25).

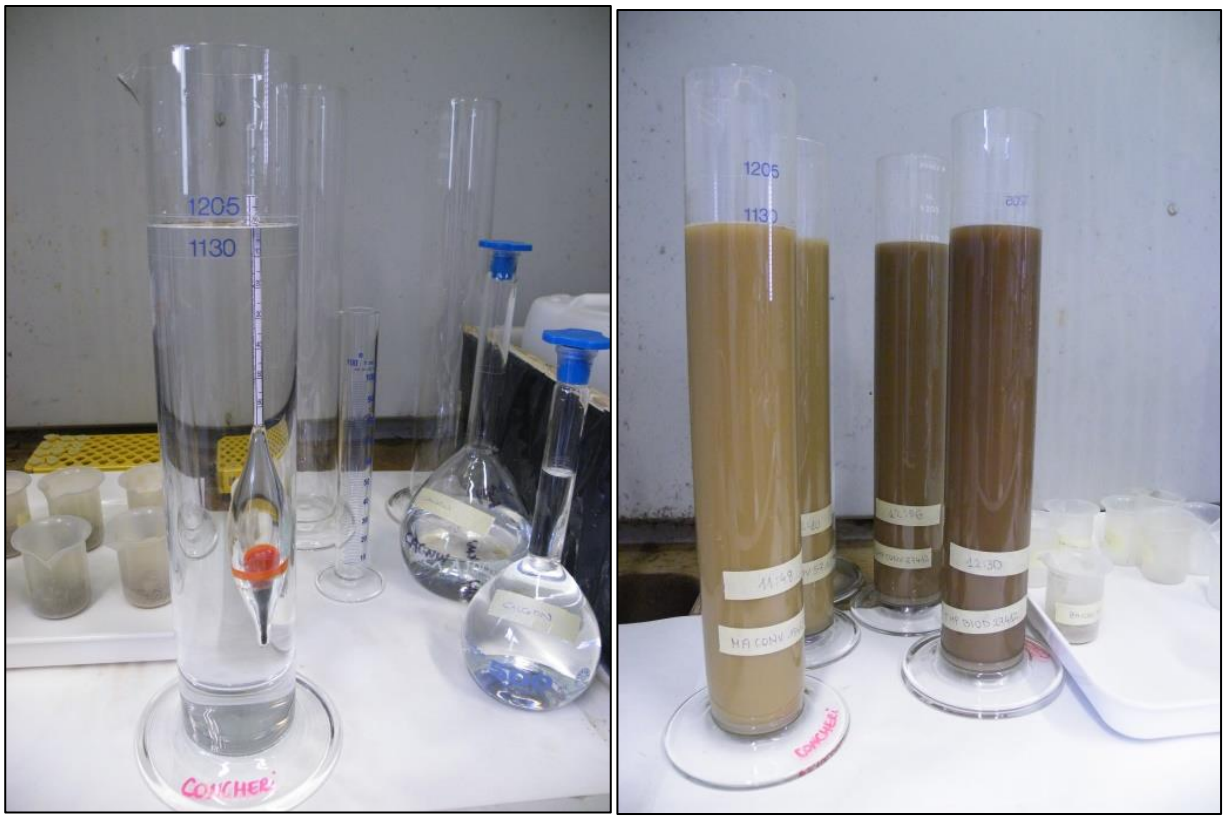


Fig. 24: Hydrometric method to determine soil texture: (left) density determination of the control with the Bouyoucos's densimeter; (right) soil samples during sedimentation time (Ph. S. Fusaro).

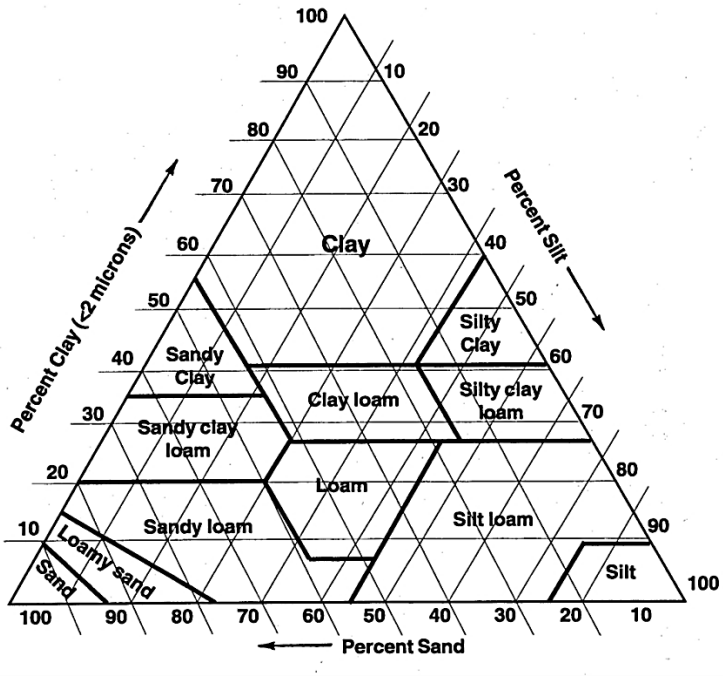


Fig. 25: USDA soil texture triangle[16]

[16] From Plant & Soil Sciences eLibrary: http://passel.unl.edu/pages/informationmodule.php?idinformationmodule=1130447039&topicorder=2&maxto=10

Dry matter

Dry matter quantification is important to calculate elemental concentration. The procedure used was the following. A ceramic crucible was weighed, 1g of soil sample was put in it and the precise weight noted. The crucible was heated in a stove at 60°C for 3-4 hours, after which it was weighed again. The difference between the weight values allowed to calculate the dry matter.

pH

The procedure to calculate soil pH in water was the following. 10g of soil sample were put in a beaker and 50ml of deionized water were added. The suspension was shaken and let to decant for 1 hour. Afterwards pH was measured with a pHmeter after calibration. For this analysis a Corning pHmeter with HI 1131 B electrode and HI 7669 temperature probe was used.

Electric conductivity

The electric conductivity was measured using a Hannah Instrument conductimeter on a suspension obtained by mixing in a beaker 30g of soil sample and 150ml of deionized water, decanted for 2 hours and subjected to two filtrations: one with normal filter paper and one with Whatman n°42 cellulose filter.

CNS analysis

CNS analysis aims to find elemental composition of soil sample. The operating principle is based on the Dumas method (1831), which provides a complete and instantaneous oxidation (flash combustion) of the sample with conversion of all organic and inorganic substances in gaseous products. To perform this analysis an elemental analyzer is necessary and the one used in this work was the "vario MACRO" (Elementar Analysensysteme GmbH). It is a completely automatic tool which allows rapid quantitative analysis of C, H, N, S, starting from various kinds of materials (soil in this case).

The preparative requires an initial homogenization of the sample which is then weighed, with the addition of an oxidant agent (tungsten oxide), in tin capsules. These are automatically closed and introduced into the instrument after air removed.

Inside the instrument the following reactions take place: in the combustion tube (first reaction tube) the high temperatures (1150°C) and the O_2 presence determine the sample incineration. The products that arise during the combustion are CO, CO_2, H_2O, NOx, SO_2 and SO_3 and they are transported by a He flow, used as a carrier gas, until the detector. In the reduction tube (second reaction tube containing

Cu in the reduced state) NOx and SO_3 are quantitatively reduced to N_2 and SO_2 and the excess oxygen is bound by silver wool (present inside the tube). The moisture present in the gas stream is removed with a first passage through a membrane and with subsequent transfer of Sicapent (highly hygroscopic compound). Inside the post-combustion tube (third reaction tube containing CuO and Pt) there is a complete oxidation to CO_2 of carbon compounds not completely oxidized (CO). The separation of N_2, CO_2, SO_2 is made blocking temporarily the CO_2 and SO_2 inside specific heated columns. N_2 comes instead directly to the detector which detects the concentration. Following the CO_2 adsorption column is heated up to 230°C causing the liberation of the compound which can be transported up to the detector. Finally, to affect the heating of the SO_2 column up to 210°C the sulfur oxides are released and detected (Concheri and Stellin, 2011). The quantification of the different elements is performed with creation of a calibration curve generated by the use of a standard (Sulfanilamide) containing known concentrations of the interest elements (N=16,25%; C=41,81%; S=18,62%; H=4,65%).

Method of the muffle

This methodology involves the splitting of soil sample in two aliquots. The first aliquot is weighed into tin foil and analyzed for quantifying the total content of N, C and S. The second aliquot is weighed in silver foil, which will be placed in a muffle furnace heated up to a temperature of 550°C for 2 hours. The use of "silver foil" is required by the temperature reached inside the muffle furnace, since the Ag is resistant up to 960 °C, while the Sn melts at 230 °C. This step allows to obtain the combustion of the organic C without affecting the carbonates content, which is determined by elemental analysis.

For each samples the content of total organic carbon (T.O.C.) is determined by the difference between the value of total C obtained with the first analysis and the value of inorganic C quantified with the second analysis.

In particular in this work the ZE 1100°C muffle (Prederi, Milano, Italy) was used.

Total calcium content

Total calcium content is obtained by dividing the inorganic C (obtained from CNS analysis after treatment in the muffle) for the percentage of C in $CaCO_3$ (12% = 0.12). It is generally expressed as $CaCO_3$ percentage even if there are other carbonates.

ICP-OES (Inductively Coupled Plasma – Optical Emission Spectroscopy)

The ICP-OES is a tool that allows to simultaneously detect all the elements between lithium and uranium with variable sensitivity and precision (with the exception of oxygen, fluorine, noble gases). The characterizing part of the plasma optical emission spectrometer is the plasma itself which is constituted by

argon gas with a high degree of ionization and at very high temperature (from 6000° up to 8000°C depending on the analysis), produced by the ionization of the gas being continuously flushed through the system. The spectrometer consists of four parts: 1-Sample introduction system: the liquid sample solution is aspirated from the tubes through a peristaltic pump whose action is combined with a nebulizer. This system aims to transform the sample solution and the Argon in an aerosol formed by droplets (< 10 μm diameter); 2- Radiofrequency generator and torch: an electric current creates a magnetic field that passes along the torch axis in which the energy produced by the generator is transferred by the electrons to the gas and so for collision the gas is heated. Therefore it has a kind of plasma "nut" where the aerosol containing the sample is injected; 3- Optical bench and detectors: the radiations emitted from the atoms of different elements go to collimate on a fixed system composed of 2 diffraction gratings that provide to separate them between 125 and 770 nm. The core of the reading system is represented by CCD detectors through which it is possible to measure continuously all wavelengths between 125 and 770 nm. The signal arrives at the CCD and then, once "clean", is sent to the PC; 4- Software: to proceed with the samples analysis is necessary to choose the length or the most appropriate wavelengths, since each element emits radiation at most frequencies. The analysis consists of three readings, of variable duration depending on the determination, carried out consecutively. The result is obtained from the arithmetic mean of the three readings.

In this work the ICP-OES spectrometer used was produced by Spectro Italia s.r.l.

Available phosphorus (Olsen method)

The procedure used to quantify the soil available P was the following. A sodium bicarbonate solution (21 g/250 ml of deionized water) was prepared, the solution mixed with a mechanical stirrer with magnetic stir bar, and the pH raised up to 8.5 with sodium hydroxide solution (NaOH). The volume was brought up to 500 ml with deionized water in a flask. 2 g of soil sample previously sieved to 2 mm in a Teflon container were weighed. 40 ml of the solution previously prepared were added and shaken. The Teflon containers were put in a Dubnoff bath for 30 minutes at 60°C for a first rough separation of the liquid and solid phases. The liquid (supernatant) was recovered (max 35 ml) and centrifuged at 10000 rpm (rotations per minute) for 5 minutes. The centrifuge used was ALC 4233R, max RCF (xg) 5289. The supernatant was filtered with Whatman n°42 cellulose filter and loaded in the ICP.

Exchangeable bases (Ca^{++}, Mg^{++}, K^{+}, Na^{+})

A $BaCl_2$ solution (100 g + 50 ml of triethanolamine and 800 ml of deionized water) was prepared, mixed by mechanical stirrer with magnetic stir bar, and the pH was raised up to 8.2 with HCl. The volume was brought up to 1000 ml with deionized water in a flask. 2.5 g of soil sample previously sieved to 2 mm in a Teflon container were weighed. 50 ml of solution previously prepared were added and shaken. The Teflon containers were placed in a Dubnoff bath for 60 minutes at 60°C for a first coarse separation of the liquid and solid phases. The liquid (supernatant) was withdrawn and centrifuged at 3600 rpm for 5 minutes. The

centrifuge used was ALC 4233R, max RCF (xg) 5289. The supernatant was filtered with Whatman n°42 cellulose filter, diluted 1:10 before proceeding with the ICP analysis.

Cations Exchangeable Capacity

The overall cations exchangeable capacity determination was performed with barium chloride and triethanolamine method. 2 g of soil sample were put in a 50 ml Falcon tube and the tube + sample were weighed (weight A). 25 ml of $BaCl_2$ * $2H_2O$ were added, the tube closed and kept stirring for 1 hour. The sample was centrifuged at 3000 rpm for 5 minutes and the clear solution decanted in a beaker. The centrifuge used was ALC 4233R, max RCF (xg) 5289. The same treatment was repeated twice, decanting the clear solutions in the same beaker. The sample was washed with 25 ml of H_2O and centrifuged at 3000 rpm for 5 minutes and after throwing away the supernatant the tube + sample was weighed (weight B). 25 ml of $MgSO_4$ * 7 H_2O solution were taken with a precision burette and transferred in the Falcon tube, the tube was closed and shaken by hand carefully until complete dispersion of the sample, kept under stirring for 1 hour and then centrifuged at 3000 rpm for 5 minutes. 100 ml of MilliQ H_2O + 10 ml of the clear solution of the sample + 10 ml of the buffer solution of ammonium chloride (pH 10) + 2 drops of indicator (Eriochrome black) were mixed and transferred in a 250 ml Erlenmeyer flask. The control solution was prepared by transferring 100 ml of MilliQ H_2O + 10 ml of buffer solution of ammonium chloride (pH 10) + 10 ml of the solution of magnesium sulfate + 2 drops of indicator (Eriochrome black) in a 250 ml Erlenmeyer flask. The control solution and the sample solution were titrated with the EDTA solution until a blue coloration was achieved.

To calculate C.E.C. the following formula was used:

$$C.E.C. = \frac{(Vb - Va) * \mathrm{M} * 1000}{M * 1000} * \frac{30}{10} * \frac{(30 + weight\ B - weight\ A)}{30}$$

where,

C.E.C. = cations exchangeable capacity (in meq*100g^{-1})

Vb = EDTA solution volume (in ml) used to titrate the control solution

Va = EDTA solution volume (in ml) used to titrate the sample solution

Weight A = tube + sample mass (in g)

Weight B = tube + sample mass (in g), after saturation with $BaCl_2 * 2H_2O$ solution and washing with H_2O

30 ml/10 ml = volumetric ratio

M = EDTA solution concentration (in cmoli *L^{-1})

M = sample mass used (in g)

The higher is the C.E.C. value, the higher is the overall quantity of exchangeable K, Mg and Ca into the soil.

Mineralization coefficient

As OM is an important component of the soil, also the processes that govern its evolution over time are critical. There are some processes of "destructive" type (mineralization) that lead to the OM disintegration and to the release of mineral elements (Giandon and Bortolami, 2007).

In this work the Remy and Marin-Lafleche (1974) mineralization coefficient was applied. It is calculated with the following formula:

$$Min.Coeff = \frac{1200}{(C + 20) * (TCC + 20)}$$

where,

C = clay content (in %)

TCC = Total Calcium Content (in %)

The value of this coefficient represents the percentage of OM mineralized in the course of one year: the speed of degradation of organic materials into the soil is inversely proportional to the total calcium content (Giandon and Bortolami, 2007).

Humification coefficient

There are other processes that affect the OM balance of "constructive" type (humification) that lead to the formation of humus (Giandon and Bortolami, 2007). The humification coefficient is calculated with the following formula:

$$\frac{C}{N} = \frac{Total\ N\ d.m.}{T.O.C.}$$

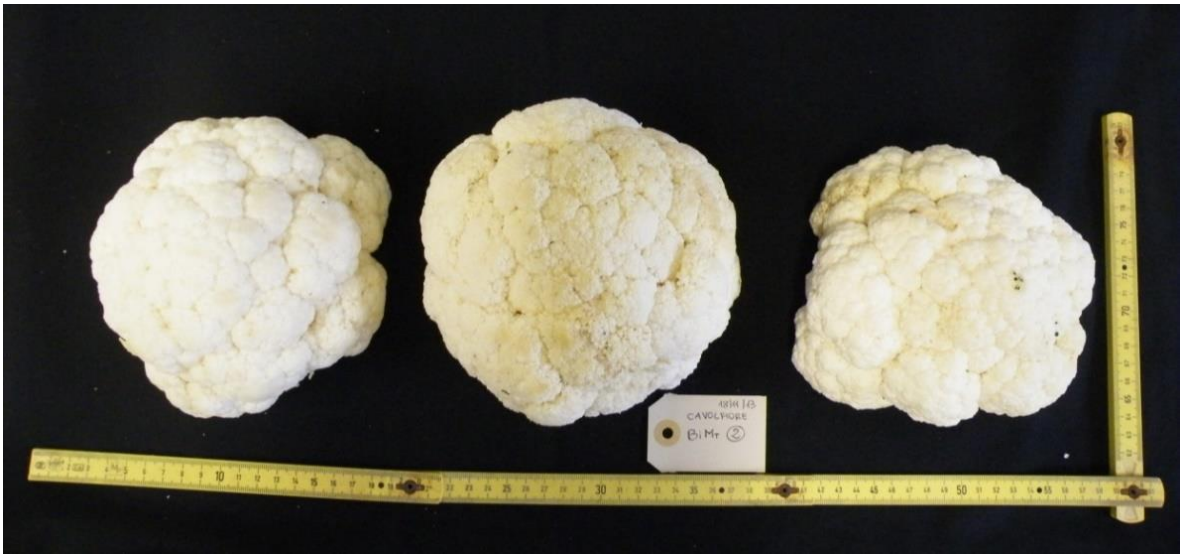
Values of this coefficient close to 10 are typical of well drained soils. Generally soils with C/N ratio between 9 and 11 have a well humified and quite stable in quantity OM; in soils with C/N < 9 oxidation reactions and the release of available N prevail, while in soils with C/N > 11 the N content is not enough to guarantee the progress of the humification process (Giandon and Bortolami, 2007).

Crop nutritional properties analyses

In order to represent the variability in crop product nutritional properties, for each field ten crop plants were collected when they were ready for human consumption and then they were subjected to

several nutritional analyses. All tests were conducted in triplicate and averaged. These analyses were performed at the RICerca OrtoFloricola PaDova laboratory (DAFNAE, Legnaro, Italy).

a)



b)

Fig. 26: (a) Commercial plant of Treviso red chicory-late variety; (b) commercial inflorescence of white cabbage during the first stage of physical characterization in the laboratory (Ph. S. Fusaro).

Physical analysis

Colour

The colour was evaluated with the optical colorimeter (Minolta CR-300), according to the Hunter Lab method concerning the L, a, b values: **L** indicates the brightness of the sample, and varies from black (0) to white (100); **a** indicates the colour of the sample in the range between green and red; and finally **b** in the range between blue and yellow by the spectrophotometer (Colour Eye XTH).

Dry matter

Samples dry matter quantification was obtained in a PID System ventilated oven (model M80-VF; Instruments s.r.l.; Bernareggio (MI), Italy) set at 65 °C for 72 hours. The difference of the sample weight between before and after heating in the oven allows to determine dry matter quantity.

Compositional analysis

Total Antioxidant Capacity

As regarding the determination of the total antioxidant capacity (TAC) and total phenols were used methods indicated in Kang and Saltveit (2002) and Benzie and Strain (1996) with appropriate adjustments to adapt the methods to the material to be analysed (Nicoletto and Pimpini, 2010). Crop samples were frozen and stored at -80°C before proceeding with the analysis. The determination of the TAC and total phenols was provided for both the tests 5 g of d.m of the sample to which 20 ml of methanol were added; the sample was homogenized for 30 seconds with the aid of the Ultra Turrax T25 at a speed of 17000 rpm and then filtered with filter paper (589 Schleicher with a diameter of 125 mm).

The TAC was determined by the method FRAP (Ferric Reducing Antioxidant Power). The FRAP reagent (1 mM 2,4,6-tripyridyl-triazine 2 [TPTZ], 2 mM ferric chloride and 250 mM sodium acetate solution at pH 3.6) was prepared daily from stock solutions of 300 mM acetate buffer, 12 mM TPTZ (in hydrochloric acid 48 mM) and 24 mM ferric chloride in ratio 10:1:1. To 100 µl of extract were added 1900 µl of FRAP reagent and it was homogenized with a vortex; after leaving the mixture at 20°C for 4 minutes, the absorbance at 593 nm was determined. The value of absorbance was compared with a calibration curve formed from solutions of ferrous ammonium sulphate with concentration from 0 to 1200 g/ml of ferrous ion. The TAC was expressed in equivalent mg of Fe^{2+} (Fe^{2+} E)/kg of dried sample.

Polyphenols

Polyphenols were estimated using the Folin-Ciocalteau method (Singleton and Rossi, 1965). In order to determine total phenols 200 µl of extract were taken, then 1000 µl of Folin-Ciocalteu's phenol reagent, 800 µl of anhydrous sodium carbonate (7.5%) were added to them and with the aim to dilute the solution, 2000 µl of deionised water were added. Afterwards the solution was agitated for 15 seconds and subsequently left to rest for 30 minutes at room temperature before reading the value of absorbance with the spectrophotometer (Shimadzu UV-1800) at a wavelength of 765 nm. The absorbance was compared with the values of solutions at known concentration of gallic acid (ranging from 0 to 600 g/ml) which underwent the same procedure of the samples. The total phenol content was expressed in mg of gallic acid equivalents (GAE)/kg of dried sample.

Free phenolic acids

For the determination of free phenolic acids, 5 g of sample were whipped and extracted in 20 ml of 100% methanol homogenizing the whole mixture with Ultra-Turrax for 30 seconds. Thereafter the sample was filtered with a 589 Schleicher filter paper and, without any dilution, it was filtrated again using cellulose acetate 0.45 µm syringe filters. The analysis was performed with High Pressure Liquid Chromatography (HPLC) using a mobile phase consisting of 0.1% formic acid (A), methanol (B) with a gradient for B of 0-100% in 50 minutes. The phenolic acids separation was obtained by using the column Tracer Exstrasil OSD2 (250 x 45 mm, 5µm) thermostated at 35°C by a temperature control system (Jasco CO-2060); the flow rate was 0.8 ml/min. For the subsequent identification of the phenolic acids the following wavelengths were used: 200-600 nm (310 nm for *p*-coumaric acid, 325 nm for caffeic, chlorogenic and ferulic acids, 330 nm for sinapic and chicoric acids, 520 nm for the anthocyanins cyanidin-3-glucoside and cyanidin-3-malonil glucoside). All standards were prepared by dissolving the compound in methanol (3 g/l) and the calibration curve was performed by using serial dilutions (0.3-30 mg/l).

Sulforaphane

Sulforaphane content was determined by using the method of Ghawi et al. (2013). It is the hydrolysis product of glucoraphanin (mainly glucosinolate present in *Brassica* vegetables) and since it is a naturally occurring cancer chemopreventive and neuroprotective molecule (Ghawi et al., 2013; Tarozzi et al., 2013), in this work its content was determined in cabbage samples. To proceed with the extraction, 0,5 g of lyophilized and grind sample were added to 10 ml of demineralized water, homogenizing the whole mixture with Ultra-Turrax for 30 seconds. Thereafter the compound was incubated in the dark at room temperature for 3 hours. Later the sample was filtered with a 589 Schleicher filter paper. 2 ml of dichloromethane were added to 1 ml of filtrate and then homogenized with a vortex for a few seconds: after the separation of two phases was waited. Only the organic part was separated and the extraction

with water was repeated. After centrifugation for 3 minutes, the organic part was separated. The organic parts were put together and made it evaporate by using the rotary evaporator. Then a new solution was made with 2 ml of acetonitrile and the last filtration was performed by using cellulose acetate 0.45 µm syringe filters. The analysis was performed with HPLC using a mobile phase consisting of water (A), acetonitrile (B) with a gradient for B of 0-60% in 20 minutes and of 60-100% in 2 minutes. The sulforaphane separation was obtained by using the column Tracer Exstrasil OSD2 (250 x 45 mm, 5µm) with a controlled temperature at 30°C by a temperature control system (Jasco CO-2060); the flow rate was 1 ml/min. For the subsequent identification of sulforaphane a wavelength of 235 nm was used. The standard was prepared by dissolving the compound (D,L-sulforaphane) in ethanol (200 mg/l) and the calibration curve was performed by using serial dilutions (0.2-20 mg/l).

Reducing sugars

As regarding the content of reducing sugars (glucose and fructose), 5 g of sample were whipped and extracted in 20 ml of demineralized water and, thereafter, the extract was filtered with Schleicher 589 filter paper. Subsequently the sample was further filtered with cellulose acetate 0.45 µm syringe filters. The analysis was performed with HPLC by using a chromatographic gradient system (Jasco PU-2080 Plus), consisting of a binary pump based on the principle of mixing at high pressure and by a refractive index detector (Jasco RI 2031 Plus). The HPLC column HyperRez XP Carbohydrate Ca^{++} used for the analysis has dimensions of 300 mm length and 7.7 mm in diameter. The data provided by this system were collected and processed by using the software ChromNAV for LC systems. The injections were made using a Jasco AS 2055 Plus autosampler, and moreover a thermostatic column compartment (Jasco CO-2060 Plus) was used to obtain reproducible data at a controlled temperature of 80°C. A standard solution of glucose (1 mM) and fructose (1 mM) and water for HPLC (Sigma-Aldrich) was used. The mobile phase used for HPLC was made by water (100%) and the flow used was 0.6 ml/min.

Ascorbic acid

The procedure adopted to know vitamin C or ascorbic acid content was the following. Samples were frozen and stored at -80 °C before proceeding with the analysis. The determination of ascorbic acid was performed according to the B method of ISO 6557, which is a standard method for the analysis of fruit and vegetables. In short terms, 5 g of sample were homogenized with Ultra turrax in 20 ml of the extraction solution (consisting of meta-phosphoric acid and acetic acid solution). A solution of 2,6-di chlorophenyl-indophenol was used as colorant. The values of the prepared samples were determined by a spectrophotometer at a wavelength of 500 nm.

Nitrogen content

The nitrogen content was measured by the Kjeldhal method (ISO1656).

Anions and Cations

The determination of the content of anions and cations was achieved by Ion Chromatography (IC). 200 mg of dry sample were weighed and extracted with 50 ml of demineralized water. Sample agitation on a rotating plate was performed for 20 minutes at 150 rpm and afterward the sample was filtered by using a 589 Schleicher filter paper. The filtrate, after appropriate dilution in demineralized water, was filtered by using cellulose acetate 20 μm syringe filters and then injected into the chromatograph. For anions analysis an Ion Pac AS23 column with dimensions 4x250 mm was used, while for cations analysis an Ion Pac CS12A column with dimensions 4x250mm was used, both thermostated at room temperature. The chromatographic run was performed at a flow rate of 1 ml/min. The eluent used was consisting of sodium carbonate (4.5 mM), sodium bicarbonate (0.8 mM) for the analysis of anions and of metensolfonic acid (20 mM) for the analysis of cations. The flow rate used was 1 ml/min. The identification of the compounds in the examined mixture was detected by comparison of retention times with standard compounds (fig.27). For the analysis of anions a mixture consisting of fluorides, chlorides, nitrites, bromides, nitrates, phosphates and sulphates was used while for the analysis of cations a mixture consisting of lithium, sodium, ammonium, potassium, magnesium and calcium was used. The quantitative analysis was performed by using the calibration curve created as a result of serial dilutions of the stock solutions.

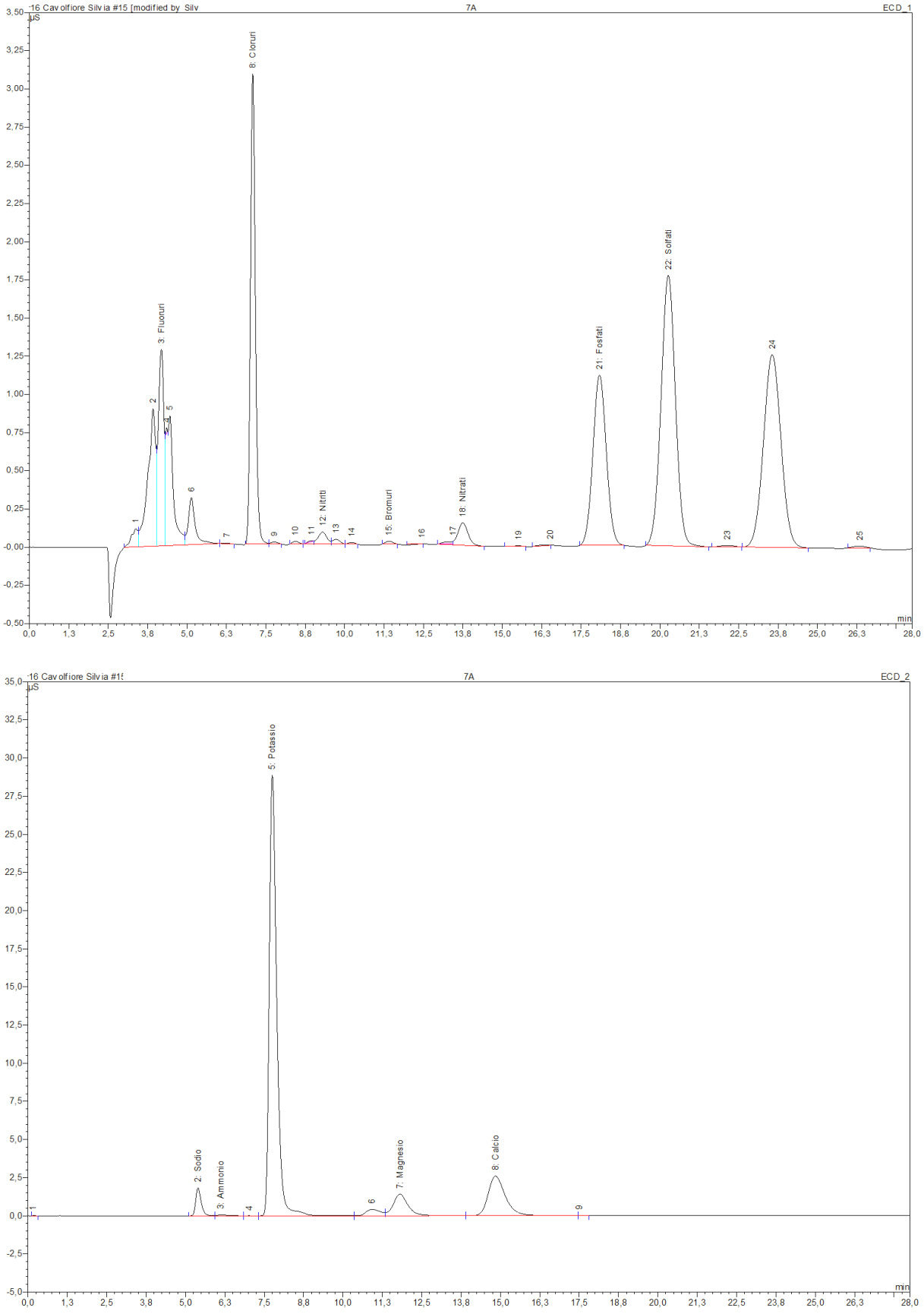


Fig. 27: Example of a cabbage sample chromatogram relative to anions (above) and cations (below).

Quantitative crop elemental analysis

As regards the detection of any kind of detectable elements, sample mineralization (1 g of dried sample) was performed in a muffle furnace at 550°C for 6 hours. Then the ashes of 1 g of dry substance were melted in 5 ml of concentrated HCl. After 30 minutes, the solution was diluted with distilled water to reach a volume of 50 ml. Subsequently, the solution was carefully filtered to proceed with the analysis of elemental content. The instrument used in this analytical phase was the ICP-AES (Inductively Coupled Plasma-Atomic Emission Spectroscopy) (SPECTRO CIROS, Spettro Italia S.r.l.) spectrometer (see above in soil analyses for details about the instrument).

Data statistical analyses

PAST software version 3.04 (Hammer, 2014) was used to perform statistical analyses. Cytoscape software version 3.2.0 was used to visualize the correlations among biotic indicators, functional indicators and measured parameters.

Indirect data ordination

Generally, data ordination techniques should be used for data exploration, finding a concise and useful summary of the patterns or trends within multivariate data (Shaw, 2003). In particular, indirect data ordination techniques detect tendency within data without the operator needing to define gradients within data (Shaw, 2003). These techniques return a new arrangement of the analysed samples recalculated on the basis of two components or axes, the first of which is always explaining the greater part of data variability.

Non-metric Multidimensional Scaling (NMDS)

Initially, data about the composition of the different bioindicators groups were processed by the non-parametric ordination data technique of Non-metric Multidimensional Scaling (hereafter defined as NMDS). Ordination data techniques are important for reducing the data dimensionality, which is useful for displaying multidimensional data sets. NMDS technique was chosen because less sensitive to data deviation from normality and therefore appropriate to elaborate ecological data coming from populations with non-normal distributions and discontinuous (Shaw, 2003; Mouhmadou et al., 2013). The reduction of data dimensionality is defined as the transformation of a given multidimensional datum in a meaningful representation of reduced dimensionality (Bessi, 2008). The NMDS two-dimensional resulting plot is a representation of a set of low-dimensional points, which reflects the relative data configuration at initial

high dimensionality, according to the proximity among these points expressed in similarity measure (Shaw, 2003; Bessi, 2008).

Principal Components Analysis (PCA)

When there was the necessity to highlight the relationships among samples and the variable meanings, the Principal Components Analysis biplot representation was used (hereafter defined as PCA). A biplot is an extension of ordination plot, in which an ordination of properties of the analysed variables are overlain on top of the main ordination plot. Such a plot can directly allow the operator to see which properties are strongly associated with each observation (datum), since proximity implies close association: therefore biplot suggests tendencies between two sets of data (Shaw, 2003).

Data classification

Data classification techniques are used to search for divisions within data, seeking to classify samples on the basis of their attributes, for example species composition. The general aim is to identify discrete subsets of samples with similar characteristics (Shaw, 2003), therefore they are intended to help the researcher explore data and generate hypotheses.

Cluster analysis

Given that ordination techniques do not directly provide probability levels (so that an ordination output cannot be said to be statistically significant) (Shaw, 2003), to objectify the interpretation of ordination plots and since the traditional form of hypotheses testing using statistical tests can be applied to the scores calculated by the software after ordination (Shaw, 2003; Gotelli and Ellison, 2004), in this study the new coordinates of the samples referred to the main axis (1) of the NMDS plot were used to perform a classification technique. The chosen one was the most commonly used classical cluster analysis which can produce a dendrogram of relationships among all the samples, based on their similarities. The rule chosen for cluster formation was the minimum variance clustering or Ward's method applied to a matrix of Euclidean distances, since generally it gives intermediate results between single-link and complete-link clustering and it is commonly used by ecologists (Shaw, 2003).

To make data analysis as objective as possible it was decided to proceed blindly, or not knowing the identity of the samples (afterwards attributed).

The different cluster analyses referred to each bioindicator, grouped the samples according to similarity: samples positioned closer in the dendrogram are more similar with respect to the bioindicator

used for the analysis. If the samples clustered in the same group were belonging to the same management, then it could be concluded that the examined group of bioindicators was sensitive to agroecosystem management. On the contrary, if the grouped samples did not come from agroecosystems with the same management, then that bioindicator was not sufficiently sensitive to the management condition.

Ordination and classification methods were used to extrapolate relationships which may exist between the community composition of considered bioindicators and the management of the agroecosystem where they came from (and therefore to answer the first question of the objectives).

Statistical tests

As regards inferential statistics, first of all Shapiro-Wilk normality test was performed to test for data normal distribution. Eventually data were transformed by using log(x + 1) or radq(x). Fisher's F-test was performed to test for homogeneity of variances within the analysed groups.

In order to process cumulative data coming from the two groups of fields under study (organic-biodynamic and conventional groups), tests for separation of means and medians were used. If data had a normal distribution, the parametric Student's t-test was performed to assess equality of means. If data were not normally distributed, Mann-Whitney U test was applied, one of the most powerful non-parametric tests (Zar, 1984), to assess the equality of the medians of the two groups. In the case the variances of the two groups were different, condition in which the use of the Mann-Whitney U test can lead to wrong results as the erroneous acceptance of the alternative hypothesis, Student's t-test was chosen to test the equality of means that allows the samples come from populations with distributions with different variances (Nachar, 2008). For completeness, when data were normally distributed and the variances were homogeneous, both the t-test value and the U test value were reported in results, since the latter has approximately 95% of the statistical power of the Student t-test (Landers, 1981; Zar, 1984) and also when the assumptions of the t-tests are seriously violated, the Mann-Whitney U test can be much more powerful (Hodges and Lehmann, 1956; van Emden, 2008).

When it was possible to collect data with a proper replication in time, two-way ANOVA was performed to test the significance of difference between the organic-biodynamic and conventional groups, establishing the two factors as the sampling period and the management. If the basic requirements to apply ANOVA test of data normality and variance homogeneity were not satisfied, the non-parametric Friedman test was performed. In particular in order to balance the statistical analyses about different groups of phytophagous agents and predators sampled during 2013 on cabbage crop, only three organic and three conventional fields were considered, those located in the Venice province.

When there was a proper data replication, but only for one factor (the management) one-way ANOVA was performed. If the basic requirements to apply ANOVA test of data normality and variance homogeneity were not satisfied, the non-parametric Kruskal-Wallis test was applied.

The multiple comparison procedure exemplified by the Tukey's (also known as Honest Significant Difference test -HSD) test was applied in order to find if means were significantly different from each other, when there were more than two groups to compare (for example among the four sampling periods of fertimeters).

Finally Chi squared (χ^2) test was applied to calculate the significance of the difference between observed data and expected data (for example in the case of *P. xylostella* parasitization and hyperparasitization rates).

Diversity Indexes

Diversity indexes are mathematical measures of species diversity in a community, they are numeric scores given to a community which reflect its diversity (Shaw, 2003). They provide more information about community composition than simply species richness; they also take the relative abundances of different species into account and so the evenness features of an assemblage (Magurran, 2004).

They were calculated using Software PAST version 3.04 (Hammer, 2014).

Taxa

Taxa_S is the simplest index that can be calculated and it represents simply the number of different taxa composing the analysed sample.

$$S = n°taxa$$

Shannon

Shannon_H is the most commonly used diversity index. It takes into account the number of individuals as well as number of taxa. It is calculated with the following formula:

$$H = -\Sigma \frac{n_i}{n} \ln \frac{n_i}{n}$$

Its value ranges from 0 for communities with only a single taxon to high values for communities with many taxa, each with few individuals.

Simpson

Simpson_1-*D* is widely used due to its conceptual simplicity: it relates to the probability that two consecutive individuals taken at random from a population belong to the same species. It is calculated with the following formula:

$$1 - D = \sum_{i=1}^{s} p_i^2$$

where $P_i = \frac{N_i}{\Sigma N}$, that is the probability of sampling species *i* that is that species' proportion of the total.

Simpson index value ranges from 0 (for highly diverse community) to 1 (for a community that consists of just one species).

Dominance

Dominace_D index is 1-Simpson index. It is calculated with the following formula:

$$D = \sum_{i} (\frac{n_i}{n})^2$$

where n_i is the number of individuals of taxon *i*.

Dominance index ranges from 0 (all taxa are equally present) to 1 (one taxon dominates the community completely).

Equitability

Equitability_J is Shannon diversity divided by the logarithm of number of taxa. This index measures the evenness with which individuals are divided among the taxa present.

$$J = \frac{H}{\log(S)}$$

It reflects the evenness of species distribution within the sample. An equitability index value near 0 shows the community to be dominated by one species, while a value near 1 shows it to have an equal balance among all species.

Evenness

Evenness_e^H/S is the Buzas and Gibson's evenness index: it is another measure of the equitability among life forms (Cardinale et al., 2012).

Correlation

The correlation is an index of the extent to which two variables change in value together.

Pearson's coefficient

In order to express the possible relationships among the diversity indexes of the analysed bioindicators, the tests of ecosystem services functionality, the soil chemical-physical analyses, the crop nutritional properties and the landscape composition categories, the Pearson's correlation coefficient (r) was calculated. Since it is a parametric coefficient, first of all data normality was verified using Shapiro-Wilk test. If data were not normally distributed, they were transformed by log (x + 1) or sqrt (x). This coefficient value ranges from 1 (positive correlation between the variables) to -1 (negative correlation). A coefficient value equal or near 0 means lack of correlation. R^2 is equal to the proportion of the variance which is explained by the linear regression (Shaw, 2003; Fowler and Cohen, 2010).

Spearman's coefficient

When data distribution was not normal also after data transformation, the Spearman's correlation coefficient (r_S) was calculated. It is a non-parametric version of Pearson's correlation coefficient, calculated by recording all data as their ranked values then calculating Pearson's correlation coefficient (Shaw, 2003).

RESULTS AND DISCUSSION

Landscape structure overview

An important factor that has to be considered in agroecological research is the landscape structure around the fields object of study. This factor does not depend directly and completely from the farmer or from his farm management, but from the context in which his farm is inserted. In this work landscape composition was analysed within different radius concentric areas from the field centre. Table XII summarises results about this analysis.

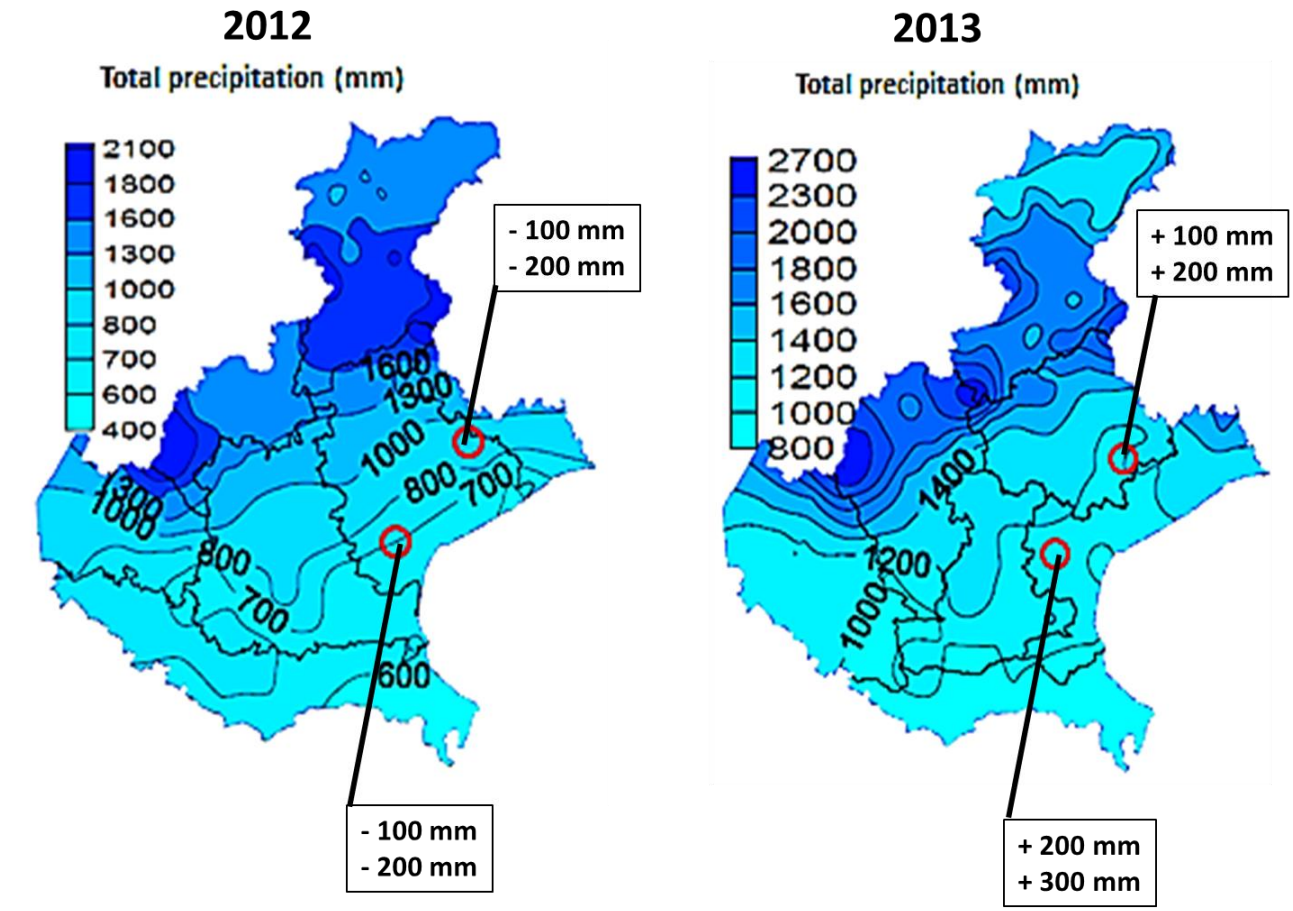
Radius from field center	**Landscape category**	**Organic-biodynamic** [Mean (S.E.)]	**Conventional** [Mean (S.E.)]	**Statistical test** (Kruskal-Wallis)
100 m	Arable	71.48 (3.28)	66.89 (6.47)	n.s.
	SemN	19.92 (3.84)	19.47 (4.46)	n.s.
	Urb	4.07 (1.79)	8.38 (3.77)	n.s.
150 m	Arable	69.68 (5.17)	57.91 (3.82)	n.s.
	SemN	24.73 (4.42)	30.70 (2.36)	n.s.
	Urb	4.05 (1.68)	9.88 (3.28)	n.s.
300 m	Arable	64.23 (5.98)	48.99 (6.53)	n.s.
	SemN	25.95 (6.71)	33.62 (5.80)	n.s.
	Urb	7.44 (2.42)	12.60 (4.03)	n.s.
500 m	Arable	59.97 (5.63)	48.73 (6.29)	n.s.
	SemN	26.24 (7.08)	31.73 (5.10)	n.s.
	Urb	12.28 (3.28)	14.54 (4.86)	n.s.
700 m	Arable	59.68 (7.94)	50.76 (6.38)	n.s.
	SemN	24.73 (7.33)	30.10 (5.56)	n.s.
	Urb	13.48 (4.86)	16.25 (4.76)	n.s.
1000 m	Arable	58.58 (8.93)	44.14 (9.65)	n.s.
	SemN	23.15 (6.93)	26.76 (4.55)	n.s.
	Urb	16.73 (6.58)	21.47 (4.34)	n.s.
Field dimension (ha)		0.21 (0.04)	0.23 (0.05)	n.s. (one-way ANOVA)

Tab. XII: Mean values of areas (in %) of different landscape categories considered within 100-150-300-500-700-1000 m radius concentric areas from the field centre. Arable: arable land use; SemN: semi-natural environment; Urb: urban environment. Significance: n.s.: p value >0.05.

From this landscape analysis emerges that there are no significant differences in landscape structure for the mean of organic-biodynamic fields and the mean of conventional fields considered. They are included in the same lowland context, characterized by a prevalence of arable land use and therefore it is possible to define the landscape structure as simple. Furthermore the mean dimension of the studied fields was comparable between the two types of management system. These reflexions are important to consider uniform the landscape structure and the field dimension in order to remove two variables (the landscape and the field dimension) from overall data interpretation.

Considerations about meteorological data

Another important consideration is to characterize the studied areas and the sampling period from a meteorological point of view and for this reason during the two years of field data collection (2012 and 2013), also weather data were downloaded from ARPAV system web service[17]. Among all, in particular precipitation data have showed anomalous trends in respect with the past reference period 1994-2012 (fig.28).



a) b)

[17] Data available on ARPAV website: http://www.arpa.veneto.it/bollettini/meteo60gg/Mappa_TEMP.htm

Fig. 28: Annual values of precipitation in Veneto region (ARPAV): a) the difference in precipitation is between 2012 and the 1994-2011 reference period; b) the difference in precipitation is between 2013 and 1994-2012 reference period. Areas object of this study are marked with red circles.

The weather diagrams show how 2012 was a dryer year, with 100-200 mm of rain less than the reference period average, while 2013 was a wetter year, with from 100 up to 300 mm of rain more than the reference period. There were not particularly marked differences in precipitation between the studied sites located in the Venice province and Treviso province.

Soil physical-chemical analyses

During the fieldwork period soil samples were characterized also from the pedological point of view. In the following table results of soil analyses are summarised.

Soil parameters	**Organic-biodynamic** [Mean (S.E.)]	**Conventional** [Mean (S.E.)]	**Statistical test** (Kruskal-Wallis)
pH in H_2O	8.08 (0.1)	8.11 (0.1)	n.s.
Electric conductivity (µS/cm)	653.4 (90.8)	633 (87.3)	n.s.
Clay (%)	18.2 (2.7)	23.3 (4.5)	n.s.
Silt (%)	17.4 (1.6)	17.7 (1.7)	n.s.
Sand (%)	64.4 (2.9)	59.1 (6.1)	n.s.
Total N d.m. (%)	0.15 (0.01)	0.12 (0.01)	*
Total C d.m. (%)	4.57 (1.8)	4.39 (1.8)	n.s.
Inorganic C d.m. (%)	3.42 (1.7)	3.49 (1.7)	n.s.
Total Organic Carbon (%)	1.15 (0.1)	0.91 (0.1)	n.s.
Organic Matter (%)	1.98 (0.2)	1.56 (0.2)	n.s.
Calcium content (%)	28.48 (14.5)	29.06 (14.0)	n.s.
Cations Exchangeable Capacity (meq/100g)	21.97 (1.5)	20.54 (0.7)	n.s.
P (Olsen method) (mg/l)	507.84 (126.6)	267.76 (41.5)	n.s.
Exchangeable K^+ (mg/l)	189 (24)	139 (21.4)	n.s.
Exchangeable Na^+ (mg/l)	441.6 (57.9)	256 (63.3)	n.s.
Exchangeable Mg^{++} (mg/l)	959 (262.8)	553.8 (107.3)	n.s.
Exchangeable Ca^{++} (mg/l)	5370 (1631.4)	5602.2 (1268.7)	n.s.
Mineralization Coefficient	0.87 (0.2)	0.63 (0.1)	n.s.
C/N (Humification)	7.9 (0.6)	8.0 (1.2)	n.s.

Tab. XIII: Mean values of soil chemical parameters. D.m.: dry matter. Significance: *: p value <0.05; n.s.: p value > 0.05.

Detailed results of soil physical-chemical analyses for each soil sample are listed in the appendix (tab. LVIII).

Concerning soil chemical parameters, it can be appreciated that among the analysed soils there are no significant differences between the two management practices (organic-biodynamic and conventional)

except for the total nitrogen (N) measured in dry matter, which was higher in organically-biodynamically managed soils. There are some evidences in literature that demonstrate the benefits of organic farming in reducing N leaching and increasing N uptake efficiency, due to the fact that techniques to reduce N losses and to increase the efficiency of N uptake are widely used in this type of farming system (Kramer et al., 2006), and these results seem to confirm this tendency. In particular Kramer and coworkers (2006) measured that annual nitrate leaching was 4.4-5.6-fold higher in conventional than in organic plots, with undesirable consequences for groundwater pollution in the surrounding of conventional fields.

(1) Biodiversity overview

In this chapter, the goal is to answer the first question of the objectives:

Can different agroecosystem managements (organic/conventional) change taxa composition of the different bioindicator groups in horticultural crops?

Therefore results of statistical analyses of taxa of each sampled bioindicator group and of functional indicators are discussed.

Soil Microbiology

Bacterial diversity overview

A.R.I.S.A.

By using A.R.I.S.A. technique it was possible to explore soil bacterial communities, obtaining a DNA fingerprint. 36 DNA fingerprint profiles were obtained for a total of 111 different amplification products found, characterized by a variable length between 100 and 800 bp. A mean of 45.9 DNA fragments was analysed for each sample. A first consideration is about the number of peaks of soil bacterial strains in the electropherogram: the difference in peak number between soils belonging to different management systems was not significant (tab.XIV).

	Organic-biodynamic [Mean (S.E.)]	**Conventional** [Mean (S.E.)]	**Statistical test** (One-way ANOVA)
N° peaks in electropherogram	43.89 (1.39)	48.06 (1.57)	n.s.

Tab. XIV: Mean number of peaks in A.R.I.S.A. electropherogram for bacterial community analyses. Significance: n.s.: p value >0.05.

A cluster diagram of all soil samples was obtained with numerical data of abundance of each bacterial strain (fig. 29).

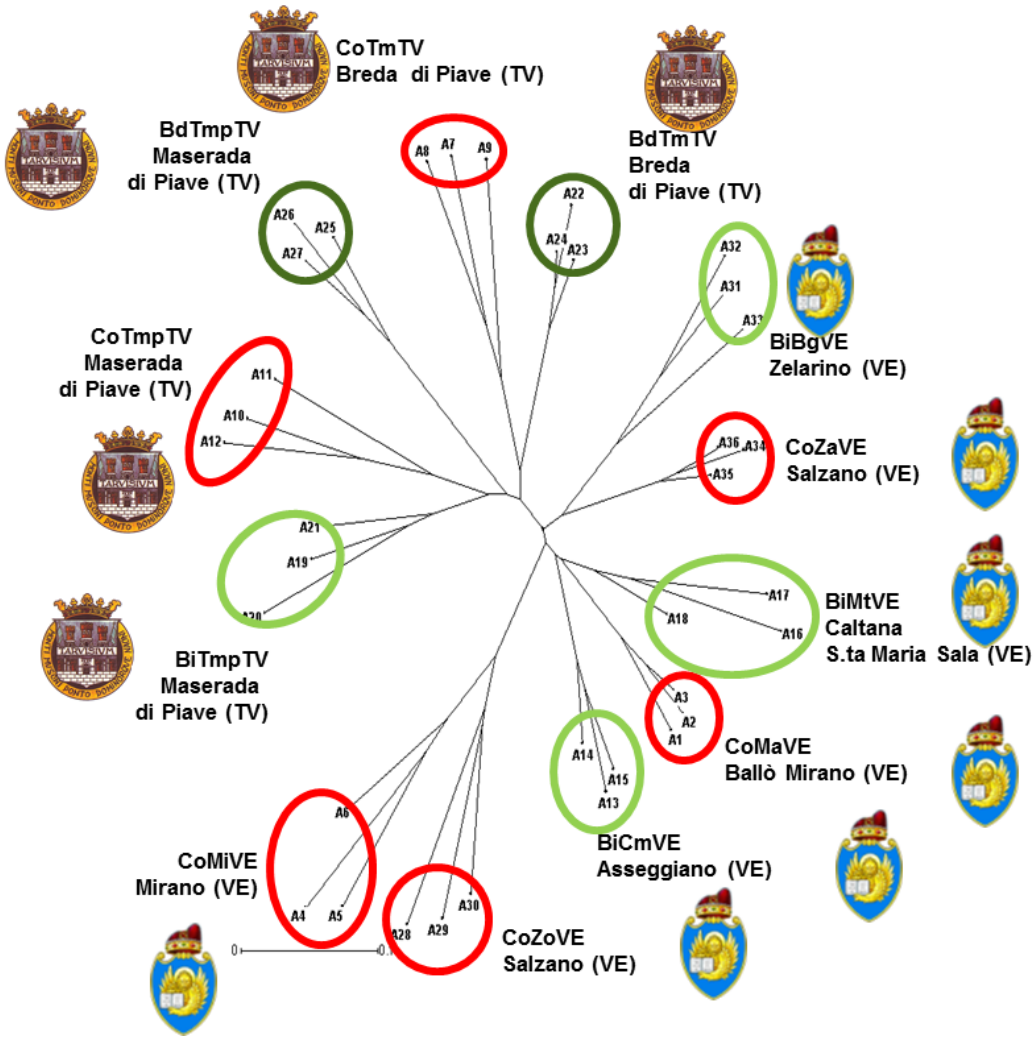


Fig. 29: Cluster diagram (neighbour-joining analysis) of soil bacterial communities analysed by the A.R.I.S.A. technique. In red: conventional farm samples; in light green: organic farm samples; in dark green: biodynamic farm samples.

: fields located in the Venice province. : fields located in the Treviso province.

Despite the known innate heterogeneity of soils and of microorganism spatial distribution and despite microbial diversity and population size could be underestimated resulting in high variability between replicates (Kirk et al., 2004), the proximity of the three replicates coming from the same field in the cluster diagram (fig. 29) supports a reproducible and faithful outcome of analysis and an appropriate representation of overall bacterial community of each field. Moreover a separation of two main clusters is evident, the Venice province samples and the Treviso province samples, independently from the management practices (in fact samples coming from organically and conventionally managed soils are joined in the same cluster). It could mean that bacterial communities are characterized more by the locality factor than by the management system and a sort of “bacterial biogeography” could be seen within the

cluster diagram, probably due to the scarce efficiency in diffusion of bacteria. A robust example of the use of bacterial communities to solve a murder case with the help of the strong bond to local geography factors can be found in literature (Concheri et al., 2011).

In order to visualize relationships of similarity among bacterial community samples in a 2D space, a multivariate statistical technique of ordination was applied since, as in most ecology studies, the initial priority is the reduction of the number of variables, which is typically high.

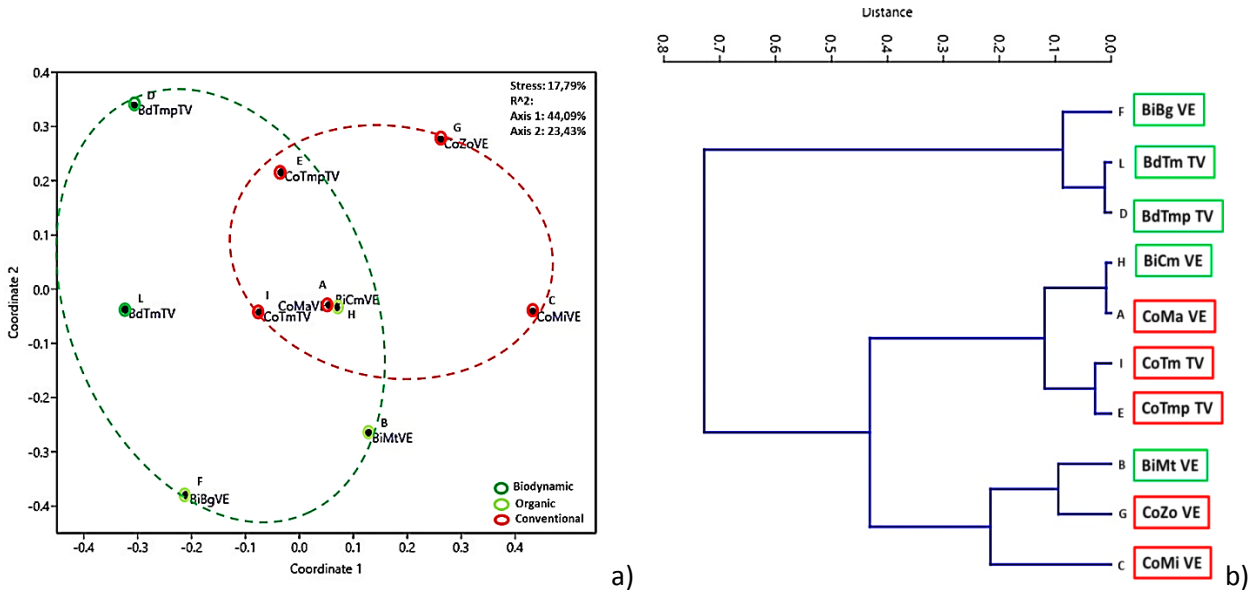


Fig. 30: a) NMDS plot of soil bacterial communities (A.R.I.S.A.) data, Bray-Curtis similarity measure. b) Classical cluster analysis of NMDS scores on axis 1 data of soil bacterial communities (A.R.I.S.A.), Ward's method- Euclidean similarity measure.

To read the NMDS plot in an objective way, by using the recalculated coordinates of each sample points on axis 1 (the one which explains the most part of samples variance), a cluster analysis was performed (fig.30 b). The aim of this analysis is to find whether samples of soil bacterial communities can be divided according to the management system.

From this cluster diagram it can be appreciated how the soil samples are divided in more than two groups and not according to the type of agriculture. Probably two main factors can have acted in this classification: management and locality. Therefore in this research, it was not possible to detected a difference among soil samples concerning just the management, as concerns the hosted bacterial communities analysed by A.R.I.S.A. technique.

Bacterial 16S amplicon sequencing

By using the 454 Roche technology, from 10712 to 18403 reads for each sample were sequenced and after the quality filtering phase, a minimal number of 6363 sequences was chosen at random for each sample. Statistical analyses were performed on these sequences. First of all a screening of the abundance of different phyla was made (fig. 31).

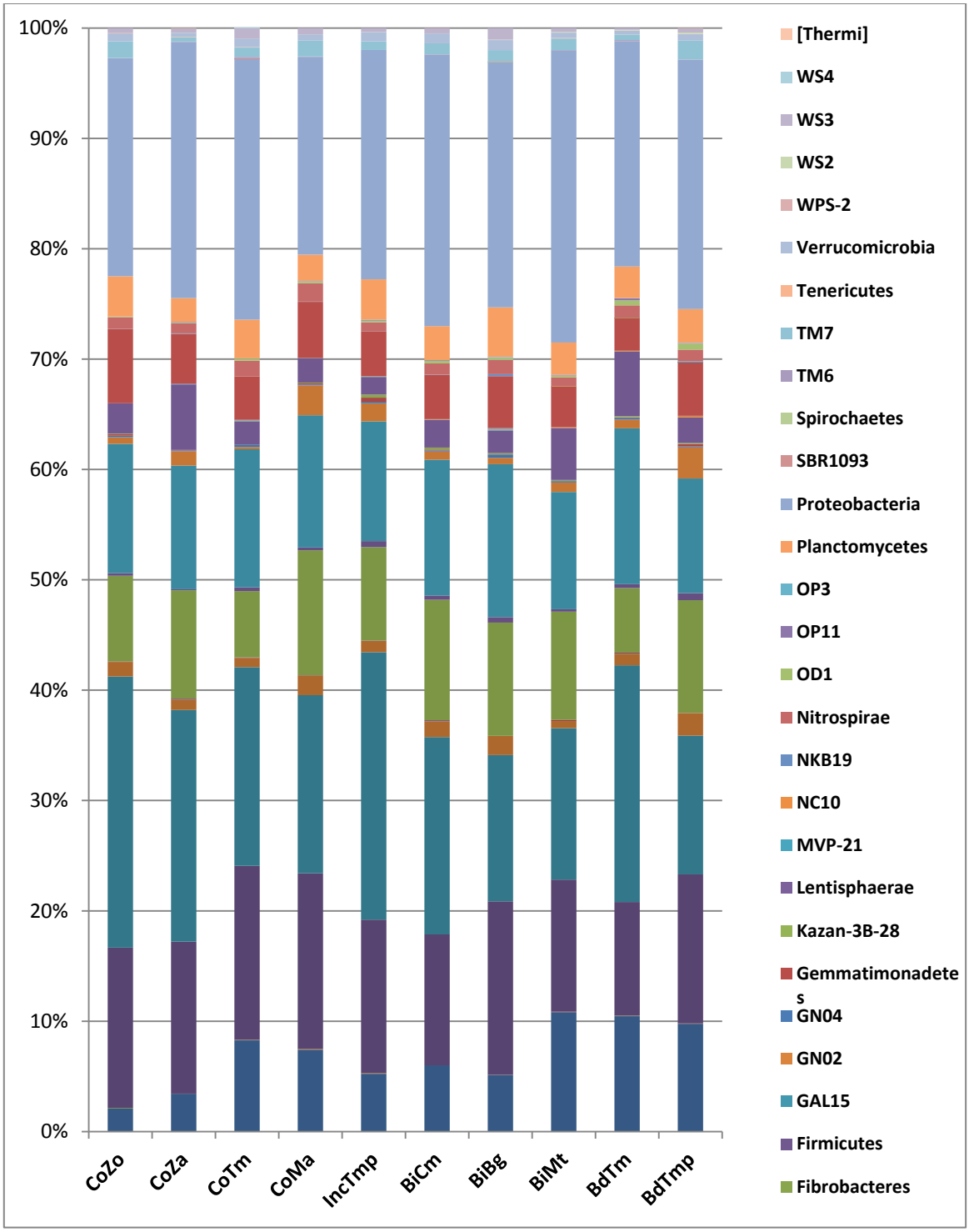


Fig. 31: Histogram of soil bacterial phyla diversity (presence in %) analysed by 16S amplicon sequencing.

The following pie charts (fig. 32) show data of the most abundant bacterial phyla (more than 2%).

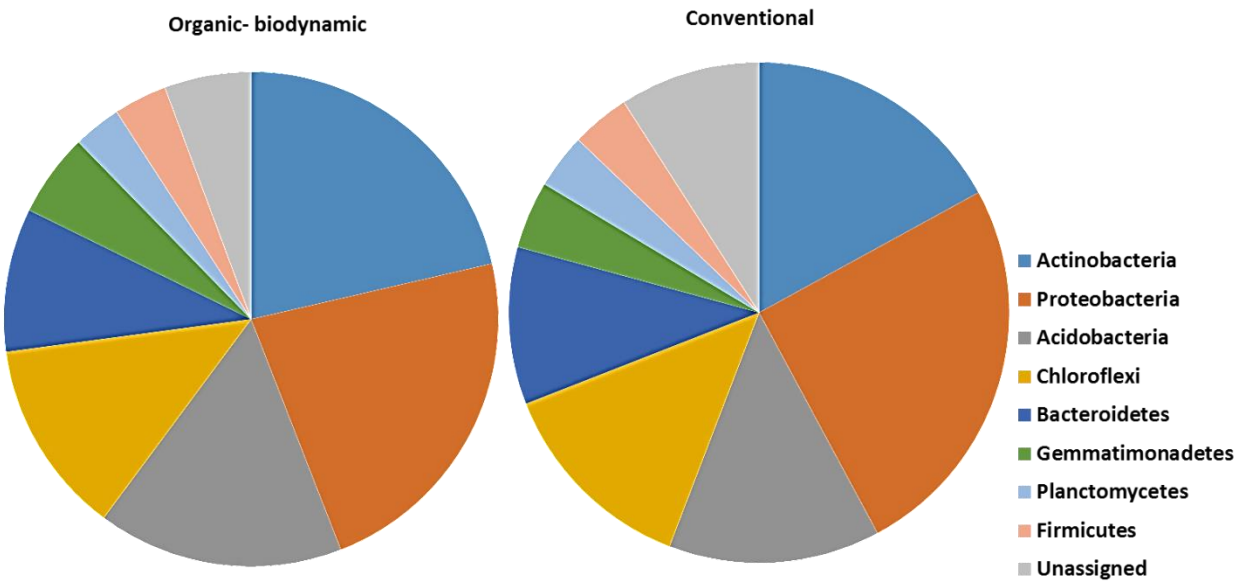


Fig. 32: Pie charts of the mean data of the most abundant bacterial phyla (> 2 %) in the two types of agriculture analysed.

As it can be also observed by the image no significant differences can be traced in abundance among the most present soil bacterial phyla in the two management systems (all p-values >0.05).

The relative abundances of the four principal classes of the Proteobacteria phylum were also compared in the two types of management systems (fig. 33).

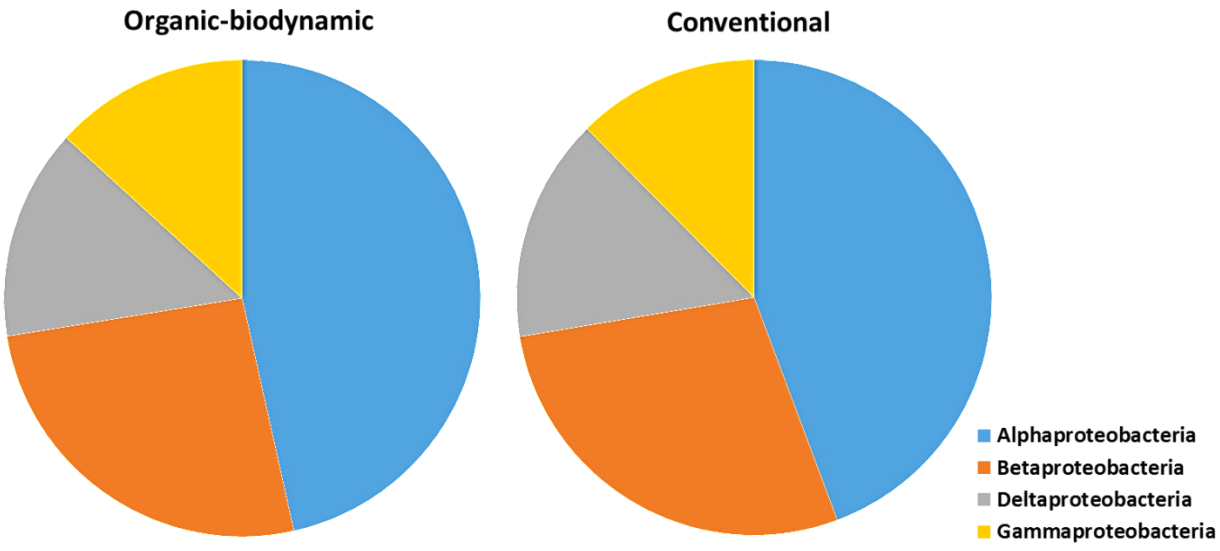


Fig. 33: Pie charts of the mean data of the four principal Proteobacteria classes in the two types of agriculture analysed.

There are neither observable nor significant differences in abundance between the four principal classes of Proteobacteria phylum in the two management systems either (all p-values >0.05).

The main phyla detected in soil samples in this work were found to be generally predominating also in other soils throughout the world and they are Actinobacteria, Proteobacteria, Acidobacteria, Chloroflexi and Bacteroidetes (Roesch et al., 2007; Ramirez et al., 2010; Fierer et al., 2012a,b), but with some differences. In fact Roesch et al. (2007) found that Proteobacteria represented the dominant phylum in each of soils they analysed coming from four sites across the western hemisphere, like in this work, but they found that Betaproteobacteria were the dominant class among the Proteobacteria, while in this work Alphaproteobacteria are the most abundant. Moreover they found that the second most abundant phylum was the Bacteroidetes (Roesch et al., 2007), while in this work it resulted Actinobacteria.

Another consideration is about bacterial phyla composition and N fertilization. Despite some authors (Ramirez et al., 2010) found that Gammaproteobacteria and Actinobacteria significantly increased with N inputs and in soil analyses of this work significant differences in the amount of soil total N (tab.XIII) between organic-biodynamic and conventional soils were found, here no significant differences were detected in the abundance of Gammaproteobacteria and Actinobacteria between the two types of agriculture.

Also less abundant phyla were considered. The following pie charts (fig. 34) show phyla present at percentages equal or lower than 2% in all soil samples.

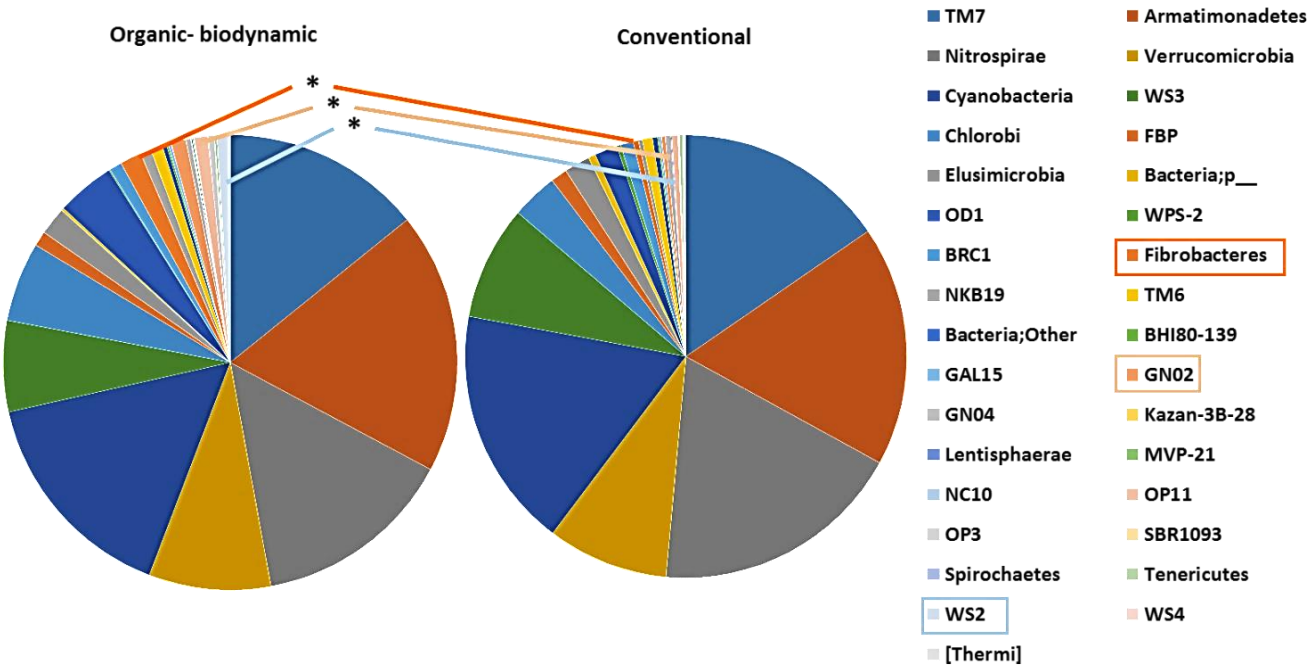


Fig. 34: Pie charts showing the mean data of less abundant bacterial phyla (< 2%) in the two types of agriculture analysed. Kruskal-Wallis test. Significance: *: p value <0.05. The three phyla that have highlighted differences in abundance between organic-biodynamic and conventional fields are marked with boxes.

Interestingly some significant differences were detected in the mean percentages of the some less abundant bacterial phyla between organic-biodynamic and conventional fields. In particular these

differences concern: Fibrobacteres, WS2 and GNO2 phyla were more abundant in organic-biodynamic managed fields.

The members of the functionally important phylum Fibrobacteres are recognised as major bacterial degraders of lignocellulosic material in the herbivore gut, but recent 16S rRNA gene-targeted molecular approaches have demonstrated that novel centres of variation within the genus Fibrobacter are present in landfill sites and freshwater lakes, and their relative abundance suggests a potential role for Fibrobacteres in cellulose degradation, beyond the herbivore gut, in environmental samples (Ransom-Jones et al., 2012). Moreover at least one species has evolved an atypical cellulose degradation mechanism, which may explain the superior hydrolytic capabilities of fibrobacters compared to other anaerobic bacterial groups (Ransom-Jones et al., 2012). WS2 and GNO2 are "candidate" phyla: this term means that no cultures yet exist to represent the group and in fact they are under studied (Rappé and Giovannoni, 2003). It could be inferred that the changes in microbiological functionality (described below) are partially due also to these differences in the less abundant phyla between organic-biodynamic and conventional soils.

The more detailed taxonomic unit which can be reached, with a reasonable reliability, by using sequencing technique is the genus level. This is mainly due to the taxonomic uncertainty that emerges when treating microbial species (Godfray and Lawton, 2001; Kirk et al., 2004). The following table summarises synthetic results about the mean number of bacterial genera that were detected in soil samples.

	Organic-biodynamic [Mean (S.E.)]	**Conventional** [Mean (S.E.)]	**Statistical test** (One-way ANOVA)
N° bacterial genera	403.6 (4.76)	378.3 (9.94)	*

Tab. XV: Mean number of genera within bacterial communities analysed by 16S sequencing. Significance: *: p-value <0.05.

On the contrary of A.R.I.S.A. results (tab. XIV), the number of bacterial genera detected with 16S amplicon sequencing was significantly higher in organically-biodynamically managed soils.

In order to visualize relationships of similarity among bacterial community samples in a 2D space, a multivariate statistical technique of ordination was performed (fig.35 a).

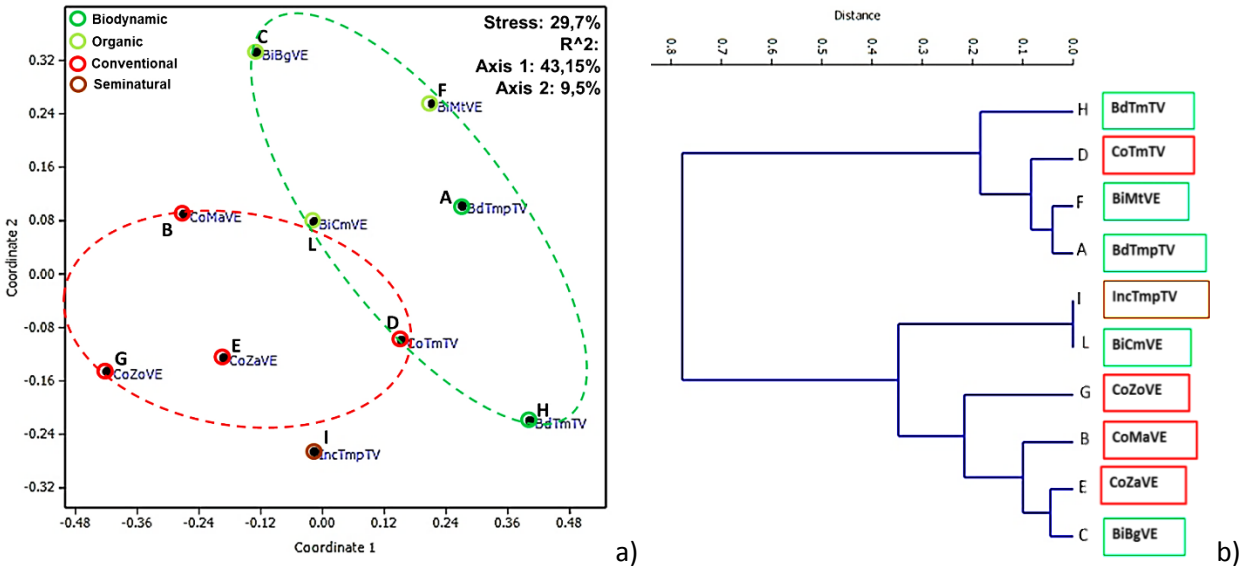


Fig. 35: a) NMDS plot of soil bacterial communities (16S sequencing) data, Bray-Curtis similarity measure. b) Classical cluster analysis of NMDS scores on axis 1 data of soil bacterial communities (16S sequencing), Ward's method- Euclidean similarity measure.

By using the recalculated coordinates of each sample points on axis 1 of NMDS plot, a cluster analysis was performed (fig. 35 b).

By analysing bacterial diversity using 16S sequencing, it was not possible to separate two groups of samples according to the management.

Fungal diversity overview

A.R.I.S.A.

By using A.R.I.S.A. technique it was possible to explore also soil fungal communities, obtaining a DNA fingerprint. 36 DNA fingerprint profiles were obtained for a total of 86 different amplification products found, characterised by a variable length between 100 and 800 bp. A mean of 30.8 DNA fragments was analysed for each sample. A first concern is about the number of peaks of soil fungal strains in the electropherogram: the difference in peak number between soils belonging to different managements was not significant (tab. XVI).

	Organic-biodynamic [Mean (S.E.)]	**Conventional** [Mean (S.E.)]	**Statistical test** (Kruskal-Wallis)
N° peaks in electropherogram	31.56 (1.60)	30.11 (1.41)	n.s.

Tab. XVI: Mean number of peaks in A.R.I.S.A. electropherogram for fungal communities analysis. Significance: n.s.: p value >0.05.

Using the numerical data of abundance of each fungal strain, a cluster diagram of all soil samples analysed was obtained (fig. 36).

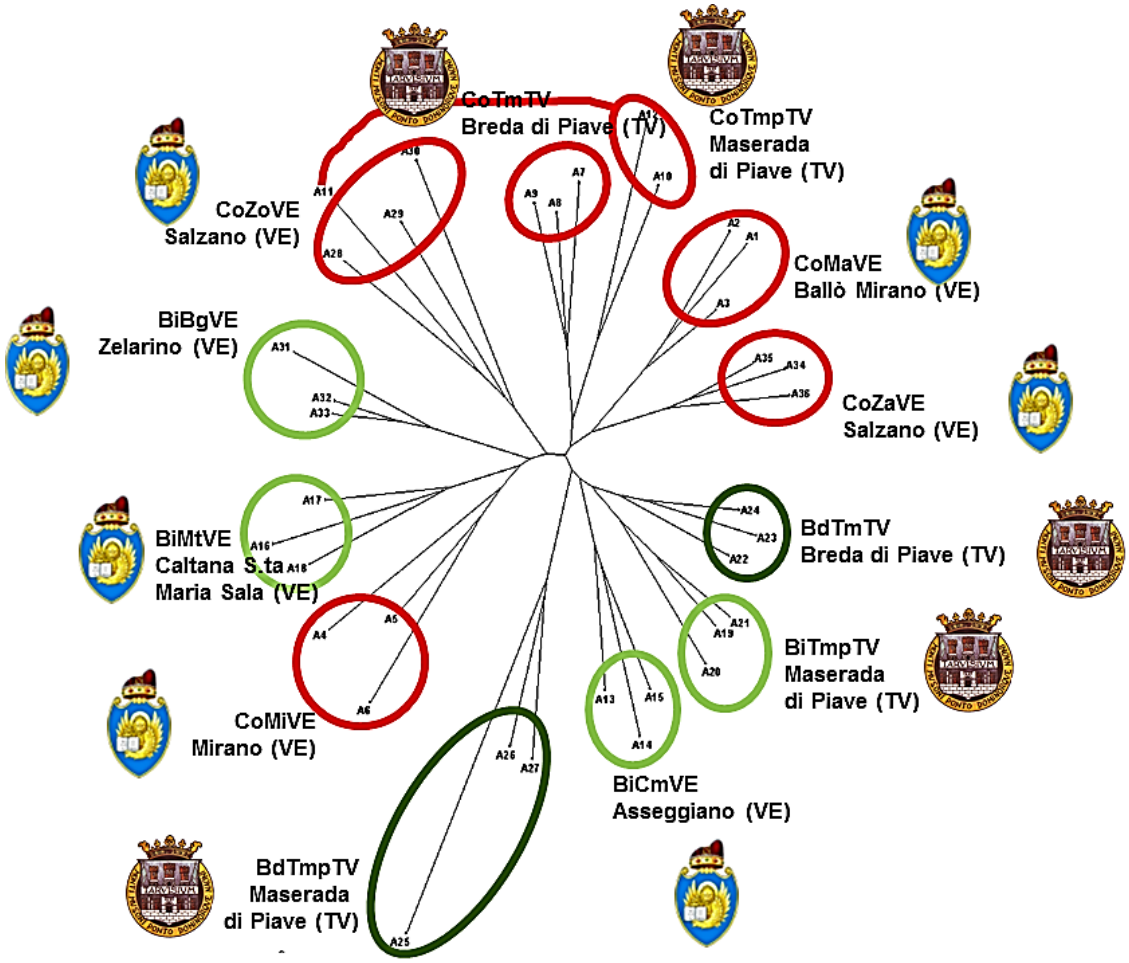


Fig. 36: Cluster diagram (neighbour-joining analysis) of soil fungal communities analysed by A.R.I.S.A. technique. In red: conventional farm samples; in light green: organic farm samples; in dark green: biodynamic farm samples.

: fields located in the Venice province. : fields located in the Treviso province.

Observing this cluster diagram (fig. 36) as for soil bacteria, it is evident that the proximity of the three samples coming from the same field (except for one case, which is CoTmpTV) seems to confirm a fairly reproducible outcome of the analysis and an appropriate representation of overall fungal community of each field. Differently from soil bacteria cluster analysis results, fungal communities appear more related to soil management and less shaped by geographical factors. This could be due to their spore phase during the life cycle, which is a very mobile phase for species diffusion helped by wind and by other external dispersion factors. When spores arrive in a place, if there are the right conditions they can germinate and for this reason, fungi could be considered a good indicator for different management practices in

agroecosystem. Also other findings (Avio et al., 2013) confirmed that fungi, and in particular AMF communities, are affected by N-fertilization and tillage, which are among the main factors of agroecosystem management.

In order to represent relationships of similarity among fungal communities samples in a 2D space, a multivariate statistical technique of ordination was applied (fig. 37 a).

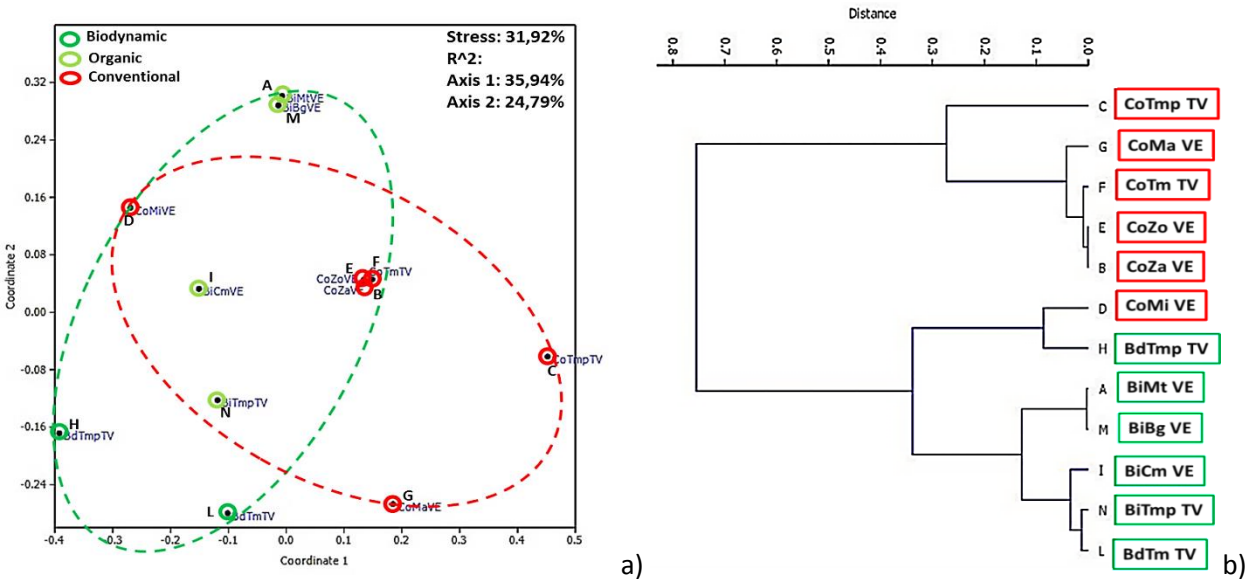


Fig. 37: a) NMDS plot of soil fungal communities (A.R.I.S.A.) data, Bray-Curtis similarity measure. b) Classical cluster analysis of NMDS scores on axis 1 data of soil fungal communities (A.R.I.S.A.), Ward's method- Euclidean similarity measure.

To read the NMDS plot objectively, by using the recalculated coordinates of each sample points on axis 1, a cluster analysis was performed (fig. 37 b).

The cluster analysis result shows how the soil samples can be divided into two main groups that are concordant, almost perfectly, with the field management. The difference in fungi communities was significant (p value = 0.04*, U test; p value = 0.04*, t test) between organic-biodynamic and conventional fields. This confirms also results obtained with the cluster analysis in fig. 36: soil fungal community can be a good indicator to discriminate agroecosystem management. Another consideration is that just counting the number of fungal taxa seems to be not enough to discriminate between agriculture management: it is necessary to consider the whole fungal community, that is to say in which extent each single taxon takes part to the entire soil community.

Fungal ITS sequencing

From 12870 to 43150 reads were obtained upon sequencing the ITS of each sample and after the quality filtering phase a minimal number of 9774 sequences was chosen at random for each sample. On

these sequences statistical analyses were performed. The screening of the abundance of different phyla is shown in fig. 38.

For reasons presumably due to the presence of inhibitors or limited DNA content in soil, it was not possible to amplify the CoMa sample.

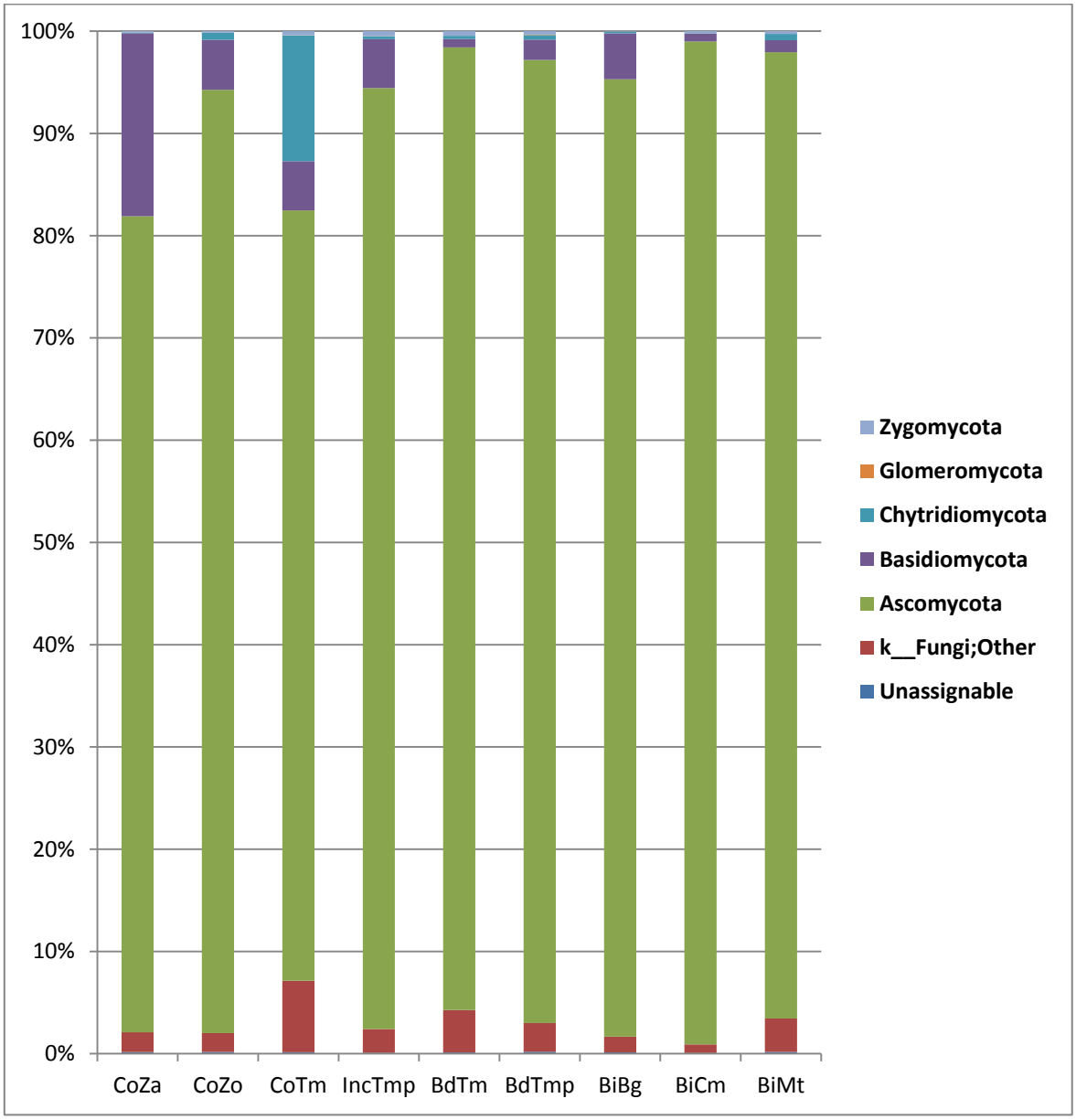


Fig. 38: Histogram of soil fungi phyla diversity (presence in %) analysed by ITS sequencing.

As in literature (Mouhmadou et al., 2013), also in this analysis the most abundant phylum in soil samples was Ascomycota. A key group, in which many species may be unculturable, is the Glomeromycota phylum (but not so abundant in respect to other ones) that forms arbuscular mycorrhizae (AM). These fungi are among the most abundant and ecologically important symbionts on earth, forming mycorrhizae with

around two-thirds of all plant species and occurring in virtually all ecosystems (Helgason et al., 2007). Again, as for bacteria, the less abundant groups could account for differences in functionality.

The following pie charts (fig. 39) show the mean values of fungal phyla in soils coming from differentially managed fields.

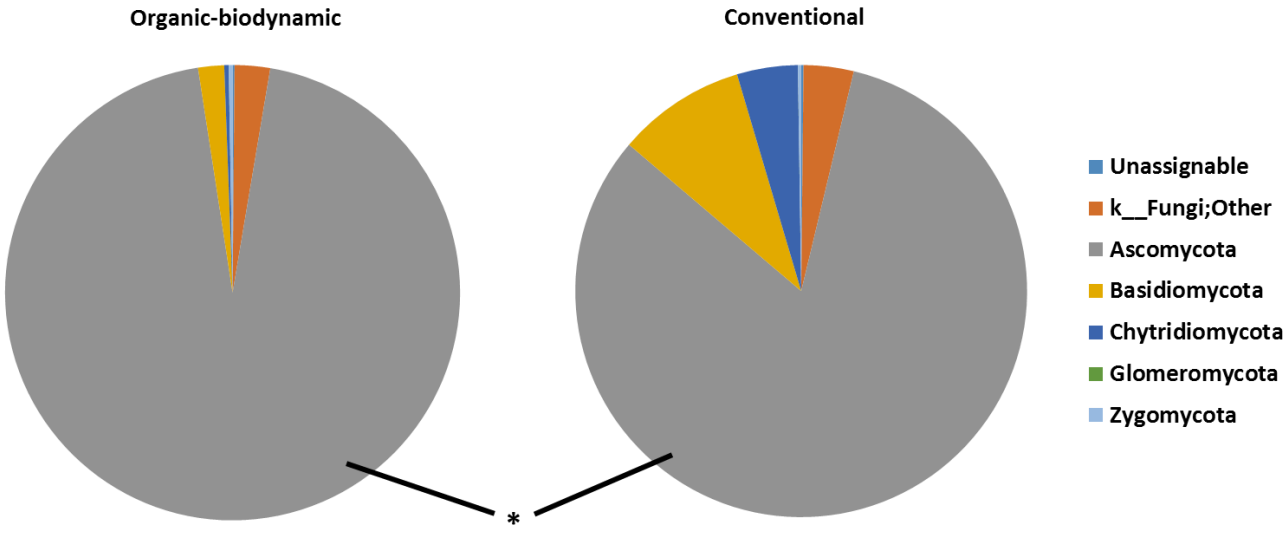


Fig. 39: Pie charts showing the mean data of the fungal phyla in the two types of agriculture analysed. Significance: *: p value <0.05.

Only the Ascomycota phylum was significantly higher in organically managed agroecosystems, while other fungal phyla were equally abundant in the two managements. Ascomycota function in the decay of organic substrates (for example wood, leaf litter and dung) and act as mutualists, parasites and pathogens of animals, plants and other fungi. More than 40% of all named Ascomycota are moreover reported as fungi that can also be potentially lichenized (Schoch et al., 2009).

The following table summarizes synthetic results of the mean number of fungal genera that were detected in soil samples by ITS sequencing.

	Organic-biodynamic [Mean (S.E.)]	**Conventional** [Mean (S.E.)]	**Statistical test** (One-way ANOVA)
N° fungal genera	109.2 (7.97)	112.7 (2.73)	n.s.

Tab. XVII: Mean number of genera within fungal communities analysed by ITS sequencing. Significance: n.s.: p value >0.05.

Confirming A.R.I.S.A. results (tab. XVI), the number of fungal genera detected with ITS sequencing was not significantly different between the two types of agriculture.

To visualize relationships of similarity across fungal communities samples in a 2D space, a multivariate statistical technique of ordination was performed (fig. 40 a).

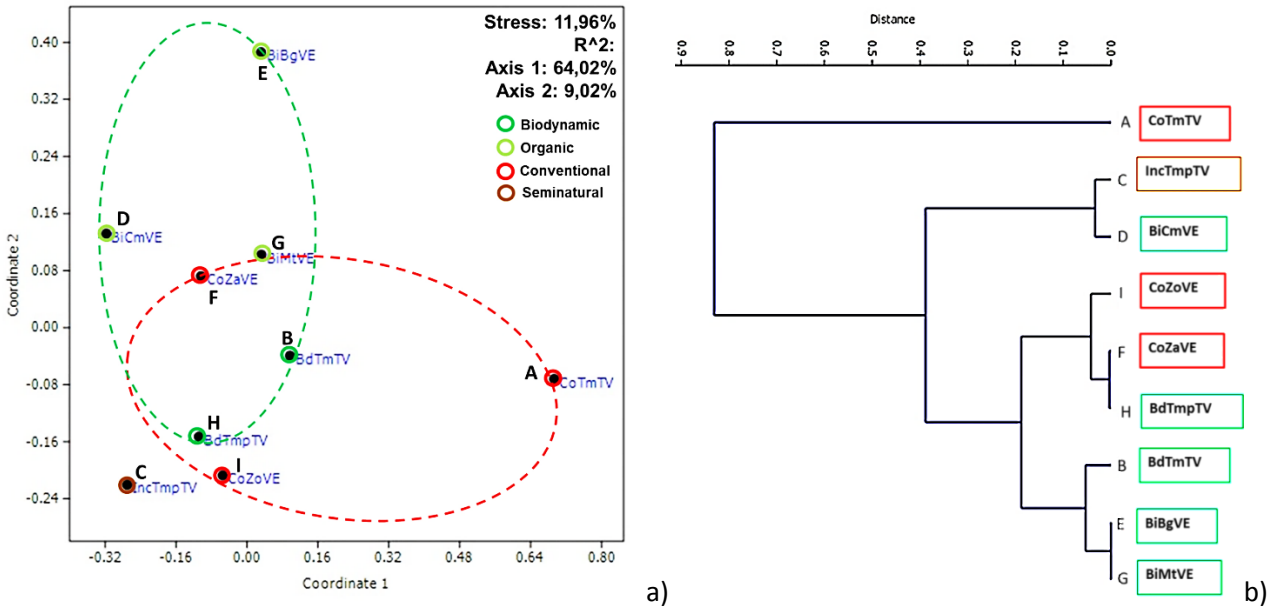


Fig. 40: a) NMDS plot of soil fungal communities (ITS sequencing) data, Bray-Curtis similarity measure. b) Classical cluster analysis of NMDS scores on axis 1 data of soil fungal communities (ITS sequencing), Ward's method- Euclidean similarity measure.

To interpret the NMDS plot objectively, by using the recalculated coordinates of each sample points on axis 1, a cluster analysis was performed (fig. 40 b).

In respect with fungal community A.R.I.S.A. analysis (fig. 37), which was able to discriminate the difference between the two management types, the ITS sequencing seems not. In fact, the cluster diagram in fig. 40 b does not allow to separate soil samples in two groups according to the management. This is probably due to the fact that there are differences just in the higher taxonomic groups (phyla) and going into a deep detail in discriminating taxa (genera) with sequencing, it does not add useful information for the research purpose.

Considerations about microbiological communities screening techniques

Having applied two different analysis techniques both to explore soil microbial diversity, it is possible to draw some considerations about the estimation on the quality of data and on the analysis costs (tab. XVIII).

	N° bacterial taxa			N° fungal taxa				
Technique	**Organic-biodyn**	**Conventional**	**Manag. difference**	**Organic-biodyn**	**Conventional**	**Manag. difference**	**Taxa identity**	**Analysis cost**
A.R.I.S.A.	43,89	48,06	n.s.	31,56	30,11	n.s.	no	15€/sample (180€)
16S (bacteria)-ITS (fungi) sequencing	403,60	378,30	*	109,20	112,70	n.s.	yes	2000€/run
Increase in detail (%)	+819,57	+687,14		+246,01	+274,29			+1011,11 [a]

Tab. XVIII: Comparison between A.R.I.S.A. and gene sequencing techniques useful in the study of soil microbial communities. Significance: *: p value <0.05; n.s.: p value > 0.05. [a] the increase % is in this column referred to the increase in economic costs.

Passing from A.R.I.S.A. technique to gene sequencing screening, the quality and detail of analysis increases substantially (up to +819,57%) also considering that sequencing allows to know taxa identity. In this study for bacterial taxa analysis, having used also the gene sequencing technique had allowed to detect differences in organic-biodynamic and conventional bacterial communities: in fact, with A.R.I.S.A. the number of taxa tended to be smaller in organic soils (even if not significantly), but with sequencing it became significantly higher in respect with conventional soils. This could suggest that organic soils are probably characterized by many less abundant bacterial taxa. For fungal taxa analysis, both techniques had not allowed to discriminate between the two types of agriculture, Justas judged upon the number of taxa. Since some differences between two managements were detected in Ascomycota abundance (fig. 39) and also in the overall fungal communities analysed with A.R.I.S.A. (fig. 37), once again probably to know just the simple number of taxa is not enough for the research purpose (the separation of managements) and it requires an enquire of the structure of the whole community.

Microbiological functionality

In this part the results from several functional tests concerning the belowground sector are shown.

Fertimeters [18]

During the field data collection season, four fertimeter samplings were done, one in the late September-early October 2012 and three in the spring 2013 (in April, May and June). The overall data are shown in fig. 41.

[18] International patent PCT N. WO2012 140523 A1, Squartini, Concheri, Tiozzo, Padova University

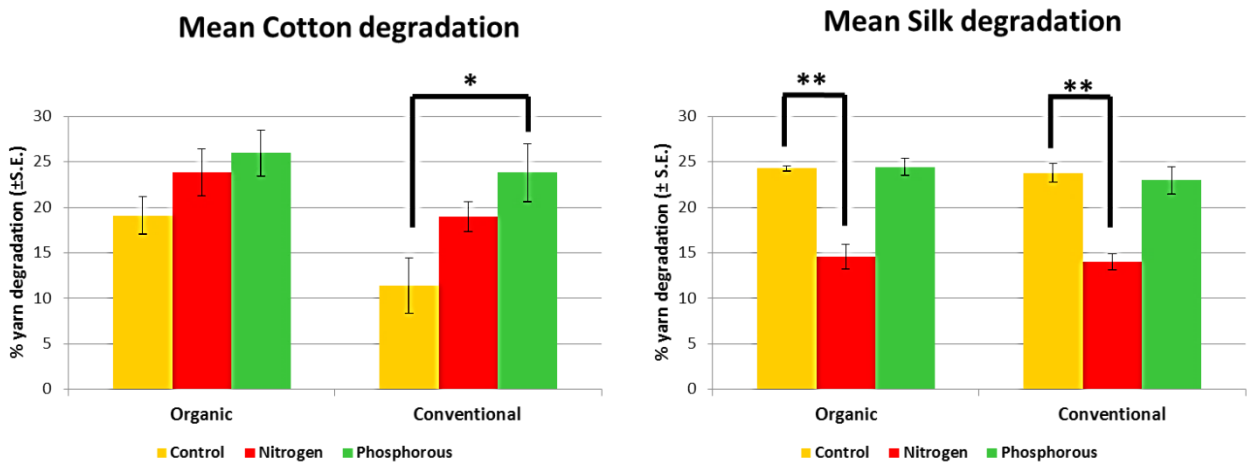


Fig. 41: Mean values of four samplings of cotton yarn and silk yarn degradation according to the agroecosystem management. Significance: *:p value <0.05; **: p value <0.01.

In tab. XIX statistical tests are summarised.

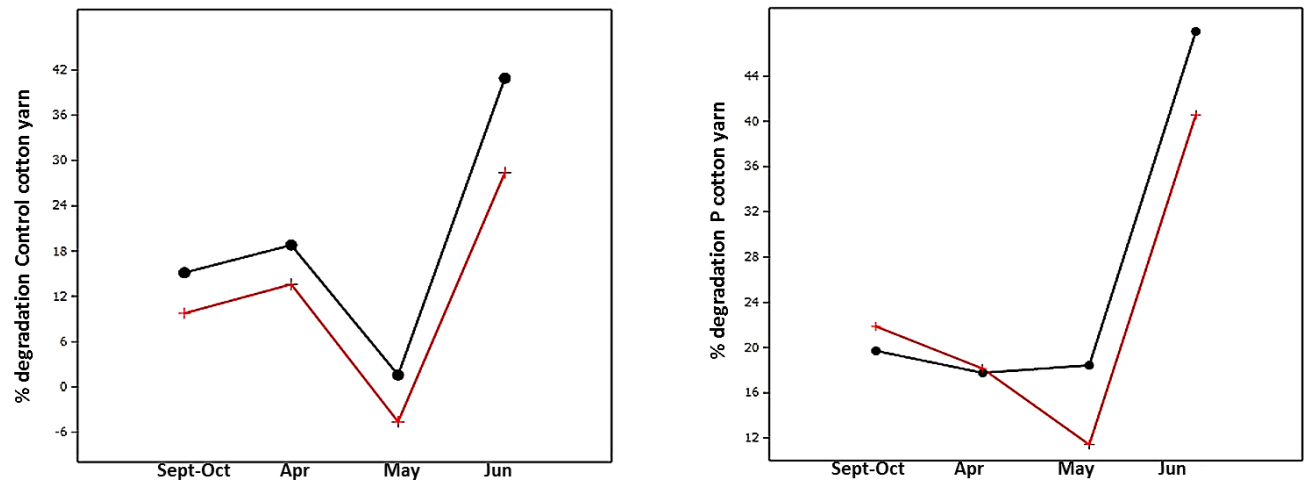
Textile yarns degradation		Management	Sampling period
Cotton	Control	*	***
	N-treated	n.s.	/
	P-treated	n.s.	***
Silk	Control	n.s.	/
	N-treated	n.s.	***
	P-treated	n.s.	/

Tab. XIX: Statistical significance concerning the overall fertimeter results. Two-way ANOVA or Friedman tests. Significance: ***: p value <0.001; *: p value <0.05; n.s.: p value >0.05.

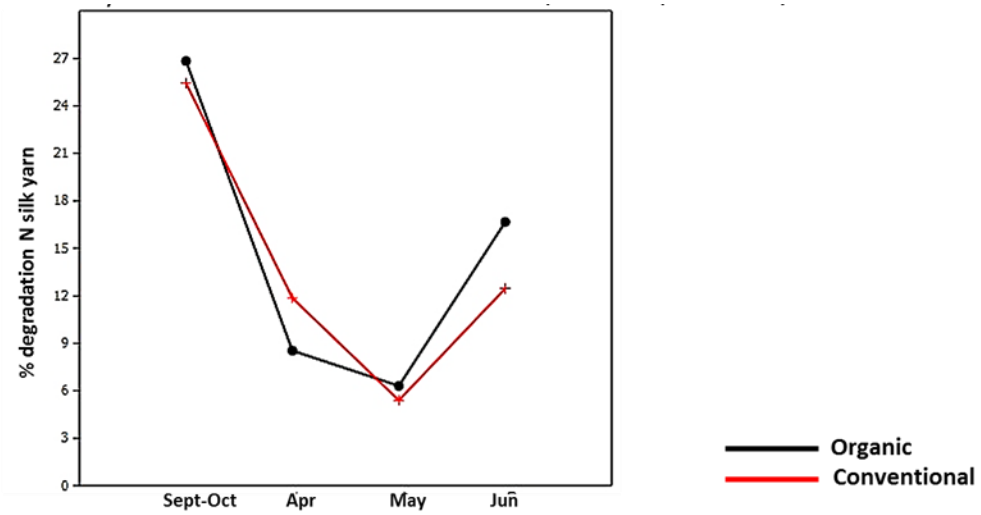
The overall data elaboration highlights how there were differences in the cotton degradation rates according to the management: indeed while in the organic management there were no differences between control vs. P-treated, and control vs. N-treated textile yarn degradation, in the conventional management there was a significant difference between control and P-treated textile yarn degradation. This would imply that in conventional fields there were marked deficiencies in P macronutrient availability.

The situation concerning silk degradation appears less clear. In fact in both agroecosystem types, there was a highly significant difference between control and N-treated yarn degradation, independently from the management. It seems to exist another factor responsible of this strong trend.

The following graphs (fig. 42) show the progression of the fertimeter experiments along the year, especially concerning the types of yarns whose degradation rate was significantly influenced by the sampling period (tab. XIX).



a)



b)

Fig. 42: Mean of yarn degradation (%) during the progression of the fertimeter experiments (from September-October to June). (a): left: Control cotton yarn; right: P-treated cotton yarn; (b): N-treated silk yarn.

Control cotton degradation	September-October	April	May	June
September-October	/	n.s.	*	***
April		/	**	**
May			/	***
June				/
P-treated cotton degradation	September-October	April	May	June
September-October	/	n.s.	n.s.	***
April		/	n.s.	***
May			/	***
June				/
N-treated silk degradation	September-October	April	May	June

September-October	/	***	***	***
April		/	n.s.	n.s.
May			/	*
June				/

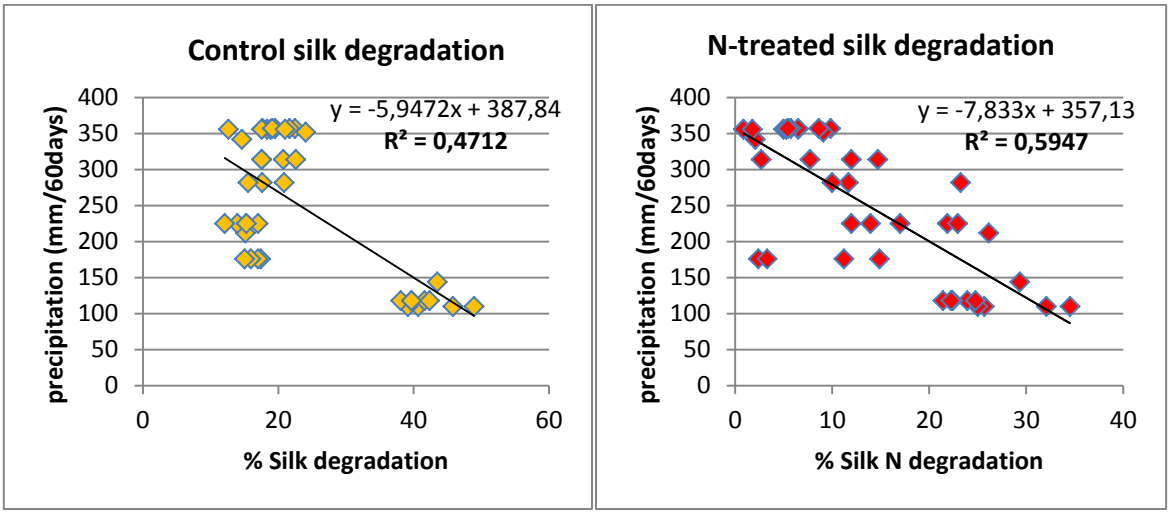
Tab. XX: Results of Tukey's HSD test of means separation about yarns degradation (control cotton, P-treated cotton and N-treated silk) in different periods of the year. Significance: ***: p value<0.001; **: p value<0.01; *: p value<0.05; n.s.: p value>0.05.

A different degradation rate can be noticed according to the yarn type: silk yarn degradation was significantly higher in autumn, meanwhile cotton yarn degradation was significantly higher in early summer (tab. XX). Only the control cotton yarn recorded a significant difference in degradation according to the management: this was higher in organic-biodynamic fields. Another consideration is that data were influenced by the weather (fig. 28), especially by the high precipitation level at the beginning of 2013. Tab. XXI lists the correlation coefficients found between the percentages of yarn degradation and the precipitation fallen within 60 days before the fertimeter samplings.

Yarn degradation	**Precipitation** (mm/60 days before sampling)	**Significance**
Control silk	-0.67	***
N- treated silk	-0.77	***
P-treated silk	-0.74	***
Control cotton	-0.30	n.s.
N-treated cotton	-0.23	n.s.
P-treated cotton	-0.32	n.s.

Tab. XXI: Pearson's correlation coefficients (r). Significance: ***: p value <0.001; n.s.: p value >0.05.

Fig. 43 shows the regression lines that put in correlation the degradation of the three silk yarns (control, N-treated, P-treated) with the precipitation.



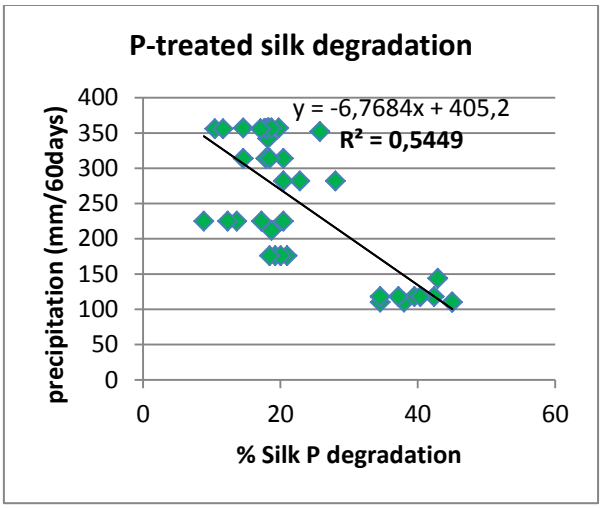
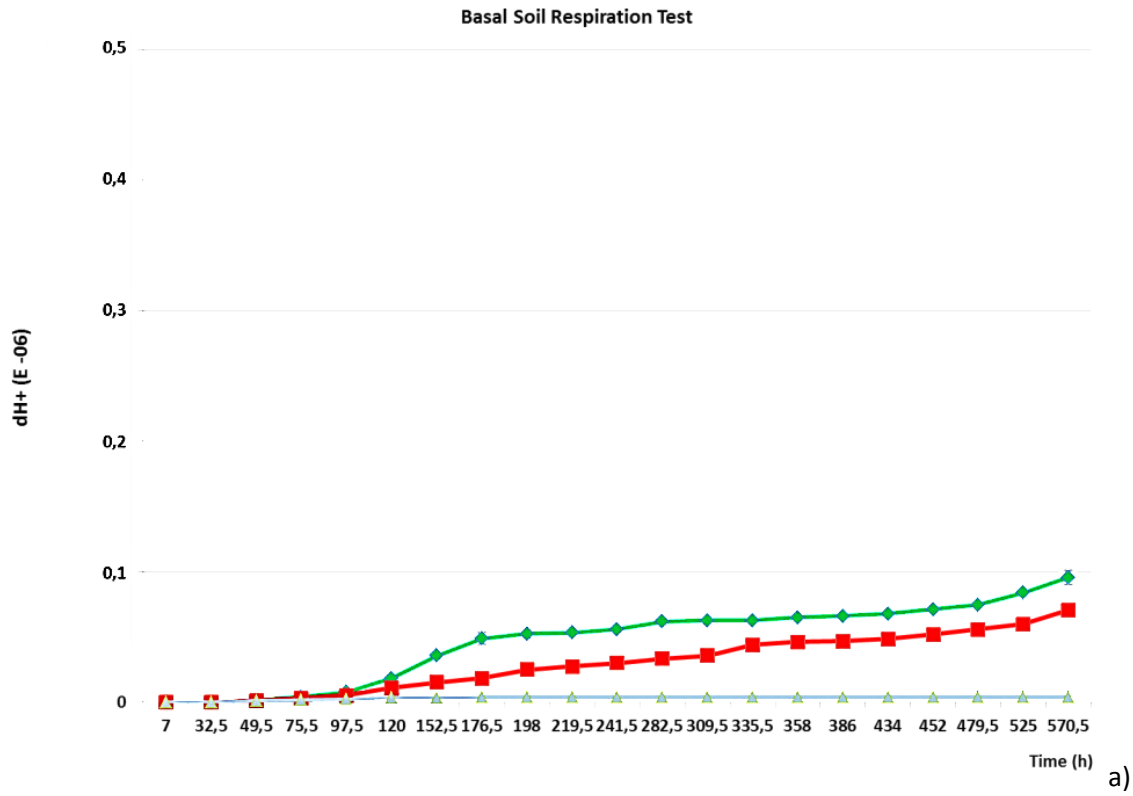


Fig. 43: Regression lines representing the correlation between the amount of precipitation in the 60 days period before fertimeter sampling and control silk yarn degradation (yellow), N-treated silk yarn degradation (red) and P-treated silk yarn degradation (green).

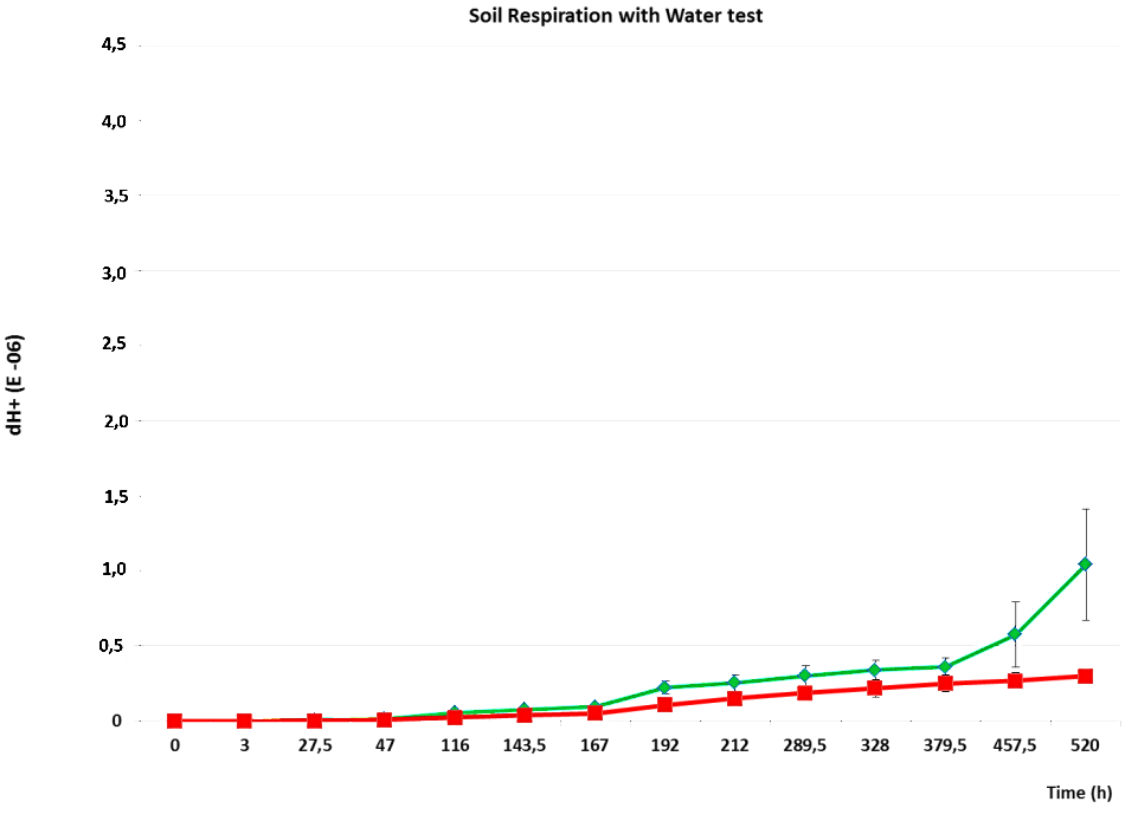
After these considerations, the factor that seems to be the responsible of the trend in silk yarn degradation could be the weather and especially the precipitation rate before sampling. In particular the significantly different values of the N-treated silk yarn in respect with the control and the P-treated ones (fig. 43) appear explainable by the higher negative correlation coefficient (-0,77). Instead cotton yarn degradation is not correlated with precipitation rate and it could be a better proxy for the discrimination of the soil management.

Soil respiration tests

Three experiments were performed with the aim to measure the soil respiration rate, by using pH variation in time, in different conditions: the dry basal respiration, just with soil sample; the re-wetted basal respiration, adding water and the S.I.R., adding the same quantity of liquid but as glucose solution in water. In practice, the re-wetted basal respiration is the negative control (glucose-minus) for the S.I.R. and the dry basal respiration is a baseline control (water-minus) for both. Results are in fig. 44.


Basal Soil Respiration Test
dH+ (E -06)
0,5
0,4
0,3
0,2
0,1
0
7
32,5
49,5
75,5
97,5
120
152,5
176,5
198
219,5
241,5
282,5
309,5
335,5
358
386
434
452
479,5
525
570,5
Time (h)

a)


Soil Respiration with Water test
dH+ (E -06)
4,5
4,0
3,5
3,0
2,5
2,0
1,5
1,0
0,5
0
0
3
27,5
47
116
143,5
167
192
212
289,5
328
379,5
457,5
520
Time (h)

b)

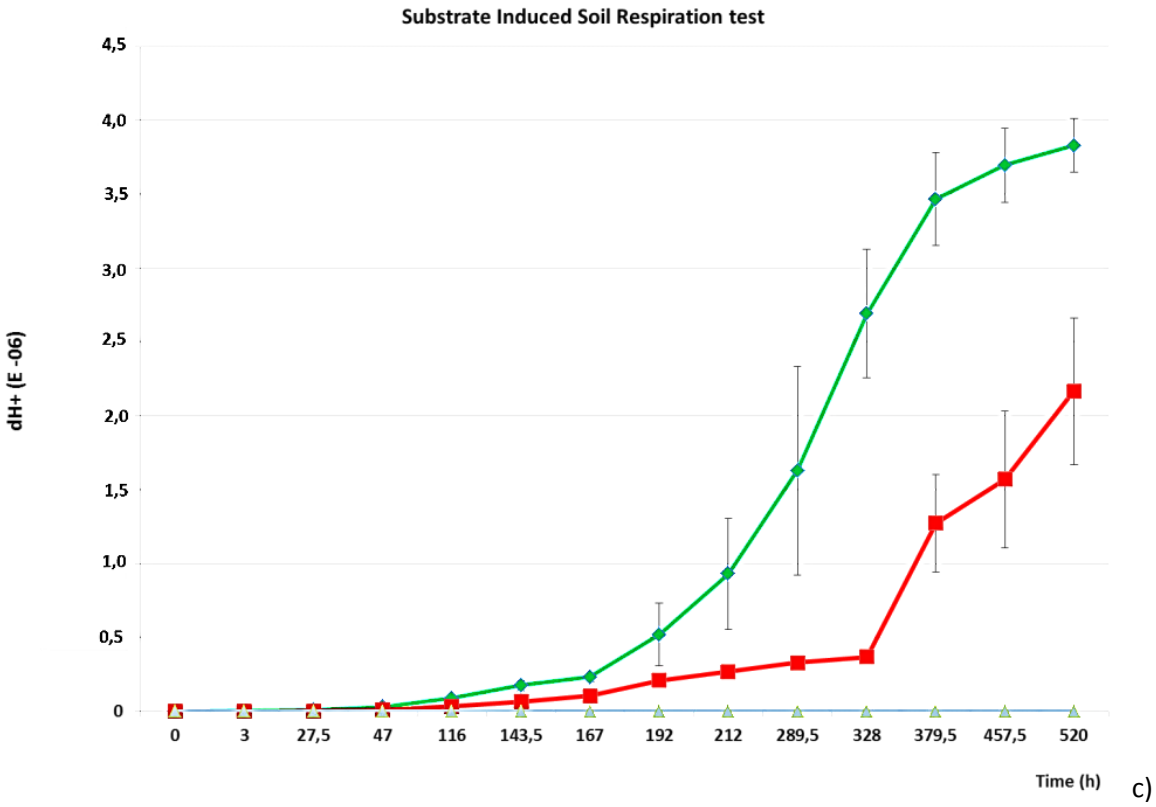


Fig. 44: Mean results (with standard error bars) concerning the three types of experiment of soil respiration rate measurement: a) dry basal respiration; b) re-wetted respiration; c) S.I.R. Green: organic-biodynamic soil samples; Red: conventional soil samples; Light blue: control without soil.

In tab. XXII there are statistical elaborations of the values of difference in liberation of protons (dH^+) reached at the end of the experiment between soils belong to different management types.

Respiration test (final results-dH^+)	**Organic-biodynamic** [Mean (S.E.)]	**Conventional** [Mean (S.E.)]	**Statistical test** (One-way ANOVA or Kruskal-Wallis)
Basal respiration	9,57 E-08 (5,44 E-09)	7,06 E-08 (4,23 E-09)	***
Respiration with water	1,04 E-06 (3,70 E-07)	2,97 E-07 (5,31 E-08)	**
Substrate induced respiration	3,83 E-06 (1,80 E-07)	2,17 E-06 (4,96 E-07)	***

Tab. XXII: Final mean results of three different respiration rate tests. Significance: ***: p value <0.001; **: p value <0.01.

The three different experiments show how in organic-biodynamic soils the respiration was always significantly more efficient. By adding water or glucose solution in water, it is possible to see an amplification of this phenomenon in comparison to the basal one. In the S.I.R. graph it is possible to recognise also the changing over time. The curve concerning organic-biodynamic soil respiration rate (fig.

44 c) is smooth and similar to a typical bacterial growth curve with an initial lag, followed by a rapid increase but presumably not synchronous or equal for all microorganisms involved (in fact the higher variation bars are in correspondence of the flex point of the curve); and subsequently the achievement of a plateau due to the consumption of food resources (glucose in this case), becoming limiting. The conventional soils curve appears instead more jerky and irregular in its stepwise increases, as well as less intense in terms of moles of CO_2 released. Concluding this part, organic-biodynamic soils seem to host a more complete microorganism community able to better use more efficiently the environmental resources and to process more promptly organic amendments. Since soil basal respiration reflects the overall activity of the microbial pool (Saviozzi et al., 2001), in organic-biodynamic soils there is a more active microbial community.

PCR for AMF

An initial investigation about the presence of Arbuscular Mycorrhizal Fungi into the soil samples was performed by Polymerase Chain Reaction analysis (fig. 45). Soil samples were collected in three periods along the year: in spring, in summer and in autumn in order to detect possible variations in AMF presence. Soil coming from the same fields was analysed three times in order to see possible AMF variation with period of the year.

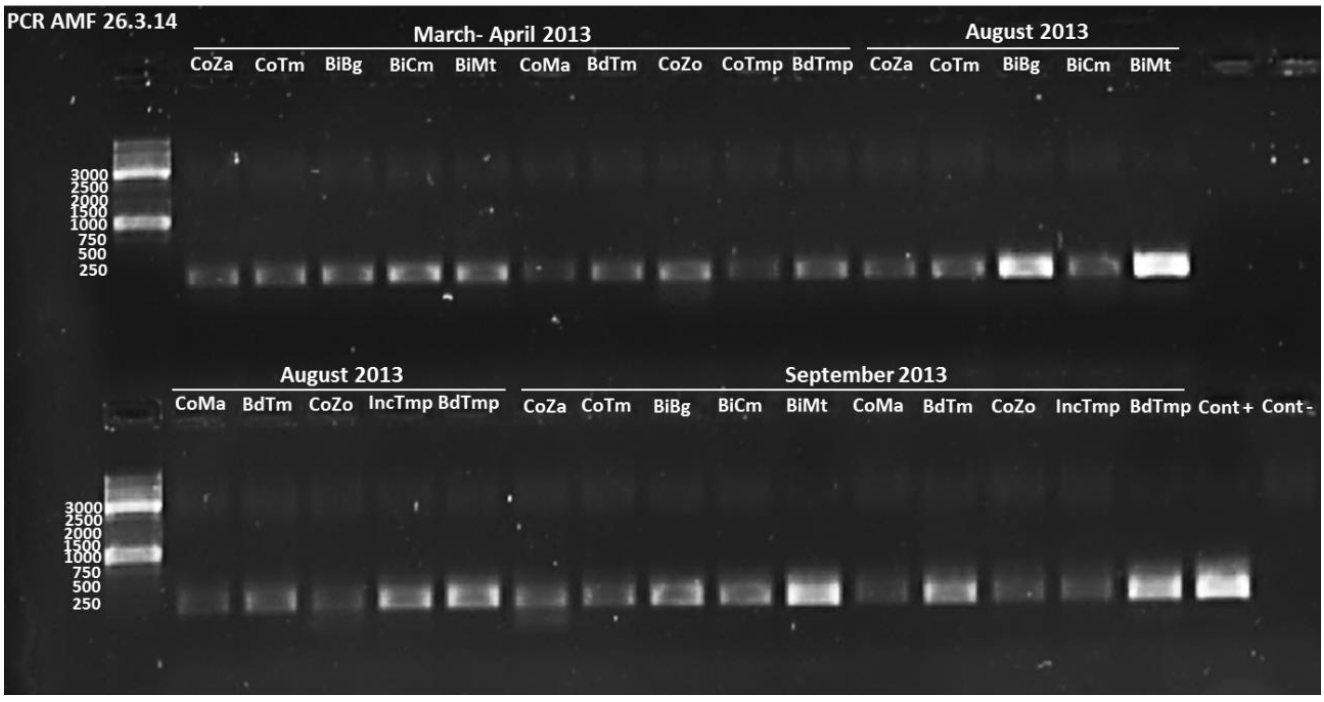


Fig. 45: Agarose gel electrophoresis showing the PCR output on AMF presence. Cont+: positive control; Cont-: negative control.

As it can be qualitatively appreciated observing this PCR output, there are marked differences in the presence of AMF. In general in spring there appear to be lower amounts of AMF with respect to summer and autumn. This could be due to soil management practices (like ploughing or rotary tillage-see tabb. LV

and LVI in the appendix) that farmers do in spring time to prepare the seed bed for the crop growing season. After this disturbing event, soils have different resilience capacity: organic and biodynamic soils seem to restore good AMF conditions quicker than conventional soils. This is probably due to the invasiveness of the adopted practices: ploughing for example is typically more invasive than just surface rotary tillage and the first is practiced only by conventional farmers.
Almost all AMF are non-specific symbionts, readily colonizing the roots of most plant species they encounter (Smith and Read, 1997), hence detecting their presence provides an important index for monitoring of the intrinsic potentialities of a soil to support crop growth.

Real time PCR for AMF quantification

In order to refine the resolution of AMF analyses the AMF gene copies quantification was addressed by quantitative Real Time-Polymerase Chain Reaction (qRT-PCR). Results are shown in fig. 46.

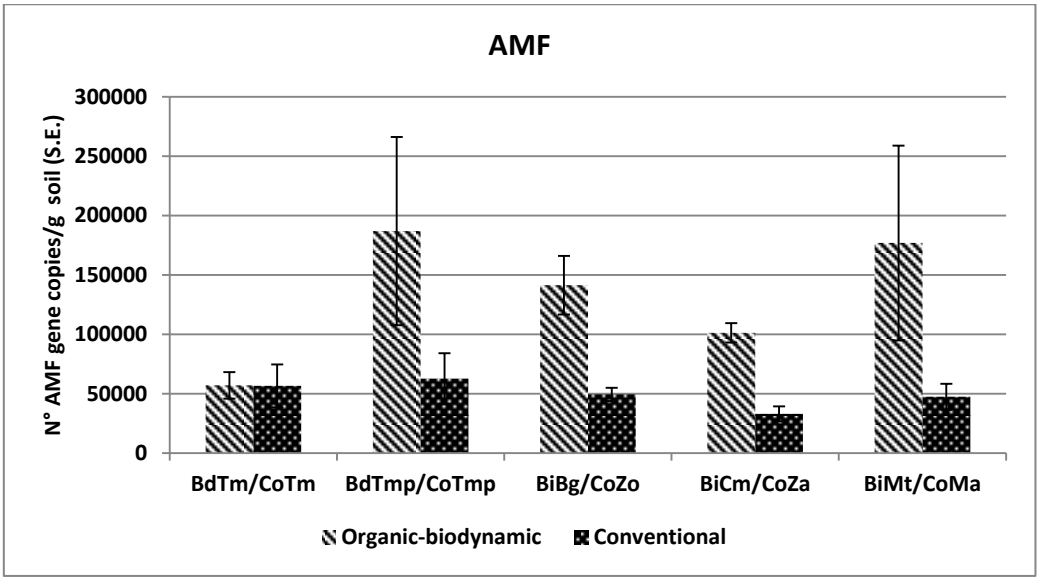


Fig. 46: Mean values (three replicates) of AMF gene copies in 1g of soil samples coming from fields with different managements.

Statistical elaborations are summarised in tab. XXIII.

	Organic [Mean (S.E.)]	**Conventional** [Mean (S.E.)]	**Statistical test** (Two-way ANOVA)	
			Management	**Period**
N° AMF gene copies/g soil	132631,4 (24170,01)	49814,5 (4990,36)	***	n.s.

Tab. XXIII: Mean values of number of AMF gene copies in 1g of soil sample. Significance: ***: p value <0.001; n.s.: p value > 0.05.

From the histogram (fig. 46) it is possible to appreciate how organically-biodynamically managed soils host a significantly higher number of AMF gene copies, and therefore these fields have better conditions to develop mycorrhizal symbioses between fungi and crop plant roots. AMF are very useful partners that help crop growth and stimulate to use natural existing resources without the necessity to provide surplus of external inputs. In fact de Vries et al. (2013) found that N leaching decreased with increasing biomass of AMF across all sites in four different European countries, moreover also laboratory studies showed that AMF reduce leaching of N and P. Others (Pankhurst et al., 1995) found that the major reduction in mycorrhizal fungi was in response to N fertilization and they thought that it might be due to the added N altering the competitive balance between mycorrhizal fungi and other microorganisms. Further studies (Avio et al., 2013) confirmed that AMF communities in the field are affected by N-fertilization and tillage. These findings are in line with the concept that AMF help to better use natural resources and they do not withstand excessive external inputs. Moreover there seems to be a link between higher levels of AMF and higher soil total N found in organic-biodynamic soils. All considered these fungi could be useful for crop production also from an economical point of view, by reducing external inputs.

In particular tab. XXIV shows data about the fold increase of AMF from the conventional fields to each of the adjacent organic-biodynamic fields.

Mean AMF gene copies/g soil			
Field pairs	**Conventional**	**Organic-biodynamic**	**Increase in AMF** (n-fold)
BdTm/CoTm	56552.5	56952.3	1.0
BdTmp/CoTmp	62668.8	186848.2	3.0
BiBg/CoZo	49379.2	141313.5	2.9
BiCm/CoZa	33033.4	101206.3	3.1
BiMt/CoMa	47438.6	176836.4	3.7

Tab. XXIV: Values of AMF gene copies/g soil in conventional fields and in the corresponding organic-biodynamic fields, with the n-fold increase when comparing conventional with organic-biodynamic management system.

From the table XXIV it emerges that there was always an increase (from 1- up to 3.7- fold) in AMF quantity in organic-biodynamic soils. Another feature reported on AMF in a renowned study (Mader et al., 2002) was about the length of roots colonized by mycorrhizae: the authors found that in organic farming systems the colonized roots were 40% longer than in conventional systems, translating into a major improvement in nutrients and water absorption.

The following plot represents the trend of AMF abundance from spring to autumn (fig. 47).

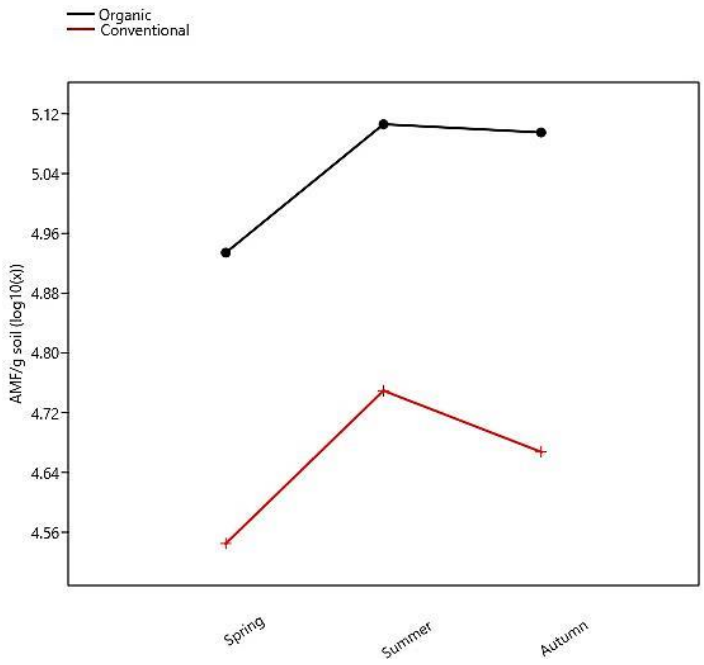


Fig. 47: Mean values of AMF gene copies in 1g of soil sample in soils with different management and during the year.

Within this graph it is possible to follow quantitatively the phenomenon indicated by the PCR data (fig. 45): conventional soils hosted less AMF and in general, both in conventional and organic-biodynamic fields, in spring there was a decrease in AMF quantity, probably due to farmer management practices. Nevertheless organic soils confirm to possess a better and more stable resilience capacity in restoring optimal environmental conditions for AMF.

To appreciate AMF presence it is important to use molecular techniques, since studies (van der Heijden et al., 2008) showed that about 60% of environmental sequences of AMF do not match with AMF that have been brought into culture. Those AMF that are easily cultured often have a ruderal lifestyle (such as *Glomus intraradices* and *Glomus mosseae*) and a global distribution (Opik et al., 2006). Another study indicated that these generalist and easily cultured AMF are also more resistant to soil perturbation (agricultural practices, agrochemicals), while specialist AMF with a narrow host range (several of them still uncultured) declined (Helgason et al., 2007).

dsDNA content

It was possible to measure the quantification of dsDNA in three pairs of farm soils, the ones situated in the Venice province. Histogram in fig. 48 shows these results.

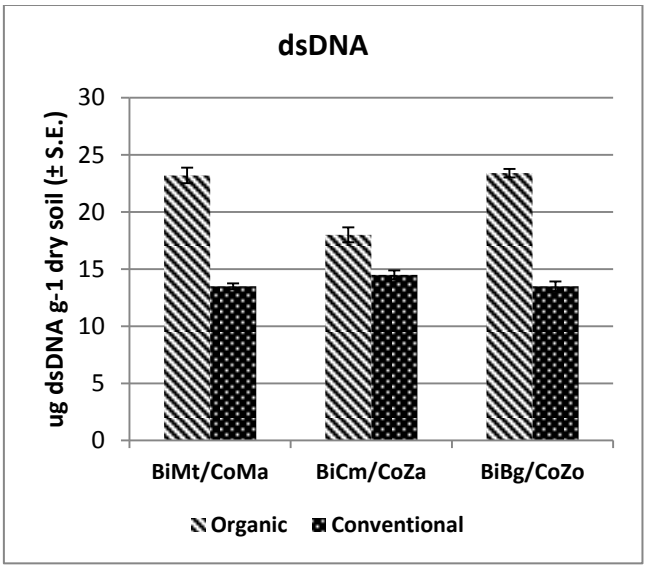


Fig. 48: Mean values (ten replicates) of dsDNA content in organic and conventional soil samples.

Tab. XXV summarizes statistical elaborations.

	Organic [Mean(S.E.)]	**Conventional** [Mean(S.E.)]	**Statistical test** (one-way ANOVA)
dsDNA (µg/g)	21.5 (1.77)	13.8 (0.33)	***

Tab. XXV: Mean values of dsDNA test. Significance: ***: p value <0.001.

The presence of dsDNA was significantly higher in organic soil samples in comparison to the conventional ones, this shows that microbial biomass was significantly higher in this kind of soils. Consistent with these results, Fliessbach et al. (2007) in a 21-years experiment found that soil microbial biomass in conventional plots amended with stacked manure was 25% lower than biodynamic plots and the systems without manure application were lower by 34%. In particular Gangneux et al. (2011) found that especially fungal dsDNA concentration, which is one of the two major components of total dsDNA (the other one consists in bacterial dsDNA), was highly related to tillage: with a lower frequency of tillage practices, there was a statistically significant increase in the amount of fungal dsDNA. The results obtained in this work confirm the same trend: in fields with more intensive and frequent mechanical practices (see tabb. LV and LVI in the appendix), a lower dsDNA quantity was detected. Also Cowie et al. (2013) found that dsDNA stocks tended to show higher values in organic treatments. Pankhurst et al. (1995) found that microbial biomass was among the soil indicators that appeared to satisfy most of the criteria advocated as important for a good indicator, such as responsiveness to management practices, ease in measure, ease in interpretation, association with major ecological soil processes, ability to reflect field conditions under a given management. Moreover the bacterial dsDNA contribution to the community dsDNA pool was the most site-dependent (Gangneux et al., 2011) and this consideration can be linked to the “bacterial biogeography”

found with cluster analysis elaboration of bacterial communities data analysed by A.R.I.S.A. technique (fig. 29).

FDA hydrolysis test

The FDA hydrolysis test was applied to four pairs of soils. Results are in the fig. 49.

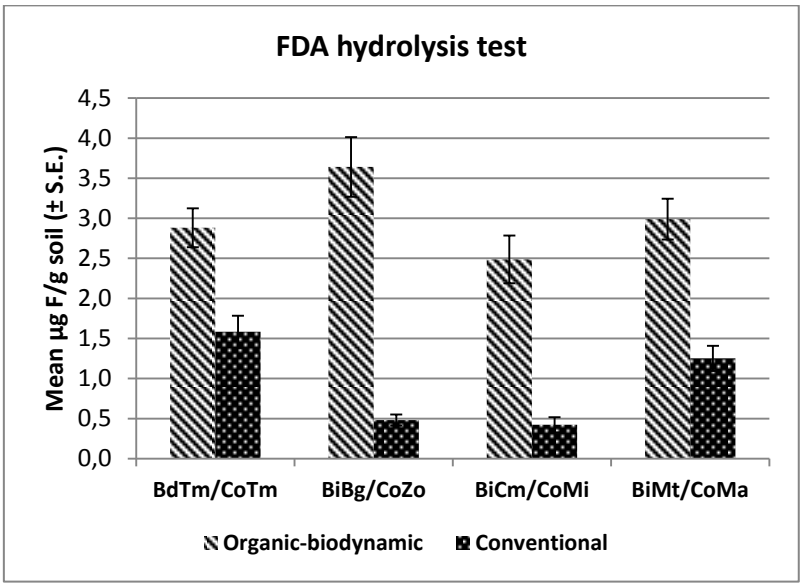


Fig. 49: Mean values (three replicates) of Fluorescein (F) in the analysed soils: organic-biodynamic and conventional.

Statistical elaborations are summarised in tab. XXVI.

	Organic [Mean (S.E.)]	**Conventional** [Mean (S.E.)]	**Statistical test** (one-way ANOVA)
Fluorescein (µg/g)	3.00 (0.24)	0.94 (0.29)	***

Tab. XXVI: Mean values of Fluorescein result from FDA hydrolysis test. Significance: ***: p value <0.001.

The fluorescein values read by the spectrophotometer were significantly higher in soil samples coming from organic-biodynamic fields, indicating that in these soils there was a significantly higher soil microbial activity. Others (Kremer and Li, 2003) found that microbial activity based on FDA hydrolytic enzymes reports that soils under grassland vegetation or high-input organic systems are metabolically more active than soils under conventional management systems, as in this study. In particular, they demonstrated that soils under an organic management system had a 0.5- to 2-fold greater FDA hydrolytic activity than soils under more intensive management. In agreement with results of Kremer and Li (2003), the ones obtained

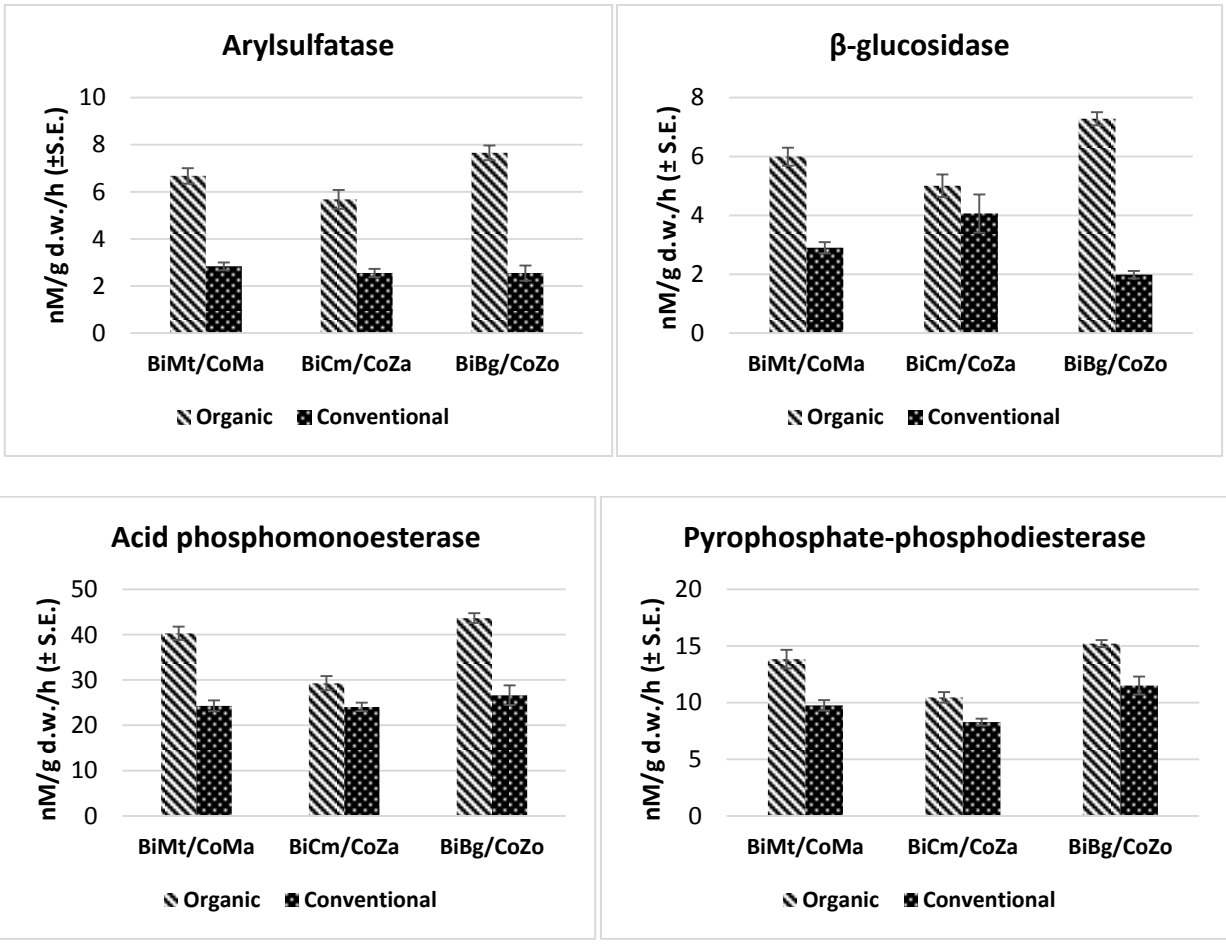
in this research, underline an even more marked increase in FDA hydrolytic activity from 1.8- up to 7.6-fold (tab. XXVII), when comparing conventional to the nearby organic-biodynamic management.

Mean F values (µg/g)			
Field pairs	**Conventional**	**Organic-biodynamic**	**Increase in FDA activity** (n-fold)
BdTm/CoTm	1.58	2.88	1.8
BiBg/CoZo	0.48	3.64	7.6
BiCm/CoMi	0.42	2.49	5.9
BiMt/CoMa	1.25	2.99	2.4

Tab. XXVII: Values of FDA hydrolytic activity in conventional fields and in the nearby organic-biodynamic fields, with the value of increase from conventional to organic-biodynamic management system.

Soil enzymatic activities

Some soil enzymatic activities, key for nutrient recycling and OM decomposition were quantified (fig. 50): all of them were significantly higher in organic soils.



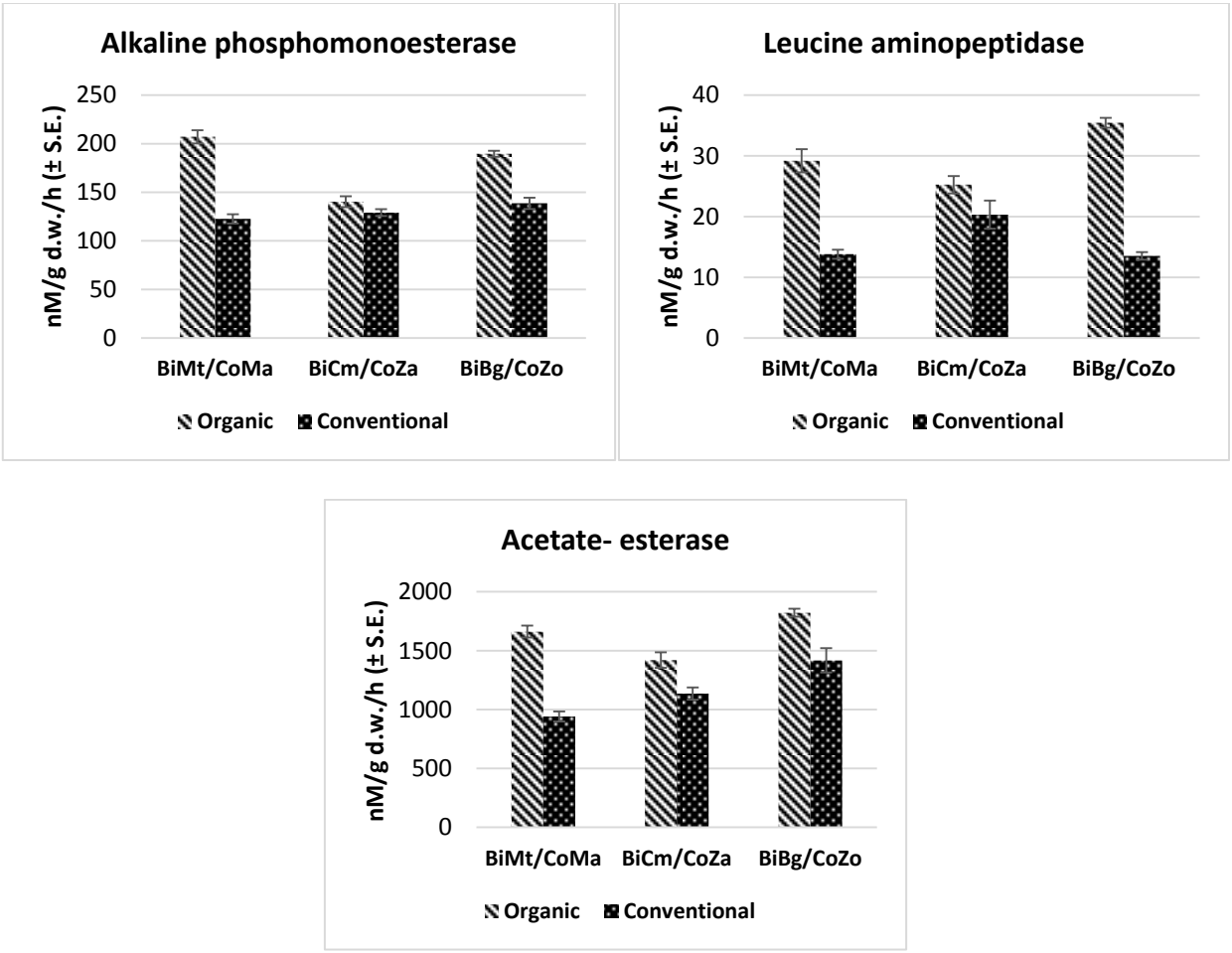


Fig. 50: Mean (ten replicates) of key enzymatic activities measured in conventional and organic soils.

Details on statistical elaborations are shown in tab. XXVIII.

Soil enzymatic activity	Mean value nM/g d.w./h (S.E.)		Statistical test (One-way ANOVA or Kruskal-Wallis)
	Organic	Conventional	
Arylsulfatase (**AryS**)	6.67 (0.57)	2.64 (0.09)	***
β- glucosidase (**Gluc**)	6.09 (1.16)	2.98 (0.60)	***
Acid phophomonoesterase (**acP**)	37.75 (4.34)	24.99 (0.83)	***
Pyrophosphate-phosphodiesterase (**Piro**)	13.17 (1.41)	9.85 (0.93)	***
Alkaline phosphomonoesterase (**alkP**)	179.01 (19.97)	130.15 (4.64)	***
Leucine aminopeptidase (**Leu**)	29.96 (2.97)	15.88 (2.22)	***
Acetate- esterase (**Ester**)	1634.66 (116.93)	1164.75 (138.29)	***

Tab. XXVIII: Mean values of key soil enzymatic activities. Significance: ***: p value <0.001.

By considering the overall picture concerning the seven key enzymatic activities analysed, it was possible to elaborate an ordination plot in order to visualize possible similarities among samples (fig. 51).

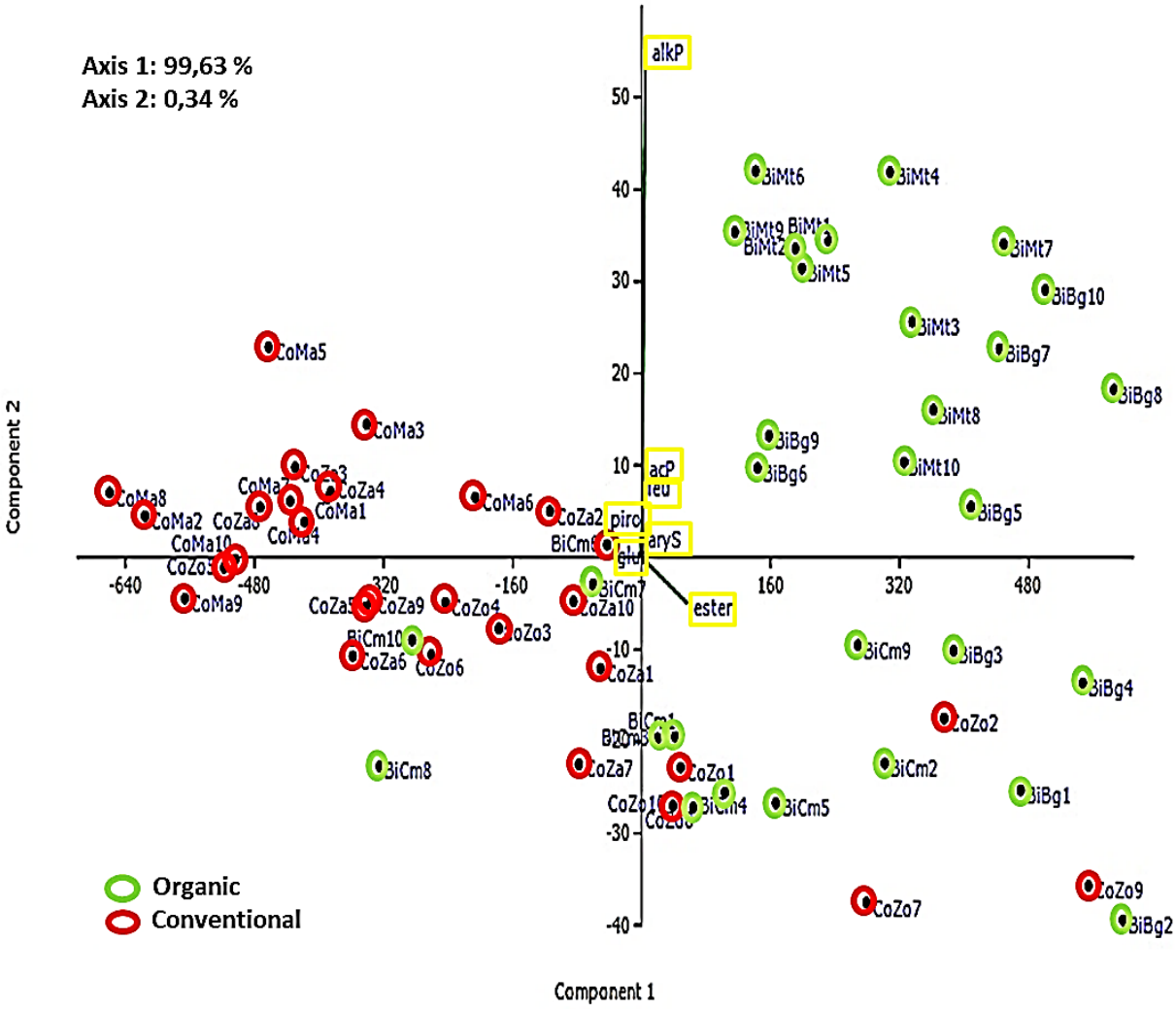


Fig. 51: Principal Components Analysis (PCA) biplot elaborated with data of seven key soil enzymatic activities (ten replicates for each field). Relationships with different enzymatic activities are also evident (yellow): aryS: arylsulfatase, glu: β-glucosidase, leu: leucine aminopeptidase, acP: acid phophomonoesterase, alkP: alkaline phosphomonoesterase, piro: pyrophosphate-phosphodiesterase, ester: acetate-esterase.

The PCA ordination plot shows how almost all the percentage of sample variance (99.63 %) is visualised on the axis 1, and along this axis a separation of samples into two groups is evident: organic samples on the right side and conventional ones on the left side. Moreover another consideration that can be made is that only acetate-esterase activity seems to characterize mainly organic samples, since the other enzymatic activities remain along axis 2. However the overall enzymatic situation seems to be different in the two types of agriculture and the mean values of all enzymatic activities are highly significantly greater in organic soils.

Considering fields in pairs (organic and conventional) the increase in each enzymatic activity was calculated in n-fold increase when passing from one management (conventional) to the other (organic) (tab. XXIX).

	Increase in enzymatic activity (n-fold)						
Field pairs	**AryS**	**Gluc**	**AcP**	**Piro**	**AlkP**	**Leu**	**Ester**
BiMt/CoMa	2.4	2.1	1.7	1.4	1.7	2.1	1.8
BiCm/CoZa	2.2	1.2	1.2	1.3	1.1	1.2	1.3
BiBg/CoZo	3.0	3.7	1.6	1.3	1.4	2.6	1.3

Tab. XXIX: Comparison between conventional and organic management with respect to the increase in each enzymatic activity considered.

By comparing the two types of agriculture the higher increases in enzymatic activity were found from conventional to organic soils in arylsulfatase, β-glucosidase and leucine-aminopeptidase (from 2.1- up to 3.7-fold). Similar results were found also in Kramer et al. (2006) for the increase in β-glucosidase activity.

Since soil quality indicators are associated with specific soil processes, they can be used as an indirect and useful measure of soil quality changes. Karaca et al. (2011) reviewed soil enzymatic activity under various soil management systems and described enzymatic activity as a useful measure for detecting the effect of soil management on carbon cycling. Among others, β-glucosidase seems to be the most sensitive enzyme to soil management practices and therefore its activity may provide a reliable long-term monitoring tool serving as early indicator of changes in soil properties induced by tillage systems (Ekenler and Tabatabai, 2003).

Jordan and coworkers (1995) found that soil phosphatases activity (acid and alkaline) can be considered important indicators of the effects of soil management systems and of the organic matter content of the soil. Considering fertilization, several studies underlined that increases in phosphatase(s) activities resulted from OM amendments (Jordan et al., 1995; Kremer and Li, 2003; Vinhal-Freitas et al., 2010) and also β-glucosidase activity increases significantly in response to the application of organic compost (Vinhal-Freitas et al., 2010). Considering differences between soils managed with intensive practices and semi-natural soils, other authors (Saviozzi et al., 2001) by studying changes in soil quality after 45 years of continuous corn production with conventional management compared with adjacent forest and native grassland, found that enzymatic activity was the most strongly depressed soil property under intensive agronomic use compared with other biochemical parameters. In particular they found that, among others, protease, β-glucosidase and urease appeared the most responsive indexes to management practices and may provide indications of the effects of soil cultivation and of their difference from the differently undisturbed ecosystems.

Concentrating their study just on agroecosystems with different management, also other authors (Mina et al., 2008) reached the conclusion that enzymatic activities were generally higher in zero-tillage practice than in conventional managed plots. From the research of other groups (Niemi et al., 2008) it emerged that arylsulfatase, phosphomonoesterase and esterase activities were greater in organic managed systems than in conventional ones. In line with these studies, also this work found that conventionally managed soils (characterised by a more intensive agronomic land use and by chemical fertilizers- tabb. LV and LVI in the

appendix) had a depressed activity in all seven key enzymes analysed. In particular the major difference between organic and conventional management was underlined by arylsulfatase and β-glucosidase activities (tab. XXIX).

Soil mesofauna

Mesofaunal diversity overview

A total of 584 individuals was collected in three sampling periods with eight replicates for field in each sampling. The main groups found are listed in tab. XXX. A distinction among different edaphic values was made for some groups according to EcoMorphological Index score (EMI) of the QBS-ar index (Parisi, 2001): the higher the score is, the more that mesofaunal group is adapted to edaphic conditions.

Mesofauna taxon	**Organic-biodynamic** [Mean(S.E.)]	**Conventional** [Mean(S.E.)]	**Statistical test** (One-way ANOVA or Kruskal-Wallis)
Coleoptera (s.1)	1.47 (0.47)	1.07 (0.27)	n.s.
Coleoptera (s.9)	/	0.07 (0.07)	n.s.
Hymenoptera (s.5)	2.67 (1.69)	0.07 (0.07)	n.s.
Orthoptera (s.20)	0.07 (0.07)	/	n.s.
Diptera (larvae)	6.27 (2.92)	1.50 (0.74)	n.s.
Diptera (adult)	0.2 (0.13)	0.07 (0.07)	n.s.
Mesostigmata	1.6 (0.19)	1.20 (0.56)	n.s.
Uropodina	/	1.87 (1.55)	n.s.
Oribatida	2.67 (0.88)	1.13 (0.59)	n.s.
Astigmata	0.07 (0.07)	0.33 (0.33)	n.s.
Collembola (s.1)	/	0.07 (0.07)	n.s.
Collembola (s.4)	0.20 (0.13)	0.40 (0.16)	n.s.
Collembola (s.6)	0.53 (0.17)	0.47 (0.17)	n.s.
Collembola (s.8)	3.87 (1.12)	1.27 (0.64)	n.s.
Collembola (s.10)	5.80 (2.77)	0.53 (0.20)	**
Collembola (s.20)	2.73 (0.99)	0.13 (0.13)	**
Araneida (s.5)	0.13 (0.08)	0.07 (0.07)	n.s.
Diplopoda	0.13 (0.13)	/	n.s.
Geophilomorpha	0.20 (0.13)	/	n.s.
Psocoptera	/	0.07 (0.07)	n.s.

Tab. XXX: Mean values of number of individuals extracted with Berlese-Tullgren extractor. Significance: *: p value <0.05; **: p value <0.01; n.s.: p value >0.05. EMI score: s. (+ number).

Numerical abundances of several mesofaunal taxa were not significantly different between the two types of agriculture, except for Collembola (s.10 and s.20) that were significantly more abundant in organic-biodynamic soils (tab. XXX). These two taxa were characterised by an EMI score among the highest ones

observed and their presence indicates that organic-biodynamic soils are less disturbed and with a well-structured profile.

In order to visualize relationships of similarity among mesofaunal community samples in a 2D space, a multivariate statistical technique of ordination was performed (fig. 52 a).

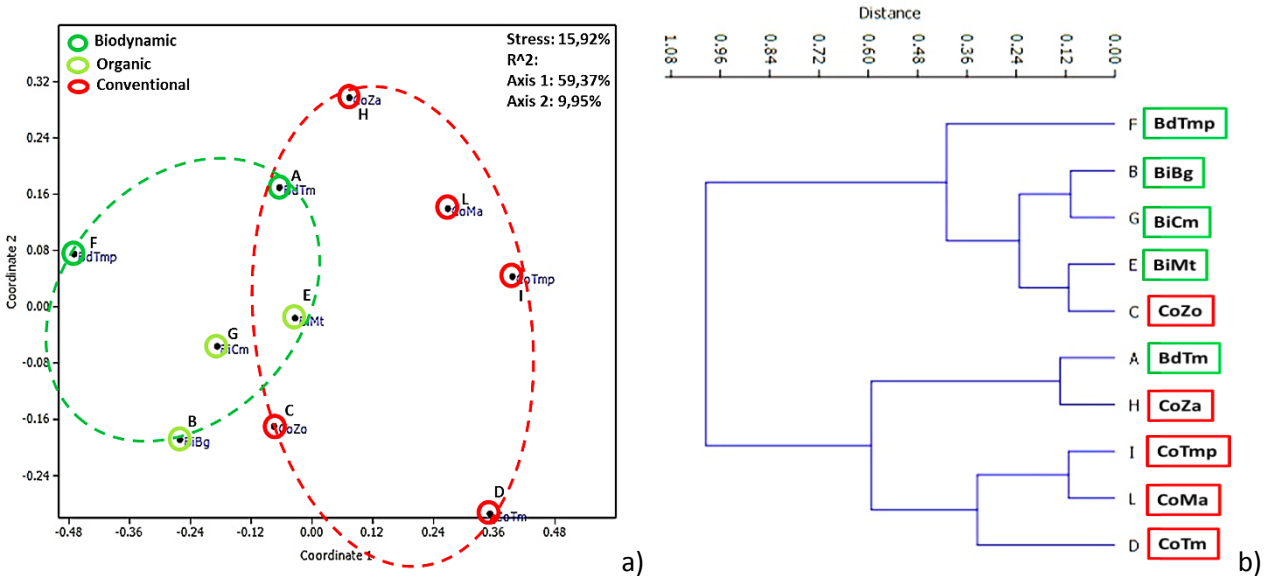


Fig. 52: a) NMDS plot of soil mesofaunal communities data, Bray-Curtis similarity measure. b) Classical cluster analysis of NMDS scores on axis 1 data of soil mesofaunal communities, Ward's method- Euclidean similarity measure.

By using the recalculated coordinates of each sample points on axis 1 of NMDS plot, a cluster analysis was performed (fig. 52 b).

Fig. 52 shows how the soil mesofaunal communities are divided in two main groups that are concordant almost perfectly with the field management. Therefore there is a significant difference, according to mesofaunal communities between organic-biodynamic and conventional fields (p value = 0.03*, U test; p value = 0.02*, t test). On the contrary other authors (Pankhurst et al., 1995) noticed that microarthropods (especially collembola, which are the only ones that in this work present significant different abundances in organic-biodynamic and conventional fields) tended to show inconsistent responses across a range of soil management practices.

QBS-ar: mesofaunal functionality

Subsequently the QBS-ar index (Parisi, 2001) was applied to mesofaunal data. Fig. 53 shows the results.

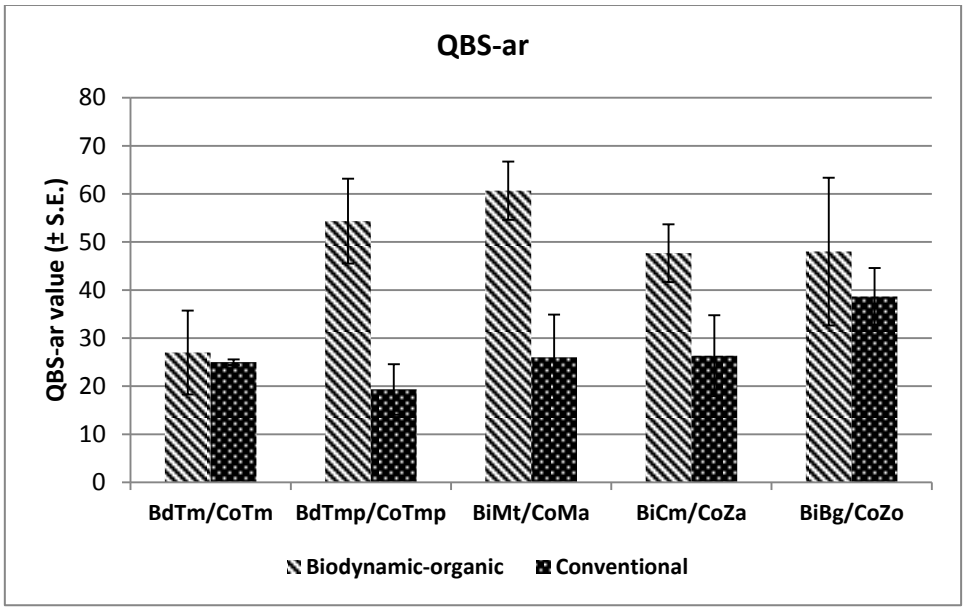


Fig. 53: Mean values of QBS-ar index (Parisi, 2001) calculated on mesofaunal samples picked up from studied fields of different management.

Statistical elaborations are summarised in tab. XXXI.

	Organic-biodynamic [mean (S.E)]	**Conventional** [mean (S.E.)]	**Statistical test** (Two-way ANOVA)	
			Management	**Period**
QBS-ar value	47.6 (5.7)	27.0 (3.3)	**	n.s.

Tab. XXXI: Mean QBS-ar value calculated for the two types of agriculture. Significance: **: p value<0.01; n.s.: p value>0.05.

By observing only the abundance of mesofaunal taxa (tab. XXX) few differences emerged between the two types of agriculture (except for Collembola), but deepening the analysis and observing mesofaunal communities these differences became more marked and the QBS-ar index analysis confirmed and highlighted the differences between organic-biodynamic and conventional management. Gardi and coworkers (2003) found that arable lands generally showed QBS-ar values lower than 100, as in this work, and moreover they found that this index was affected by agronomic management, showing the highest values in organic farming soils and/or low input crops. Results obtained in this research confirm this tendency.

Earthworms

Earthworm diversity overview

Four samplings of hand sorting were repeated in each field and with 7 replicates each time. The summary of sampled species number is in tab. XXXII.

	Organic-biodynamic [mean (S.E)]	**Conventional** [mean (S.E.)]	**Statistical test** (One-way ANOVA)
N° earthworm species	11.0 (1.9)	4.8 (1.0)	*

Tab. XXXII: Mean values of species number in the two types of agroecosystem analysed. Significance: * : p value<0.05.

The mean number of earthworm species was significantly higher in organic-biodynamic soils.

The earthworm community structure of organic-biodynamic and conventional fields was described in terms of ecological categories and age of earthworms (tab. XXXIII).

Community structure parameters		**Organic-biodynamic** [mean (S.E.)]	**Conventional** [mean (S.E.)]	**Statistical test** (Mann-Whitney)
Ecological Categories	Anecic	1.22 (0.9)	/	n.s.
	Endogeic	71.52 (8.3)	17.18 (4.2)	**
	Epigeic	3.0 (1.8)	0.08 (0.1)	**
	Coprophagic	0.03 (0.02)	/	n.s.
	Hydrophilic	0.55 (0.5)	0.05 (0.04)	n.s.
Age	Adult	29.58 (8.2)	5.21 (1.6)	**
	Juvenile	46.74 (6.9)	12.09 (3.4)	**
Total		76.32 (9.9)	17.35 (4.3)	**

Tab. XXXIII: Mean values (ind/m^2/sampling) of earthworms divided according to the five ecological categories and to age. Significance: **: p value <0.01; n.s.: p value >0.05.

The overall amount of earthworms was significantly higher in organic-biodynamic fields and moreover all ecological categories were present in organic-biodynamic fields in respect with the conventional ones that hosted only 3/5 categories. In particular there were statistically more endogeic and epigeic earthworms in organic-biodynamic soils. On the contrary of these results, considering just the abundance of earthworms Bengtsson et al. (2005) found no significant difference between organic and conventional farming systems and also Pankhurst et al. (1995) noticed that earthworms tended to show inconsistent responses across a range of soil management practices.

Other considerations can be done about the presence of different ecological categories. Since recent OM is buried into the soil, whereas soil from deep is brought to the soil surface by the deposition of

casts above-ground particularly by the anecic species (Blouin et al., 2013), the importance of the presence of anecic species is evident and they were found only in the organic-biodynamic soils. Moreover Valckx et al. (2010) found that erosion rates decreased exponentially as a function of anecic earthworm biomass and they underlined the need to promote appropriate soil ecosystem management by farmers to support populations of anecic earthworm species, such as non-inversion tillage, direct drilling. Continuing with the eco-physiological actions produced by anecic species into the soil, Blouin et al. (2013) pointed out that they can dig semi-permanent vertical burrows at depth down to 1-m and therefore efficiency in drainage is likely to be increased. Also Valckx et al. (2010) underlined how earthworms and in particular anecic species, such as *Lumbricus terrestris,* significantly reduce runoff and soil loss in arable land. They may have other effects also in soil structure; in fact, in spite of the huge deposition of casts at the soil surface, most anecic and endogeic earthworm species probably deposit their casts primarily below ground, which markedly affects bulk density and aggregation (Blouin et al., 2013).

Also adult and juvenile earthworms were more abundant in organic-biodynamic soils. It is important to characterize the community for different ages, because adults are able to reproduce if there are appropriate conditions, they represent a more stable environment that allowed juvenile to become adults and often they are larger than juvenile individuals (more biomass) and therefore their physiological influence on soil is more incisive, while the presence of juveniles indicates that there had been good conditions for earthworms reproduction (Pérès et al., 1998). Similar results can be found also in literature. In fact Hole et al. (2005) indicated a general trend for higher earthworm abundance under organic management, and with greater detail further studies (Pfiffner and Mader, 1997) found a higher number of earthworm species, a higher density and more anecic and juvenile earthworms under organic management, regardless of crop type within the rotation.

Going into detail of species determination, tab. XXXIV shows results of differences between the two types of managed soils.

Species (Ecological category-age)	**Organic – biodynamic** [Mean (S.E.)]	**Conventional** [Mean (S.E.)]	**Statistical test** (One-way ANOVA or Kruskal-Wallis)
Allolobophora caliginosa (END AD)	38.74 (11.58)	8.15 (2.43)	*
Allolobophora cfr. caliginosa (END J)	26.04 (7.03)	12.28 (7.37)	n.s.
Allolobophora chlorotica (END AD)	39.84 (16.10)	3.40 (2.05)	*
Allolobophora cfr. chlorotica (END J)	5.50 (4.35)	2.15 (1.31)	n.s.
Allolobophora cfr. georgii (END J)	0.05 (0.05)	/	n.s.
Allolobophora jassyensis (END AD)	4.99 (1.87)	0.66 (0.61)	*
Allolobophora cfr. jassyensis (END J)	1.84 (1.84)	/	n.s.
Allolobophora rosea (END AD)	8.91 (6.47)	1.18 (0.50)	n.s.
Allolobophora cfr. rosea (END J)	9.41 (7.60)	0.23 (0.23)	**
Allolobophora sp. (END J)	119.77 (19.20)	19.06 (5.35)	***
Dendrobaena byblica (END AD)	0.14 (0.09)	/	n.s.
Dendrobaena veneta (COP AD)	0.05 (0.05)	/	n.s.
Eisenia foetida (COP AD)	0.05 (0.05)	/	n.s.
Eiseniella tetraedra (IDR AD)	1.68 (1.52)	0.15 (0.11)	n.s.
Eiseniona handlirschi (EPI AD)	1.27 (1.27)	0.04 (0.04)	n.s.
Eiseniona cfr. handlirschi (EPI J)	0.63 (0.39)	/	n.s.

Eiseniona sineporis (EPI AD)	5.50 (5.00)	/	n.s.
Eiseniona cfr. sineporis (EPI J)	2.40 (2.40)	/	n.s.
Eiseniona sp.(EPI J)	0.23 (0.23)	/	n.s.
Helodrilus antipai (END AD)	0.41 (0.41)	/	n.s.
Lumbricus castanues (EPI AD)	0.41 (0.35)	/	n.s.
Lumbricus cfr. castaneus/rubellus (EPI J)	0.18 (0.08)	/	*
Lumbricus rubellus (EPI AD)	0.14 (0.09)	0.08 (0.08)	n.s.
Lumbricus cfr. terrestris (ANE J)	0.05 (0.05)	/	n.s.
Lumbricus sp. (EPI J)	0.45 (0.34)	0.11 (0.11)	n.s.
Microeophila nematogena (END AD)	0.41 (0.41)	0.04 (0.04)	n.s.
Microscolex sp. (END J)	0.41 (0.41)	/	n.s.
Octodrilus complanatus (ANE AD)	1.15 (0.99)	/	n.s.
Octodrilus cfr. complanatus (ANE J)	0.63 (0.63)	/	n.s.
Octodrilus lissaensis (END AD)	0.09 (0.09)	0.04 (0.04)	n.s.
Octodrilus cfr. lissaensis (END J)	0.05 (0.05)	/	n.s.
Octodrilus sp. (ANE J)	2.82 (2.20)	/	n.s.
Octodrilus transpadanus (END AD)	0.36 (0.23)	/	n.s.
Octolasium lacteum (END AD)	0.09 (0.09)	/	n.s.
Octolasium sp. (END J)	0.05 (0.05)	/	n.s.
Unidentified	2.18 (1.54)	0.08 (0.08)	

Tab. XXXIV: Mean values of earthworm species (ind/m2) in organic-biodynamic and conventional soils. Ecological categories: END: endogeic; EPI: epigeic; ANE: anecic; COP: coprophagic; IDR: hydrophilic. Age: AD: adults; J: juvenile. One-way ANOVA or Kruskal-Wallis test. Significance: *: p value <0.05; **: p value <0.01; ***: p value <0.001; n.s.: p value >0.05.

Differences in soil management seem to affect the abundance of some species, such as *A. caliginosa*, *A. chlorotica*, *A. jassyensis* and *A. rosea* that are endogeic species living in the first ten centimetres of soil depth, but also of *L. cfr. castaneus/rubellus* that is an epigeic species living in the litter. It is possible to conclude that organic-biodynamic soils, that present higher values of abundance of these species, are characterised by a well-structured profile, with a good aeration and drainage and also they remain for a longer period protected by litter, cover crops or crop residues, allowing also the presence of epigeic species. This fact indicates that these soils are less subjected to erosion of the surface fertile humic layer.

Trying to quantify this effect it is possible to say that the contribution of earthworms to the burial of surface litter (leaves, twigs and so on) at some locations may reach 90–100% of the litter deposited annually on the soil surface by the above-ground vegetation from both natural vegetation or crops (Knollenberg et al., 1985), representing up to several tonnes per ha per year of organic material (Blouin et al., 2013).

In order to visualize relationships of similarity among earthworm communities samples in a 2D space, a multivariate statistical technique of ordination was performed (fig. 54 a).

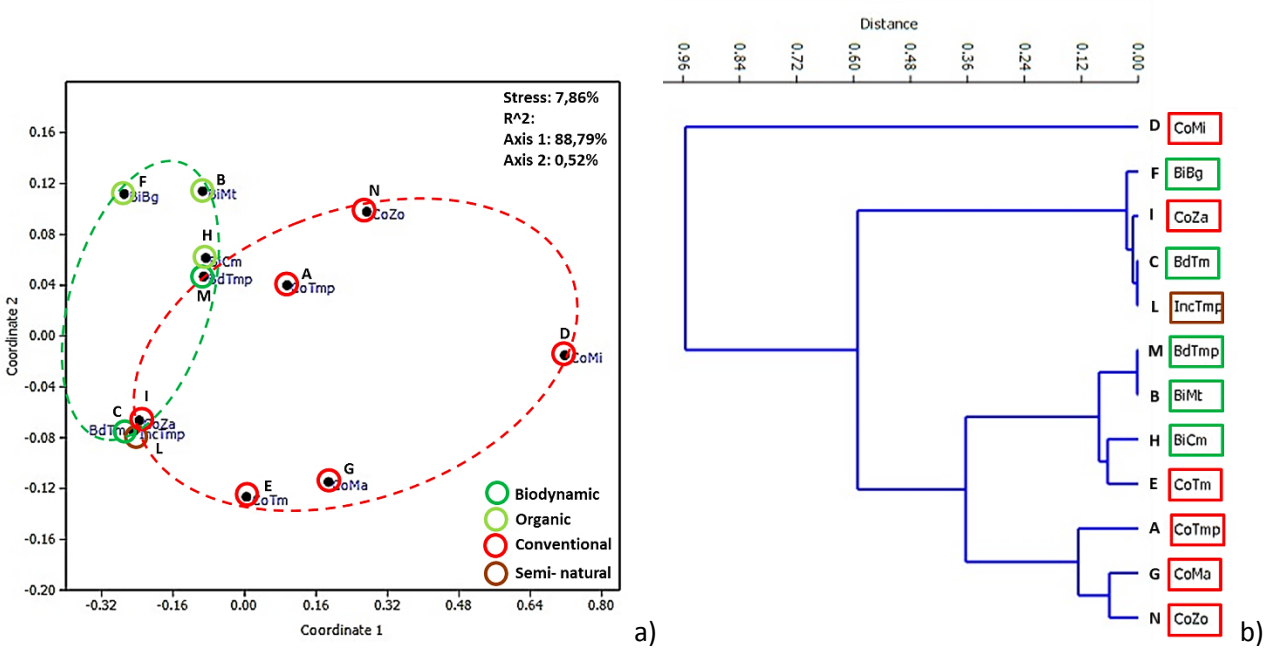


Fig. 54: a) NMDS plot of data concerning soil earthworm communities (species ind/m^2), Bray-Curtis similarity measure. b) Classical cluster analysis of NMDS scores on axis 1 data of earthworm communities, Ward's method- Euclidean similarity measure.

By using the recalculated coordinates of each sample points on axis 1 of NMDS plot, a cluster analysis was performed (fig. 54 b).

Even if considering species abundance and community structure parameters it was possible to distinguish different agroecosystem managements, it was not the same when earthworm communities (all species and their relative abundances) were considered. In fact observing the cluster diagram (fig. 54 b) there is not a clear separation into two groups according to management type.

The following ordination plot shows mean data of ecological categories for each field and each year of sampling (fig. 55).

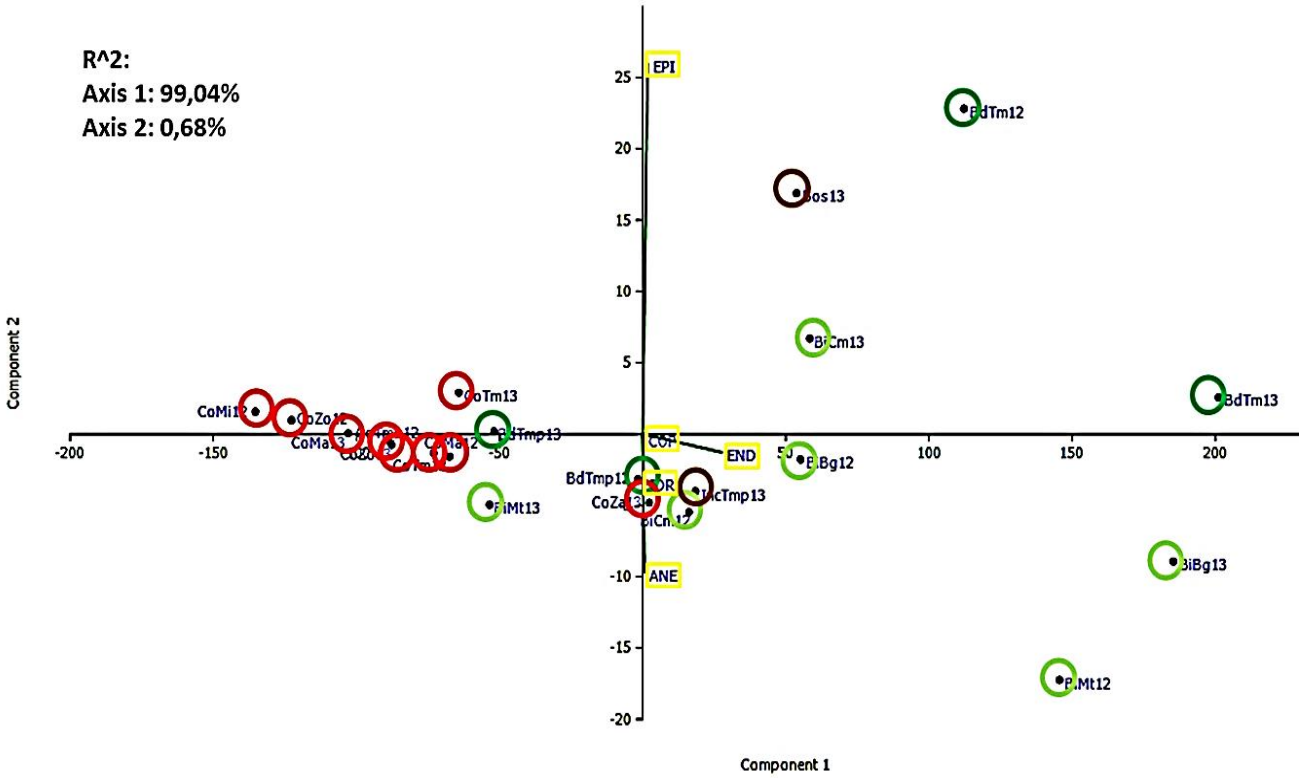


Fig. 55: Principal Components Analysis (PCA) biplot elaborated with data from earthworm ecological categories (ind/m^2). END: endogeic; EPI: epigeic; ANE: anecic; COP: coprophagic; IDR: hydrophilic. Data are about each year of sampling (2012 and 2013). In light green: organic; dark green: biodynamic; red: conventional; brown: semi-natural samples.

The PCA ordination plot shows how almost all the percentage of sample variance (99.04%) is visualised on axis 1, and along this axis it is evident a separation of samples into two groups: organic-biodynamic samples on the right side and conventional ones on the left side. Moreover another consideration that can be made is that organic-biodynamic samples are distributed also along the whole axis 2, while conventional ones are not. Endogeic species (along axis 1), but also anecic and epigeic species (along axis 2) seem to characterize mainly organic-biodynamic samples. However the overall presence of earthworm ecological categories seems to be different in the two types of agriculture.

Concluding the considerations about soil management, some studies (van Groeningen et al., 2014) pointed out that organic farming systems, typically have large application rates of organic manure or high-quality crop residues, providing excellent conditions for earthworm activity. In those agronomic systems, earthworm activity might be crucial in closing the yield gap with conventional agriculture and for this reason they highlighted that future research in these systems should focus on management strategies in order to increase earthworm populations.

QBS-e: earthworm functionality

Subsequently, the QBS-e index (Paoletti et al., 2013) was applied to earthworm data. Results are shown in fig. 56.

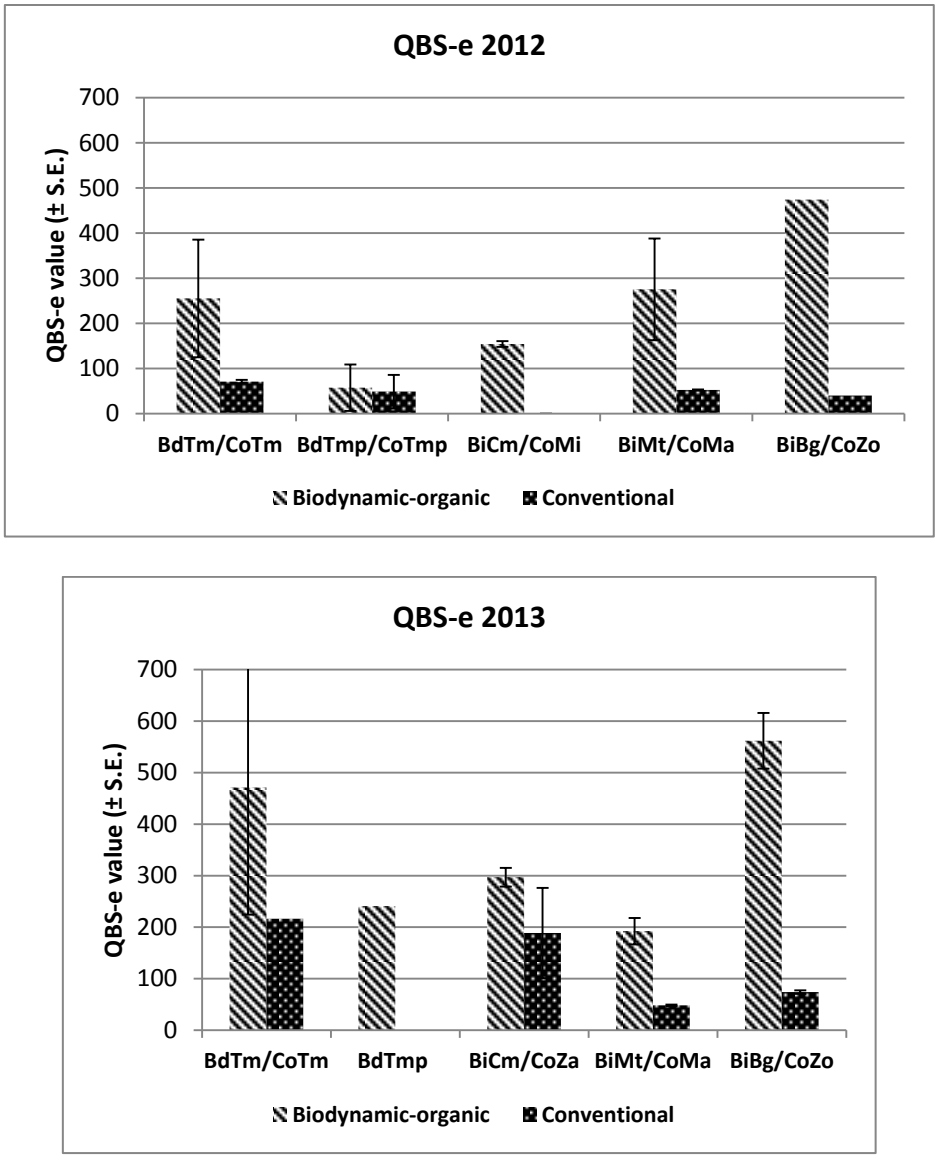


Fig. 56: Mean values of the QBS-e index (Paoletti, et al., 2013) calculated on earthworm samples picked up from studied fields during the two years of sampling.

Statistical elaborations are summarised in tab. XXXV.

	Organic-biodynamic [mean (S.E)]	**Conventional** [mean (S.E.)]	**Statistical test** (two-way ANOVA)	
			Management	**Period**
QBS-e value	267.8 (41.7)	76.4 (18.3)	***	n.s.

Tab. XXXV: Mean values of the QBS-e index (Paoletti et al., 2013). Significance: ***: p value <0.001; n.s.: p value >0.05.

According to the QBS-e index (Paoletti et al., 2013), organic-biodynamic fields totalized a sufficient quality class (1) of soil, while conventional fields reached just a poor quality class (0). Even if the organic-biodynamic QBS-e value was significantly higher than the conventional QBS-e value, these low values are probably due to the fact that generally agroecosystems (and in particular annual ones) are food production sites and consequently they are much more disturbed by human intervention in comparison to more natural ecosystems, where one can reasonably expect a higher QBS-e value. For a comparison with a less disturbed ecosystem, on demand of one of the farmers involved in the research (Andrea Giubilato of the Madre Terra farm) also a little area of plain woodland located nearby the cropped areas of his farm (BosVE on the map fig.11) was sampled. In this more natural ecosystem, the QBS-e index was applied to earthworm data and its value was 616.2, indicating a good soil quality (3). Therefore by using QBS-e it would be possible to monitor the soil quality class of an agroecosystem and to improve it by adopting always less invasive management practices, as underlined by van Groeningen and coworkers (2014).

Phytophagous agents

Crop pests overview

Treviso red chicory

In 2012 three visual control samplings were made in each field during vegetative period of *Cichorium intybus*. Six replicates were done for each field in each sampling. Results of the main phytophagous agents observed on the crop plants are summarised in tab. XXXVI.

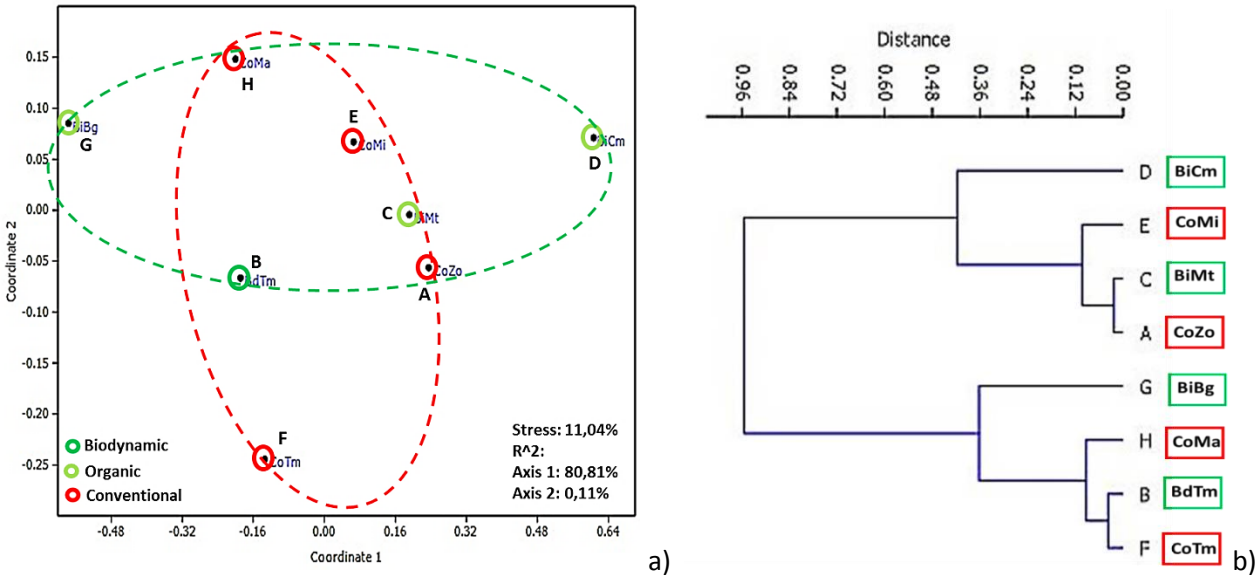
Phytophagous taxa	**Organic-biodynamic** [Mean/4 plants (S.E.)]	**Conventional** [Mean/4 plants (S.E.)]	**Statistical test** (Two-way ANOVA or Friedman)
Agromyzidae (larvae)	0.31 (0.09)	0.24 (0.17)	n.s.
Aphididae	12.49 (8.36)	6.56 (1.81)	n.s.
Chrysomelidae	0.27 (0.16)	0.02 (0.02)	*
Cicadellidae	0.85 (0.18)	0.47 (0.4)	n.s.
Curculionidae	0.06 (0.02)	0.15 (0.12)	n.s.
Chrysomelidae (Halticinae)	0.13 (0.05)	0.10 (0.04)	n.s.
Lepidoptera (larvae)	1.46 (0.51)	2.42 (0.69)	n.s.
Miridae	1.74 (0.07)	0.91 (0.16)	*
Orthoptera	0.08 (0.01)	0.01 (0.01)	n.s.
Pentatomidae	0.24 (0.02)	0.17 (0.09)	n.s.

Pulmonata		0.10 (0.03)	0.13 (0.13)	n.s.
	Total	17.71 (1.10)	11.18 (0.59)	n.s.

Tab. XXXVI: Mean presence per sampling point of crop pests on Treviso red chicory in 2012. Significance: *: p value <0.05; n.s.: p value > 0.05. (Fusaro et al., in prep).

Observing tab. XXXVI it emerges that just chrysomelids and miridae were significantly more abundant in organic-biodynamic fields, but the overall presence of crop pests was not significantly different in the two types of agroecosystem. Also other authors (Bengtsson et al., 2005) found that there were no differences in abundance of crop pests between organic and conventional managements and these results confirm that trend.

In order to visualize relationships of similarity among crop pest community samples in a 2D space, a multivariate statistical technique of ordination was performed (fig. 57 a) and then by using the recalculated coordinates of each sample points on axis 1 of NMDS plot, a cluster analysis was carried out (fig. 57 b).



a) b)

Fig. 57: a) NMDS plot of data concerning phytophagous agent communities (mean/4 plants) on Treviso red chicory, Bray-Curtis similarity measure. b) Classical cluster analysis of NMDS scores on axis 1 data of phytophagous agent communities on Treviso red chicory, Ward's method- Euclidean similarity measure.

From the cluster analysis it emerges that crop pest community samples can be divided into two groups, but there are not correspondences with different managements.

White cabbage

In 2013 three visual control samplings were made in each field during vegetative period of *Brassica oleracea,* in the same way than for red chicory. In tab. XXXVII results of main phytophagous agents occurrence are summarised.

Phytophagous taxa	**Organic-biodynamic** [Mean/4 plants (S.E.)]	**Conventional** [Mean/4 plants (S.E.)]	**Statistical test** (Two-way ANOVA or Friedman)
Agromyzidae (larvae)	0.07 (0.03)	0.06 (0.03)	n.s.
Aleyrodidae	2.88 (2.38)	1.28 (0.43)	n.s.
Aphididae	2.46 (0.54)	1.48 (0.37)	*
Cicadellidae	0.06 (0.02)	0.11 (0.03)	n.s.
Lepidoptera (larvae)	5.74 (0.52)	9.49 (3.42)	n.s.
Lygus sp.	0.58 (0.34)	0.41 (0.17)	n.s.
Pentatomidae	0.94 (0.43)	0.06 (0.06)	n.s.
Phyllotreta sp.	4.53 (0.91)	28.20 (15.81)	n.s.
Pulmonata	2.08 (1.21)	0.25 (0.25)	n.s.
Thripidae	0.33 (0.13)	/	*
Total	19.67 (0.62)	41.34 (2.83)	*

Tab. XXXVII: Mean presence per sampling point of crop pests on white cabbage in 2013. Significance: *: p value <0.05; n.s.: p value > 0.05. (Fusaro et al., in prep).

On organic-biodynamic cabbages significantly more aphididae and thripidae were found but the overall presence of crop pests was significantly higher in conventional cabbages. This underlines an outbreak of phytophagous agents (mainly flea beetles) that could damage crop production. There are evidences in literature that pests prefer plants which have been nurtured with synthetic fertilizers rather than those growing in organically managed soil (Gomiero et al., 2011) and this could explain also results obtained in this work due to different fertilization techniques adopted by farmers (tabb. LV and LVI in the appendix) and different crop pest abundance between organic-biodynamic and conventional agroecosystems.
The higher amount of crop pests in conventional fields is mainly due to the conspicuous presence of flea beetles (*Phyllotreta* sp). Altieri and coworkers (1998) by studying various fertilization regimes in broccoli crop (*Brassica oleracea*), found that conventionally fertilized monoculture consistently developed a larger infestation of flea beetles than the organically fertilized broccoli systems and they concluded that insect pest preference can be moderated by alterations to the type and amount of fertilizer used. Having a look at the tabb. LV and LVI in the appendix concerning the management practices, it seems that the same situation has occurred in the present study.

Focusing on lepidopteran larvae presence, it is interesting to notice the differences between organic-biodynamic and conventional fields (fig. 58).

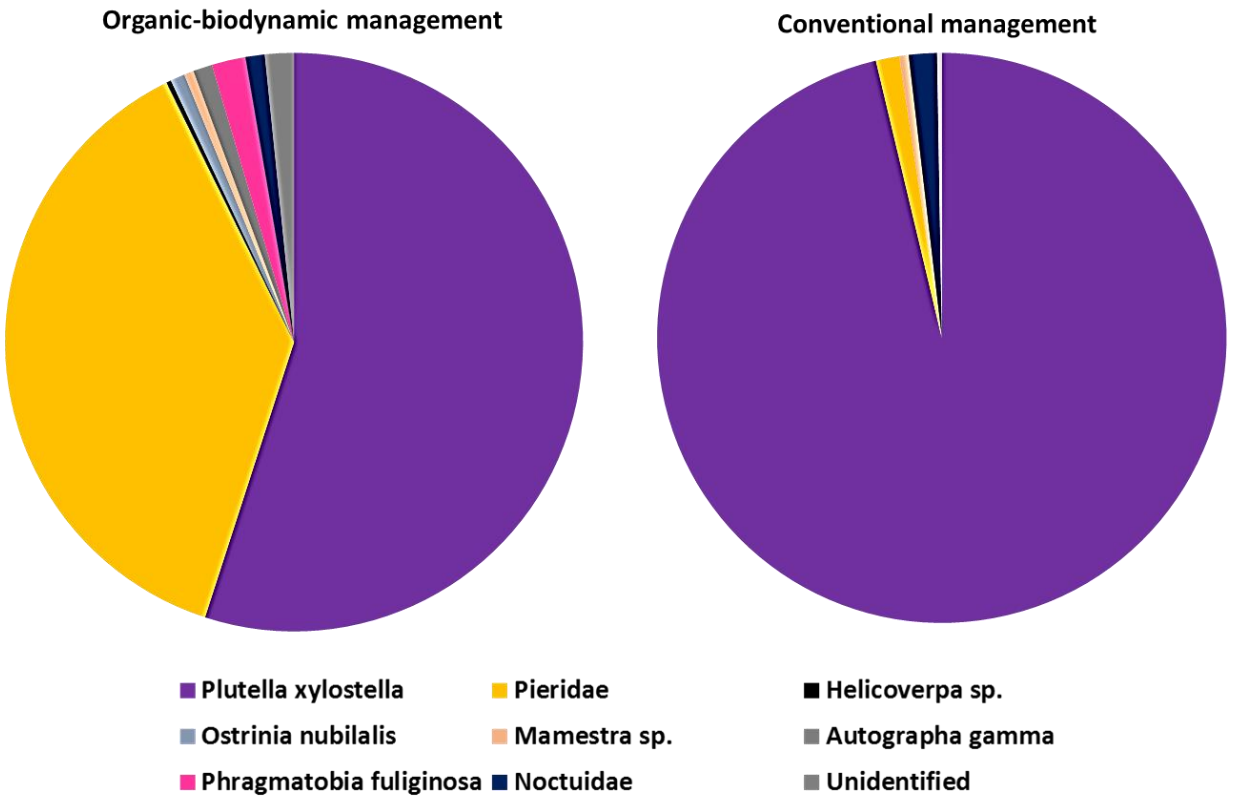


Fig. 58: Composition of different lepidopteran pest fauna on cabbage according to the field management (Fusaro et al., in prep).

Both in organic-biodynamic and conventional fields, *P. xylostella* was the dominant species, but with different abundance: 55.0% of all specimens collected in organic-biodynamic fields were *P. xylostella*, while almost all specimens (96.3%) in conventional ones belonged to this species.

In order to visualize relationships of similarity among crop pest community samples in a 2D space, a multivariate statistical technique of ordination was performed (fig. 59 a) and then by using the recalculated coordinates of each sample points on axis 1 of NMDS plot, a cluster analysis was made (fig. 59 b).

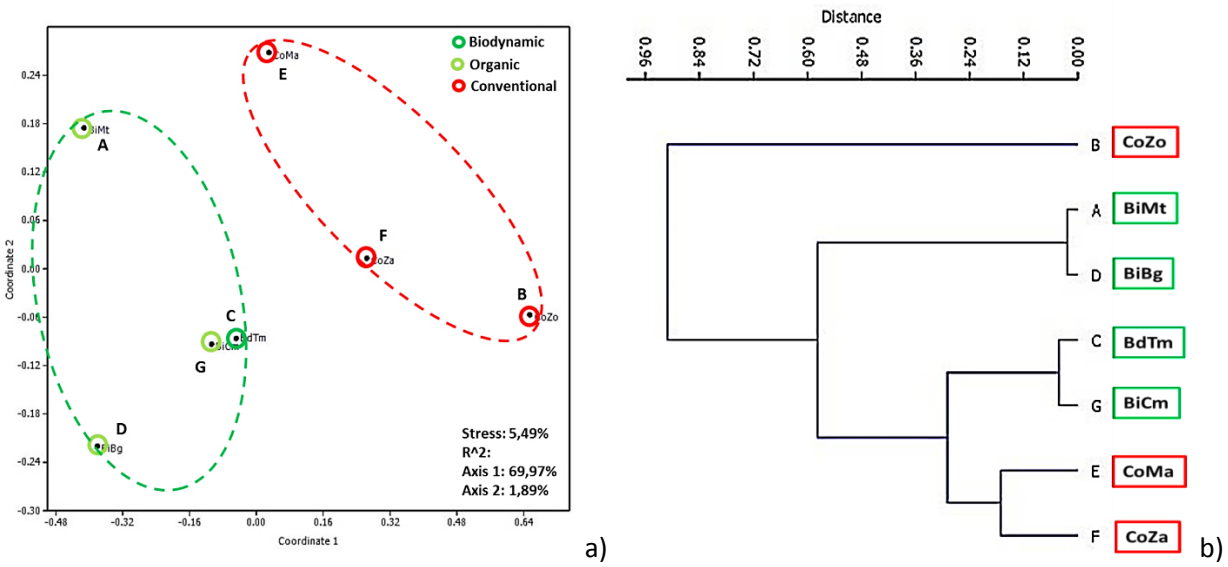


Fig. 59: a) NMDS plot of data concerning phytophagous agent communities (mean/4 plants) on cabbage, Bray-Curtis similarity measure. b) Classical cluster analysis of NMDS scores on axis 1 data of phytophagous agent communities on cabbage, Ward's method- Euclidean similarity measure.

This cluster diagram highlights how crop pest community samples cannot be separated according to management practices of the fields.

Considering both red chicory and cabbage results, partially different evidences were found by Crowder and Jabbour (2014) that pointed out that management intensification might exacerbate pest problems by concentrating arthropod resources and with consequent decrease in populations of natural enemies.

Crop damage

Only in 2013 on white cabbage was possible to evaluate the crop damage, discriminating the damage caused by strip feeders (mainly lepidoptera caterpillars) and pit feeders (mainly flea beetles). This analysis was made in order to see if there were any relation between a higher presence of crop pests and an effective higher damage in crop plants.

In the two following charts these results are shown (fig. 60).

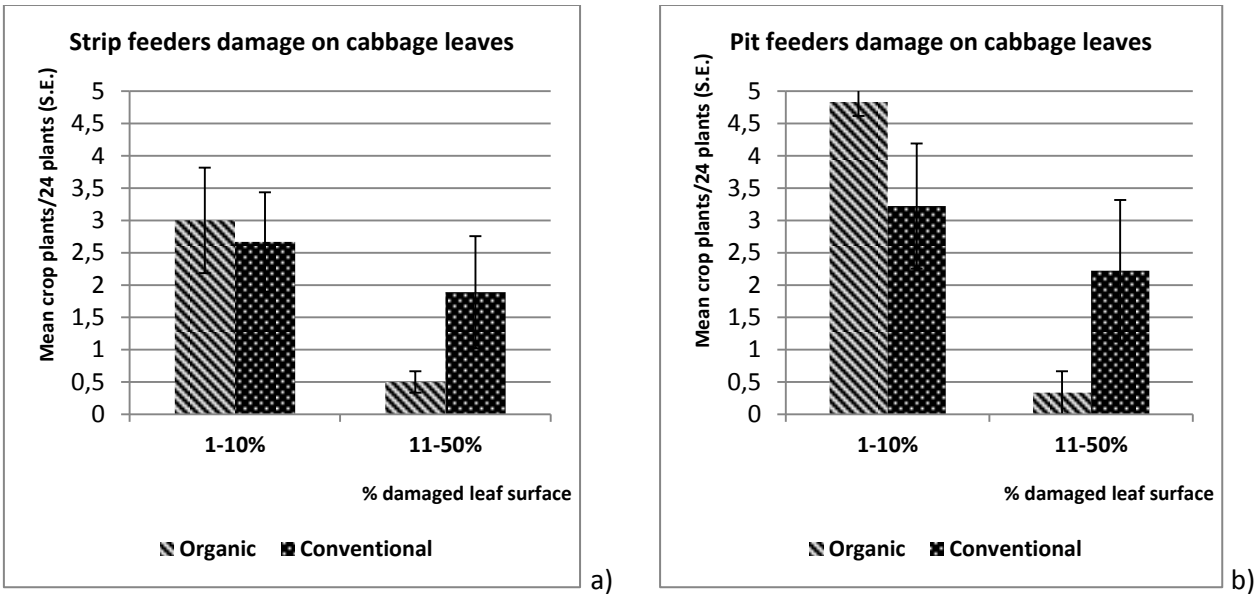


Fig. 60: Leaves damage estimation on white cabbage due to different phytophagous agents: strip feeders (a) and pit feeders (b) (Fusaro et al., in prep).

Looking at the figure 60, it is possible to appreciate how there was a tendency of a more consistent damage on leaves (11-50% of leaf surface damaged) caused both by strip feeders and by pit feeders in conventional fields, despite a more intensive use of pesticides (tab. LVII in the appendix), but these differences were never significant (Strip feeders: 1-10% p value = 0.8, U test; 11-50% p value = 0.26, U test; Pit feeders: 1-10% p value = 0.29, U test; 11-50% p value = 0.09, U test).

Natural control agents of crop pests

To explore natural control agent communities different sampling methods were applied: pitfall trap samplings (seven samplings with six pitfall traps for each field for each sampling) in order to trap carabid beetles, visual control (in the same way for phytophagous agent survey) and subsequent indoor breeding of collected insects (mainly lepidoptera caterpillars) in order to quantify and determine eventual parasitoids and hyperparasitoids.

Carabid diversity overview

A total of 65 species of carabids were collected in all fields during 2012 and 2013. The mean values of species collected in fields of different management are shown in tab. XXXVIII.

	Organic-biodynamic [mean (S.E)]	**Conventional** [mean (S.E.)]	**Statistical test** (one-way ANOVA)
N° carabid species	22.4 (1.1)	17.7 (1.3)	*

Tab. XXXVIII: Mean values of species number of carabids sampled in organic-biodynamic and conventional fields. Significance: *: p value <0.05.

The total number of carabid species found in this study (65) can be considered high if compared with the one of other studies made in organic and conventional agroecosystems (from 15 to 50) [see pg. 192 in Kromp (1999)]. The mean number of carabid species was significantly higher in organic-biodynamic managed fields (tab. XXXVIII). Also other authors (Bengtsson et al., 2005) found that in organic fields significantly more carabid species are hosted. Doring and Kromp (2003) found that the more the carabid species are typical of agricultural fields, and the less they are bound to woodland, the more they benefit from organic agriculture. Therefore, organic agriculture is considered to support higher carabid diversity in comparison to conventional agriculture, especially referring to the typical field species. Since the major part of carabid species sampled in this work are typical field species (Lupi et al., 2007), the higher mean number of species found in organic-biodynamic fields also confirms literature results (Doring and Kromp, 2003).

In tab. XXXIX data on activity density of the 26 most common carabid species (that is to say species found in more than two farms) are shown. Results on all species are listed in the appendix (tab. LIX).

	Organic-biodynamic [Mean (S.E.)]	**Conventional** [Mean (S.E.)]	**Statistical test** (one-way ANOVA or Kruskal-Wallis)
Acupalpus meridianus	0.004 (0.004)	0.03 (0.02)	n.s.
Amara aenea	0.15 (0.05)	0.18 (0.11)	n.s.
Anchomenus dorsalis	0.08 (0.05)	0.05 (0.05)	n.s.
Anisodactylus signatus	0.03 (0.02)	0.01 (0.0)	n.s.
Asaphidion stierlini	0.01 (0.01)	0.03 (0.03)	n.s.
Bembidion quadrimaculatum	0.78 (0.37)	0.38 (0.21)	n.s.
Calathus fuscipes graecus	0.40 (0.18)	0.13 (0.07)	n.s.
Clivina collaris	0.05 (0.04)	0.08 (0.06)	n.s.
Clivina fossor	0.03 (0.02)	0.07 (0.04)	n.s.
Egadroma marginatum	0.88 (0.61)	1.01 (1.01)	n.s.
Harpalus affinis	0.07 (0.03)	0.25 (0.21)	n.s.
Harpalus distinguendus	1.47 (0.34)	0.84 (0.28)	n.s.
Harpalus oblitus	0.01 (0.004)	0.002 (0.002)	n.s.
Harpalus pygmaeus	0.004 (0.004)	0.01 (0.004)	n.s.
Microlestes corticalis	0.30 (0.14)	0.20 (0.13)	n.s.
Metallina properans	0.01 (0.01)	/	*
Ophonus diffinis	0.02 (0.01)	0.02 (0.02)	n.s.
Poecilus cupreus	1.50 (0.36)	3.99 (2.84)	n.s.
Pseudoophonus griseus	0.12 (0.06)	0.04 (0.02)	n.s.
Pseudoophonus rufipes	1.61 (0.72)	0.28 (0.06)	n.s.

Pterostichus melanarius	0.17 (0.09)	0.004 (0.004)	*
Pterostichus melas	1.23 (0.77)	0.20 (0.19)	n.s.
Pterostichus niger	0.55 (0.26)	0.31 (0.27)	n.s.
Stenolophus skrimshiranus	0.03 (0.02)	0.08 (0.06)	n.s.
Stenolophus teutonus	0.06 (0.04)	2.17 (2.08)	n.s.
Trechus quadristriatus	0.25 (0.09)	0.20 (0.07)	n.s.

Tab. XXXIX: Mean values of activity density (DA_{10}) of 26 most common species sampled in all fields. Significance: *: p value <0.05; n.s.: p value >0.05.

From this table it emerges that there are no significant differences between the activity density of almost all the most common species, except for *Metallina properans* and *Pterostichus melanarius* that were more active in organic-biodynamic fields. Prior studies (Doring and Kromp, 2003) by using an index designed to calculate how much a carabid species benefits from organic management, found that among others, *Metallina properans* (*Bembidion properans*) belongs to the group of species which benefit more than the carabids in total from organic management, while *Pterostichus melanarius* benefits less than the carabids in total from organic cultivation. Therefore these results partially confirm the ones obtained by Doring and Kromp (2003).

In order to visualize relationships of similarity among carabid community samples in a 2D space, a multivariate statistical technique of ordination was performed (fig. 61 a) and then by using the recalculated coordinates of each sample points on axis 1 of NMDS plot, a cluster analysis was done (fig. 61 b).

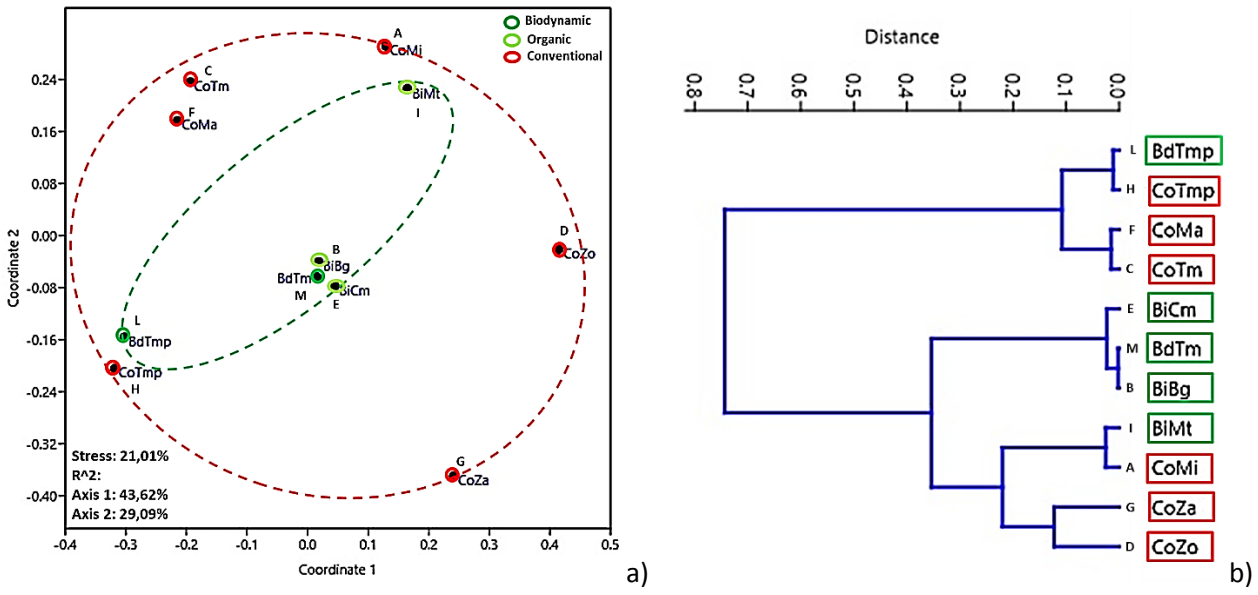


Fig. 61: a) NMDS plot of data concerning carabid communities (annual mean DA_{10} of all species), Bray-Curtis similarity measure. b) Classical cluster analysis of NMDS scores on axis 1 data of carabid communities, Ward's method- Euclidean similarity measure.

Observing the cluster diagram it emerges that it is not possible to separate carabid community samples into two groups according to the agroecosystem management.

Carabid functional traits

In literature routinely studies that have carabids as object, take in consideration not only the species diversity but also some particular functional traits of each species, such as wing development, diet and body dimension (Brandmayr et al., 2005; Gobbi and Fontaneto, 2005, 2008; Gobbi, 2009). Therefore also in this study these functional traits were considered (tab. XL).

Eco- morphologic traits		**Organic-biodynamic** [Mean (S.E.)]	**Conventional** [Mean (S.E.)]	**Statistical test** (Kruskal-Wallis)
	Total DAy	9.72 (3.18)	11.54 (5.68)	n.s.
Wing development	Macropterous species (%)	93.93 (0.53)	96.17 (1.07)	n.s.
	Pteridimorphous species (%)	3.26 (0.76)	3.64 (1.04)	n.s.
	Brachypterous species (%)	2.81 (1.10)	0.18 (0.18)	n.s.
Diet	Zoophagous species (%)	48.19 (10.47)	52.01 (10.08)	n.s.
	Zoospermophagous species (%)	51.81 (10.47)	47.99 (10.08)	n.s.
Body dimension	Big species (%)	24.72 (7.97)	6.82 (4.33)	n.s.
	Medium species (%)	63.29 (7.48)	74.92 (9.00)	n.s.
	Small species (%)	11.98 (3.38)	18.26 (8.96)	n.s.

Tab. XL: Mean values (%) of abundance of species belong to different functional traits. DAy: annual activity density. Significance: n.s.: p value >0.05.

As carabid community analysis, also functional trait analysis in this work did not produce any significant difference between the two types of agriculture. Despite Lupi et al. (2007) found that land use seems to have a significant effect on the number and composition of the species: in fact in that study catches were lower in the conventional farm and higher in biological farms, but in this work such trend was not observed. Another consideration of the cited research (Lupi et al., 2007) and that can be valid also for this work, is that all the species detected have already been recorded as frequent in agricultural fields and are characteristic of lowland agroecosystem in Northern Italy.

It is possible to make other considerations about the presence of some species. In particular Brandmayr et al. (2005) pointed out that in cultivated and in urban environments the accumulation of opportunistic forms of genera *Harpalus* and *Amara* has always been observed; in crop fields for example it is common to find very dense populations of *Pseudoophonus rufipes* and *Harpalus distinguendus*, the first

in some years is so common in the agricultural landscape that results in outbreaks and consequent aggregations of individuals on the clear walls of the farmhouses, there attracted by light sources of public lighting. The same species were found as common also in this study.

Now speaking about functional traits, Gobbi and Fontaneto (2005) found that generally predator, wingless and large species were significantly more frequent in forests than in crops, whereby small, phytophagous and flying species were more common; intermediate values were observed in meadows and in poplar stands. Carabid results in Gobbi and Fontaneto (2005) demonstrated that "functional groups", previously proposed to indicate coenose stability, are a better index of the impact of human activities in the landscape than species similarity: lower number of species, but higher frequency of predator, wingless and large species, found in forests, are connected to stability and, therefore, environmental quality. Communities sampled in agroecosystems are characterised by a high number of species with a wide ecological spectrum and therefore a generalist diet, wholly developed wings and small body size. Species with atrophied wings are able to colonize new areas only by walking; these species, for this reason, are the first to disappear in highly degraded or fragmented environments, since they are not able to move rapidly to new more stable areas. Bigger species have a longer larval stages (in some cases more than one season) and this fact makes them vulnerable to soil perturbation factors, such as ploughing (Gobbi and Fontaneto, 2008; Gobbi, 2009). In this work no differences were observed in wing development, diet and body dimension between organic-biodynamic and conventional fields; this could be due to the fact that both are annual agroecosystems and very different from a more natural environment (like forest or meadow) and these functional traits could be not sufficient to distinguish between agroecosystem managements.

Others generalist and specialist predator overview

Treviso red chicory

In 2012 three visual control samplings were made in each field during vegetative period of *Cichorium intybus*. In tab. XLI results of main generalist and specialist predators are summarised.

Predator taxa	**Usual preys**	**Organic-biodynamic** [Mean/4 plants (S.E.)]	**Conventional** [Mean/4 plants (S.E.)]	**Statistical test** (Two-way ANOVA or Friedman)
Araneae	Generic	6.00 (0.73)	0.53 (0.20)	***
Chrysopidae	Aphids	0.08 (0.04)	/	n.s.
Coccinellidae	Aphids	0.31 (0.02)	/	**
Nabidae	Generic	0.62 (0.07)	/	**
Opiliones	Generic	0.13 (0.07)	0.03 (0.02)	*
Scolopendromorpha	Generic	0.17 (0.05)	0.01 (0.01)	*
Staphylinidae	Generic	1.32 (0.18)	0.04 (0.01)	*
Syrphidae	Aphids	0.17 (0.12)	0.04 (0.04)	n.s.
Total		8.78 (0.72)	0.65 (0.06)	***

Tab. XLI: Mean presence per sampling point of predators on Treviso red chicory in 2012. Significance: ***: p value <0.001; **: p value <0.01; *: p value <0.05; n.s.: p value >0.05 (Fusaro et al., in prep).

The predator community sampled on Treviso red chicory plants was significantly richer in variety and abundance in organic-biodynamic fields with respect to the conventional ones. Also the overall presence of predators was significantly higher in this type of agroecosystem. Also previous reports (Bengtsson et al., 2005) found that both richness and abundance of predator insects were significantly higher in organic fields in comparison with the conventional ones.

In order to visualize relationships of similarity among predator community samples in a 2D space, a multivariate statistical technique of ordination was performed (fig. 62 a) and by using the recalculated coordinates of each sample points on axis 1 of NMDS plot, a cluster analysis was added (fig. 62 b).

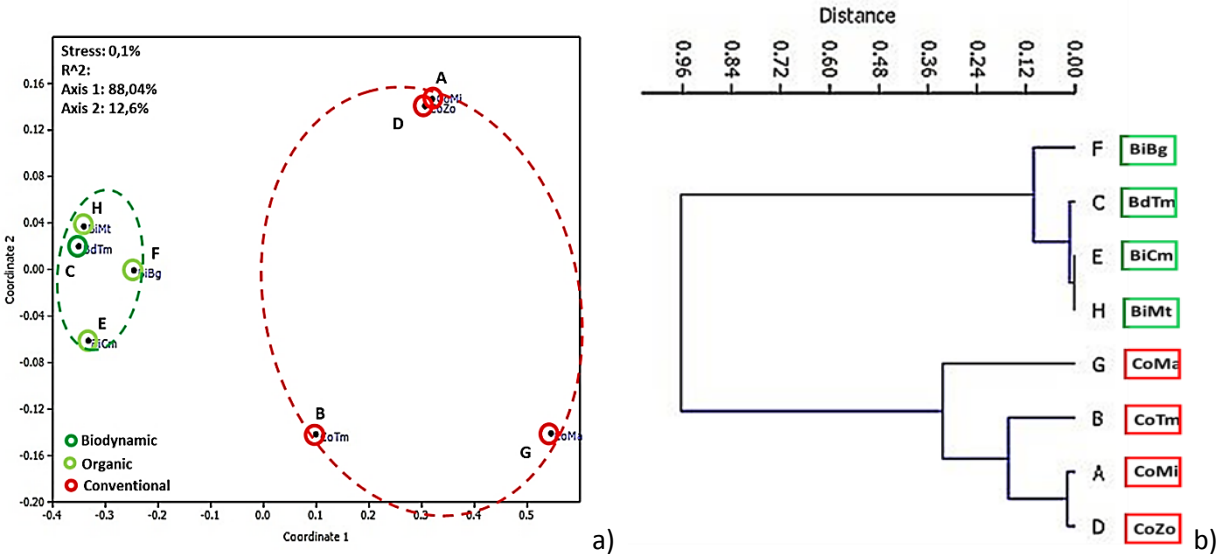


Fig. 62: a) NMDS plot of data concerning predator communities (mean/4 plants) on Treviso red chicory, Bray-Curtis similarity measure. b) Classical cluster analysis of NMDS scores on axis 1 data of predator communities on Treviso red chicory, Ward's method - Euclidean similarity measure.

The cluster diagram in fig. 62 b allows to discriminate the predator community samples into two groups perfectly according to the agroecosystem management (p value = 0.02*, t test).

White cabbage

In 2013 three visual control samplings were made in each field during vegetative period of *Brassica oleracea,* in the same way than for red chicory. In tab. XLII results of main generalist and specialist predators are summarised.

Predator taxa	Usual preys	Organic [Mean/4 plants (S.E.)]	Conventional [Mean/4 plants (S.E.)]	Statistical test (Two-way ANOVA or Friedman)
Araneae	Generic	7.43 (0.79)	0.74 (0.16)	**
Chrysopidae	Aphids	0.46 (0.23)	0.52 (0.44)	n.s.
Coccinellidae	Aphids	0.08 (0.08)	0.06 (0.06)	n.s.
Formicidae	Generic	0.54 (0.18)	/	n.s.
Nabidae	Generic	0.31 (0.05)	0.04 (0.02)	n.s.
Opiliones	Generic	0.17 (0.12)	/	n.s.
Staphylinidae	Generic	0.10 (0.04)	0.03 (0.03)	n.s.
Syrphidae	Aphids	0.29 (0.07)	0.14 (0.07)	n.s.
Total		9.38 (0.90)	1.52 (0.10)	***

Tab. XLII: Mean presence per sampling point of predators on white cabbage in 2013. Significance: ***: p value <0.001; **: p value <0.01; n.s.: p value >0.05 (Fusaro et al., in prep).

On cabbage plants only spiders were significantly more abundant in organic-biodynamic fields, but numerically the overall predator community was significantly more conspicuous in the same type of fields. Spiders were more abundant in organic-biodynamic fields both in 2012 and in 2013 and this confirms the tendency found also by Bengtsson et al. (2005) according to which spiders are significantly more abundant in organic agroecosystems.

Concerning other predators found, a similar study in almost the same area (the northern Italy agroecosystems) found that Coleoptera (Coccinellidae) and Rhynchota (Nabidae) were the most abundant groups sampled in weedy margins (Burgio et al., 2006). In this work, on crop plants (red chicory and cabbage) in the field area, almost the same predator groups described by Burgio and coworkers (2006) were found, but a major difference was in the absolute dominance of spiders, both in organic-biodynamic fields and conventional ones. Menalled et al. (1999) by studying annual crops, found that generalist natural enemies such as spiders and carabid beetles had the potential to maintain a variety of pests below outbreak levels. Other surveys (Sunderland et al., 1987) by studying the diet of several predators in cereal fields found that spiders had the highest predation indexes and this underlines the key role of spiders in pest control.

In order to visualize relationships of similarity among predator community samples in a 2D space, a multivariate statistical technique of ordination was performed (fig. 63 a) and by using the recalculated coordinates of each sample points on axis 1 of NMDS plot, a cluster analysis was carried out (fig. 63 b).

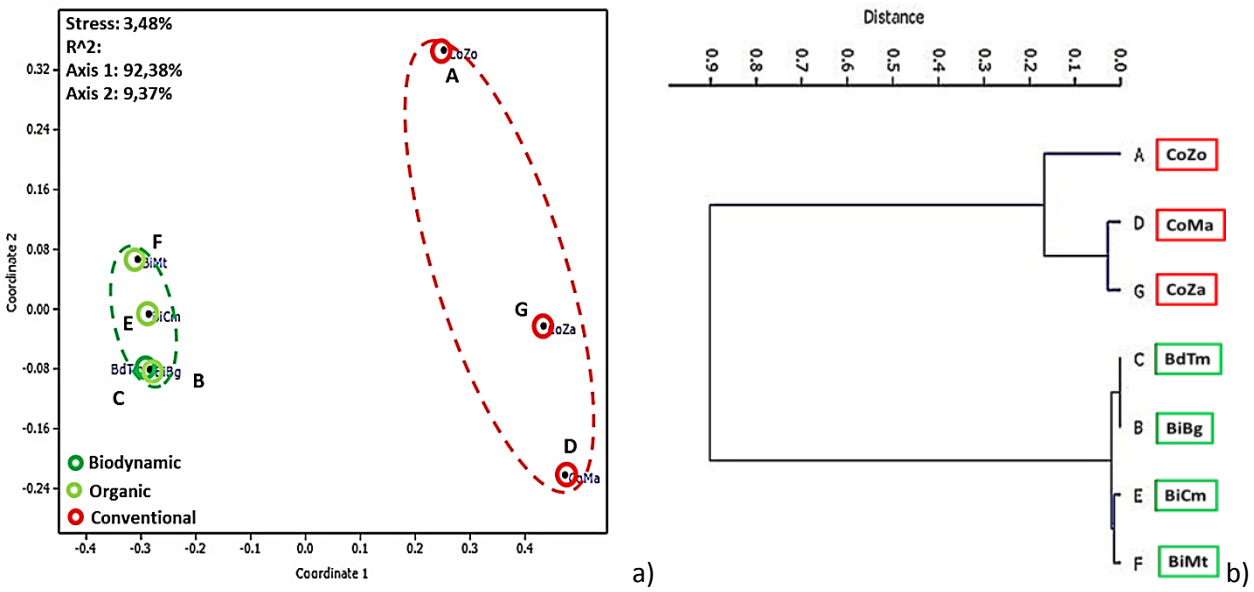


Fig. 63: a) NMDS plot of data concerning predator communities (mean/4 plants) on cabbage, Bray-Curtis similarity measure. b) Classical cluster analysis of NMDS scores on axis 1 data of predator communities on cabbage, Ward's method- Euclidean similarity measure.

As for predators on red chicory, also the predator communities on cabbage were perfectly divided into two groups according to the management type (p value = 0.03*, U test). In general terms some authors (Crowder and Jabbour, 2014) reviewed the topic of pest control and highlighted that more intensive systems decrease the abundance and biodiversity of beneficial species such as natural enemies: the same situation was found in this study.

Parasitoid and hyperparasitoid overview

White cabbage

In 2013-2014 insects, mainly lepidoptera caterpillars collected on cabbage plants during visual control in 2013, were reared in order to detect the presence of parasitoids. The main host species were *Plutella xylostella*, *Pieris* sp, *Mamestra* sp. and *Autographa* sp. (fig. 58), with an absolute predominance of the first one. In detail, 580 *P. xylostella* larvae and pupae were reared, 207 individuals coming from organic fields and 373 coming from conventional ones. The breeding success was 77,5% for organic-biodynamic management and 67,9 % for conventional one. Results on overall insect hatching are presented here (tab. XLIII).

Host	Parasitoids hatched	Organic-biodynamic [Mean(S.E)]	Conventional [Mean(S.E)]	Statistical test (One-way ANOVA or Kruskal-Wallis)
Plutella xylostella	*Cotesia glomerata*	1.00 (0.41)	0.33 (0.33)	n.s.
	Cotesia plutellae	5.50 (2.10)	8.33 (2.73)	n.s.
	Cotesia pieridis	0.25 (0.25)	/	n.s.
	Dolichogenidea	1.25 (0.75)	3.00 (1.15)	n.s.
	Glyptapanteles sp.	0.50 (0.50)	/	n.s.
	Braconidae (unidentified)	0.25 (0.25)	0.33 (0.33)	n.s.
	Diadegma sp.	15.00 (1.73)	22.67 (8.01)	n.s.
	Mesochorinae (Hyp)	1.25 (0.95)	0.33 (0.33)	n.s.
	Ichneumonidae (unidentified)	/	0.67 (0.33)	n.s.
	Trichomalopsis sp. (Hyp)	0.75 (0.75)	1.33 (0.88)	n.s.
	Oomyzus sp. (Hyp)	15.25 (6.68)	6.33 (1.20)	n.s.
	Baryscapus sp. (Hyp)	3.25 (3.25)	/	n.s.
TOTAL		44.3 (1.6)	43.3 (1.9)	n.s.
Pieris sp.	*Cotesia glomerata*	197.00 (50.53)	n.a.	/
	Cotesia cfr pieridis	2.75 (2.75)	n.a.	/
	Trichomalopsis sp. (Hyp)	1.25 (1.25)	n.a.	/
	Tachinidae	0.25 (0.25)	n.a.	/
	Diadegma sp.	4.50 (4.17)	n.a.	/
	Baryscapus sp. (Hyp)	22.75 (11.00)	n.a.	/
	Euritomydae	6.25 (4.73)	n.a.	/
	Braconidae (unidentified)	0.25 (0.25)	n.a.	/
Mamestra sp.	*Trichogramma* sp.	9.25 (9.25)	n.a.	/
Autographa sp.	*Trichomalopsis* sp. (Hyp)	9.50 (9.50)	n.a.	/

Tab. XLIII: Data of mean values of parasitoids (ind/72 cabbage plants (3 samplings)) hatched from collected lepidoptera caterpillars. Hyp: Hyperparasitoids. n.a.: non available data. Significance: n.s.: p value >0.05.

On conventional cabbages almost only individuals of *P. xylostella (*96,3%) were collected and for this reason it was possible to compare only results on parasitoids hatched from this species in organic-biodynamic and conventional fields.

Observing tab. XLIII it is possible to make some considerations. First of all, in conventional fields the absolute predominance of one crop pest (fig. 58) caused the overall impoverishment of the parasitoid community that could be supported only by one type of host resource. On the contrary a wider diversity of crop pests lived in organic-biodynamic fields and this allowed the presence of a richer parasitoid community. Moreover, there were parasitoid species, for example *Cotesia glomerata*, that can exploit more than one host (in this case *P. xylostella* and *Pieris* sp.) and this lack of host specificity allows an insurance for

pest control ES, because if there is no more one host species, the other one remains and as a consequence the parasitoid can develop and continue its useful role. Also in literature there are some evidences of this phenomenon: for example Macfadyen et al. (2011) findings demonstrated the existence of a significant positive relationship between parasitoid species richness and temporal stability in parasitization rate and moreover a greater parasitoid species complementarity in organic farms.

In order to visualize relationships of similarity among parasitoid community samples in a 2D space, a multivariate statistical technique of ordination was performed (fig. 64 a) and by using the recalculated coordinates of each sample points on axis 1 of NMDS plot, a cluster analysis was made (fig. 64 b).

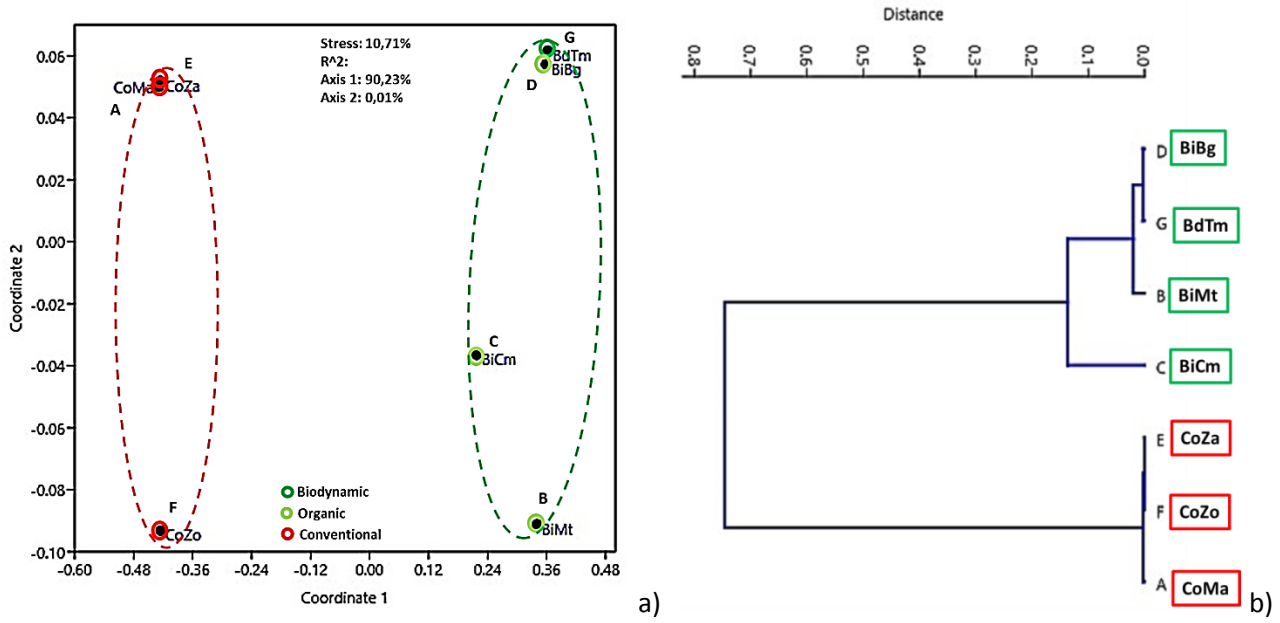
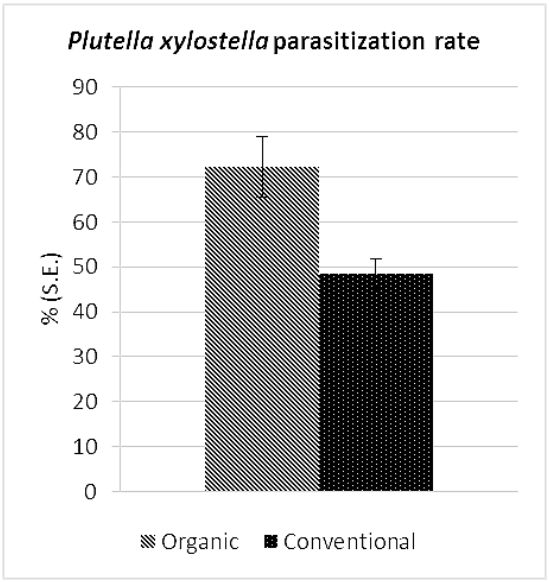


Fig. 64: a) NMDS plot of data concerning parasitoid communities (ind/72 crop plants) on cabbage, Bray-Curtis similarity measure. b) Classical cluster analysis of NMDS scores on axis 1 data of parasitoid communities on cabbage, Ward's method- Euclidean similarity measure.

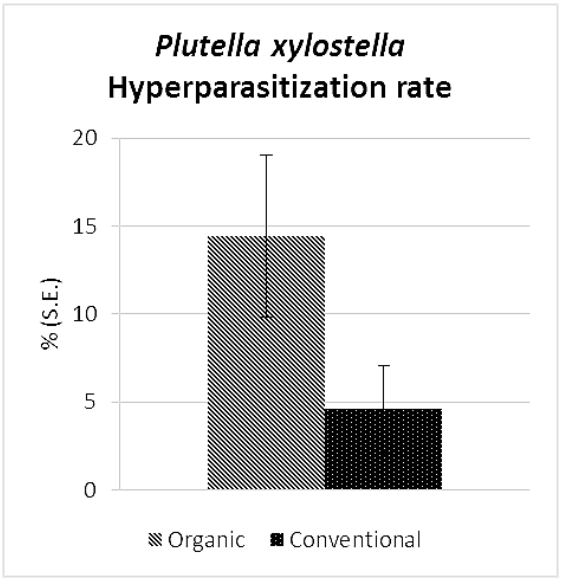
Considering the overall parasitoid communities hatched from the fields object of study, it is evident how they are different based on field management (p value = 0.03*, t test).

Plutella xylostella's parasitization and hyperparasitization rate

This part of analysis was possible only for *P. xylostella*, the main crop pest found on cabbage, due to the scarcity of data concerning the other species. Fig. 65 shows results on parasitization and hyperparasitization rates.



a)



b)

Fig. 65: (a) Percentage of parasitization and (b) hyperparasitization of *P. xylostella* according to different field managements (Fusaro et al., in prep).

Statistical elaborations are summarised in tab. XLIV.

Rate	Organic-biodynamic [Mean (S.E.)]	Conventional [Mean (S.E.)]	Statistical test (χ^2 test)
Parasitization (%)	72.28 (6.72)	48.60 (3.30)	***
Hyperparasitization (%)	14.40 (4.60)	4.58 (2.50)	***

Tab. XLIV: Mean values of *Plutella xylostella's* parasitization and hyperparasitization rates in the two types of agriculture. Significance: ***: p value <0.001 (Fusaro et al., in prep).

Both the rates of parasitization and hyperparasitization were significantly higher in organic-biodynamic fields in respect with the conventional ones, it ensues that *P. xylostella* natural control is better guaranteed in the former management.

In terms of general parasitization rate, Macfadyen et al. (2009) found no differences in percentage of parasitization across a variety of host species, despite crop pests on organic farms were attacked by more parasitoid species in respect with crop pests on conventional farms.

Considering parasitoid community and landscape structure, some studies (Marino and Landis, 1996) found that parasitoid species diversity was similar in simple and complex landscape, but the mean parasitization percentage was significantly higher in complex landscape than in simple landscape. In this study on *P. xylostella* parasitization, the landscape structure resulted not to be significantly different in the two groups of fields analysed (tab. XII) but the parasitization rate was significantly higher in organically-biodynamically managed fields and therefore the leader factor that controls parasitization ES seems to be agroecosystem management and not the landscape structure.

Pest control considerations

Regarding to the control of phytophagous agents in different agricultural management, it was reported that herbivores were attacked by more parasitoid species in organic farms than in conventional farms (Macfadyen et al., 2009). However, differences in network structure did not translate into differences in robustness to simulated species loss and they found no differences in parasitization percentage across a variety of host species. Also the landscape structure is a very important factor for pest control ES. In fact other authors (Gagic et al., 2011) studying the food web of cereal aphids in eighteen agricultural landscapes different in structural complexity, discovered higher primary parasitization and hyperparasitization rates in complex landscapes, but unexpectedly, in the same environments, there was a food web with lower linkage density, interaction diversity and generality. Therefore they underlined that landscape complexity can improve the parasitization rate, but it is not linked to the improvement of food web complexity. Not the same findings emerge from this research: in fact parasitization and hyperparasitization rates were found to be higher in organic-biodynamic fields with respect to the conventional ones, despite being located in the same simple landscape (see tab.XII).

Specific agronomical problems inherent to *Plutella xylostella*

Damage and costs

Cruciferous crops, primarily brassicas, are important components of the human diet and are grown on small subsistence farms as well as large scale farms (Shelton, 2001). Worldwide the brassicaceous production is very consistent (FAO, 2013), for this reason it is important to investigate the problems that reduce it. *P. xylostella* (Diamondback moth, DBM) has the most extensive distribution of all lepidoptera (Talekar and Shelton, 1993). It is a destructive pest of brassicaceous crops, such as cabbage, cauliflower, broccoli, Brussels sprouts and turnip in the world (Talekar and Shelton, 1993; Azidah et al., 2000; Shelton, 2001; Sarfraz et al., 2005; Alizadeh et al., 2011; De Bortoli et al., 2013; Furlong et al., 2013) and it can do up to 13-15 generations per year in tropical environments (Thian Hua, 1965). Now it is present worldwide wherever its host plants exist (Shelton, 2001). With global change and temperature increase it could become a more and more serious problem also in temperate and cold regions, as can be seen in the world map of future perspective for species distribution (Zalucki et al., 2012). In fact for example, DBM is reported to be well established on remote subantartic Marion Island where the mean monthly air temperature ranges from 3.6 to 7.5 °C, largely below the stated threshold for development elsewhere. This suggests a measure of rapid cold adaptation may develop once the moth is exposed to suboptimal temperatures (Coulson et al., 2002).

Zalucki et al (2012) estimated that annual control of DBM in brassicaceous crops costs US$ 1,4 billion worldwide, but this cost can rise up to US$ 2,7 billion if yield losses are included and up to US$ 4-5 billion if DBM losses and control costs to the worldwide canola industry are added. Up to now six

international workshops have been done concerning the DBM management (International Working Group on Diamondback Moth, Plutella xylostella (L.), and Other Crucifer Insects, Cornell University). In Italy few studies regard the presence of DBM like a brassicaceous crops problem (Hamid et al., 2006). This research also intends to contribute to an actualized overview upon the DBM in respect with different agroecosystem managements.

Considering data about phytophagous community composition on cabbage (tab. XXXVII), we can say that in North-Eastern Italy conventional agroecosystems seem to host a simplified crop pests community and, with the absolute dominance of DBM among lepidoptera, while in organic-biodynamic managed fields the phytophagous community is more diverse, in fact in addition to DBM also Pieridae were well represented (fig. 58).

Pesticide resistance

The DBM problem is emphasized if the development of pesticide resistance of this species is considered. Pesticide resistance develops in a population when certain individuals possess genes which allow them to better avoid or survive in contact with pesticides. Treating such a population with a pesticide confers differentially greater survival or fitness on these tolerant individuals, and the frequency of the resistant genotype increases when the tolerant individuals reproduce (Van Driesche and Bellows, 1996). DBM is one of the few insect species that has developed field resistance to all major classes of insecticides (Furlong et al., 2013) and it is ranked second in the Arthropod Pesticide Resistance Database (APRD) for the highest number of insecticides with reported resistance in at least one population (APRD, 2012). Up to now DBM is reported to have developed resistance against 92 different active ingredients (APRD, 2012) and some populations of it in certain areas have developed resistance to all known classes of insecticides (Shelton, 2001). Moreover DBM is the only species that has evolved resistance to *Bacillus thuringiensis* in open field populations (Heckel et al., 2001). In the present study it emerges that also in North-Eastern Italy this trend of pesticide resistance of DBM can be confirmed. In fact, despite the more intensive use of pesticides in the conventional fields (see tab. LVII in the appendix), the DBM seems not to decline and it is the only phytophagous species that can dominate. When pests develop resistance, farmers may respond by increasing pesticide dosage, changing pesticides or combining several ones, but if resistance is severe, as reported for DBM, chemical control may be abandoned and management systems based on biocontrol may be implemented (Van Driesche and Bellows, 1996). Another important feature to consider about pesticide resistance is if also DBM parasitoids can develop it with the same rapidity as DBM does. In this respect Xu et al. (2001) demonstrated that *D. insulare,* one of the most important DBM parasitoids, increases its tolerance to permethrin much more slowly than DBM and appears limited in the extent of resistance that it can develop.

Natural enemies

Primary parasitoids

Natural enemies of DBM, with particular regard to parasitoids, have been reviewed (Sarfraz et al., 2005; Furlong et al., 2013). There are specific studies in many parts of the world: Argentina (Bertolaccini et al., 2011), United States (Xu et al., 2001a; b), Iran (Hasanshahi et al., 2013; Hasanshahi et al., 2014), South Africa (Nofemela, 2004; Kfir, 2005), Senegal and Benin (Arvanitakis, 2013), Africa and Asia (Grzywacz et al., 2010), Malaysia (Ooi, 1985; 1992), Romania (Moldavia) (Mustata, 1992). In Europe it was reported that parasitoids alone may keep DBM populations under control (Mustata, 1992). In Italy there are very few records about DBM parasitoids: the only species of primary larval parasitoid of which there are confirmed distribution records is *Oomyzus sokolowskii* (Furlong et al., 2013). This study increases the knowledge of the distribution of other DBM parasitoid species and genera. This analysis shows how in organic-biodynamic agroecosystems there was a higher DBM parasitization rate with respect to conventional ones (fig. 65 a). Considering also the damage of leaves surface on cabbage, which was smaller in organic-biodynamic fields (even if not significantly), it is possible to conclude that in these fields, DBM outbreaks are better controlled using less pesticides and taking advantage of natural control of crop pests ES.

Hyperparasitoids

This research highlights that also the hyperparasitization rate was higher in organic agroecosystems (fig. 65 b). This can be interpreted as a positive control over the parasitoids population, which otherwise would grow up to deplete DBM population. If this occurs, the following season the parasitoids would no longer have the host on which to develop and they would die, resulting in new good conditions for another crop pest outbreak. This overview can be inserted in the famous Lotka-Volterra model on prey-predator relationship. It is possible to make another consideration about the influence of hyperparasitization: Nofemela (2013) by studying populations of DBM, its primary parasitoids and hyperparasitoids found that the higher efficiency of *Cotesia vestalis* (a dominant primary parasitoid in that system) in utilizing younger host larvae at lower hyperparasitization level limited host availability to other major primary parasitoids, but at increasing of hyperparasitization level with consequent decline of *C. vestalis* population, the populations of two other primary parasitoids significantly increased as they were able to parasitize a greater proportion of available hosts. The author found that the impact of hyperparasitoids did not result in trophic cascades and their impact on total primary parasitization level and infestation level was insignificant.

Generalist predators

Another important control agent for phytophagous insects in general and DBM outbreaks in particular is the predator activity (Furlong et al., 2013; Ditner et al., 2013) and in pest control studies often

is omitted. Predators feed on all host stages: egg, larval (or nymphal), pupal and adult (Van den Bosch et al., 1982), therefore their action spectrum is wider in respect with the one of parasitoids. In this research the presence of generalist predators, such as spiders, rove beetles, harvestmen, ants and damsel bugs was also analysed, which can prey on DBM eggs, larvae and pupae, reducing consistently its population. The results underline how in organic-biodynamic agroecosystems the predator community was richer in groups and more abundant. The causes can be the use of non-selective pesticides in conventional managed fields that kill the overall insect community, both crop pests but also useful control agents (Pimentel, 2005).

Management strategy: conservation biological control

Starting from the point that it is difficult to take under control the outbreaks of some crop pests, such as DBM, using pesticides because of their resistance development, it can be farsighted to choose a more long-lasting measure. Some authors (Eilenberg et al., 2001) tried to make clearance within the argument of biological control, defining it as "*the use of living organisms to suppress the population density or impact of a specific pest organism, making it less abundant or less damaging than it would otherwise be*". Biological control includes four strategies: classical b.c., inoculation b.c., inundation b.c. and conservation b.c.. Among them, the conservation b.c. or natural enemy conservation is the only one strategy in which natural enemies are not released, but it is a combination of limiting and selective use of pesticides, protecting biological control agents and providing resources so that they can be more effective, such as refuges next to crops and alternative food: it involves environmental manipulation to enhance the fecundity and longevity of natural enemies, modify their behaviour and provide shelters from adverse environmental conditions (Debach, 1974; Van Driesche and Bellows, 1996; Pickett and Bugg, 1998; Eilenberg et al., 2001; Zehnder et al., 2007; Burgio et al., 2007). Therefore it is a strategy directly applicable by a farmer. There are many examples of research focused on efficiency of this strategy. Jonsson et al. (2010) reviewed habitat management experiments, published during the period 2000-2010, which aimed to improve biological control of invasive pests and they concluded that habitat manipulation experiments have repeatedly demonstrated positive effects on natural enemy populations and/or on parasitism and predation rates. Others (Zehnder et al., 2007) analysed pest management methods available for organic agriculture, recognizing four progressive phases, starting from cultural practices up to approved insecticides and mating disruption. It is important that sufficient source habitat patches are available for naturally occurring predators and parasitoids, that these are sufficiently close to the areas under production or that corridor features are implemented and that the crops themselves are made attractive to natural enemies. Also Landis and coworkers (2000) underlined that conservation b.c. involves manipulation of the environment to enhance the survival, fecundity, longevity and behaviour of natural enemies to increase their effectiveness. In detail, the aim of habitat management is to create a suitable ecological infrastructure within the agricultural landscape to provide resources such as food for adult natural enemies, alternative prey or hosts, and shelters from adverse conditions (Landis et al., 2000). For example, Ditner et al. (2013) after studying arthropods community in seven white cabbage organic fields in the northern Swiss lowlands, concluded that habitat management practices like flower strips on field margins and intersowing with flowers, which are primarily added to attract and enhance parasitoids for pest control, also benefit

biodiversity conservation in spiders and ground beetles. Other authors (Hemerik, 2007) with a simulation study demonstrated that fed parasitoids have a longevity that is on average four times higher than that of unfed parasitoids, with consequently a higher parasitization percentage. Moreover concerning in particular DBM biological control some studies have been done upon *D. semiclausum,* one of its commonest parasitoids. It has been verified in field condition that *D. semiclausum* populations can be improved when wildflowers bordering the crop fields serve as nectar sources for the parasitoid (Winkler et al., 2006). They concluded that access to carbohydrate-rich food can be indispensable to parasitoid fecundity and stress the importance of providing suitable nectar sources as an essential part of b.c. programs (Winkler et al., 2006). Further researches (Lavandero et al., 2005) demonstrated that the presence of flowering plants next to the crop field improve the parasitization rate of DBM by *D. semiclausum*. Even though it has been verified that some plant species like the buckwheat (*Fagopyron esculentum*) can enhance the parasitoid fitness, the double-edge sword is that it can improve also DBM longevity (Lavandero et al., 2006), so they suggested to obtain a more effective conservation b.c. by the provision of selective floral resources. In detail in order to select the more useful plant species, that selectively fulfil the needs of the beneficials without promoting the pest species, for the enhancement of biological control it is good to consider plant features (annual/perennial; weed potential; floral architecture; pollen/nectar quality; quantity and nectar flow; suitability for plant-feeding arthropods), pests (host range; dispersal rate) and parasitoids (mouthpart morphology and body size, dispersal rate) (Burgio et al., 2007).

Concluding, to better ensure sustainable food production for the growing human population, there is greater need to dedicate resources for implementation of ES-enhancement strategies by improving new mechanisms and policies to maintain and enhance agricultural sustainability without compromising yield (Sandhu et al., 2010). The efficiency of the important ES of natural control of crop pests seems to depend on agroecosystem management: in organic ones the efficiency is higher and also this study confirms it. About the DBM problem, as many studies have underlined up to now, the solution has to include not only a high efficiency of parasitoids activity but also a high activity of predators. Therefore a forward-looking perspective appears to be the preservation of marginal environments, sources of shelters for overwintering and of alternative food for parasitoids and predators, instead of simply to use new chemical pesticides. This can be a more durable and sustainable solution.

Spontaneous plants and weeds

Plant species overview

Eight samplings of plants survey were made, four each year. Ten replicate plots were analysed within the field area and ten in the grassy field margin. Tab. XLV summarises results of the mean number of species sampled in each management and habitat.

	Organic-biodynamic		Conventional		Statistical test (Two-way ANOVA)		
	Field Margin [Mean (S.E.)]	**Crop field** [Mean (S.E.)]	**Field Margin** [Mean (S.E.)]	**Crop field** [Mean (S.E.)]	**Manag.**	**Hab.**	**Interac.**
N° plant species	50.4 (5.1)	24.4 (2.5)	36.5 (3.0)	23.2 (2.8)	*	***	n.s.

Tab. XLV: Mean values of number of species sampled in the crop field and in the field margin in both managements. Significance: *: p value <0.05; ***: p value <0.001; n.s.: p value >0.05.

Noteworthy is the significant difference in species number between crop field (with less species) and grassy margin (with more species), which is probably due to agricultural practices (see tabb. LV and LVI in the appendix), while there is also a significant difference in species number also within grassy margins: organic-biodynamic ones have more species than conventional ones (tab. XLV). These results confirm the ones obtained by Bengtsson et al. (2005) regarding a higher plant species richness in organic agroecosystems. Other studies (Crowder and Jabbour, 2014) found that weed communities were consistently more abundant and richer in less-intensive agricultural systems, but different studies (Roschewitz et al., 2005) demonstrated that local weed species diversity was influenced by both landscape complexity and farming system. In fact species diversity under organic farming system was clearly higher in simple landscape and conventional vegetation reached similar diversity levels when the surrounding landscape was complex. Considering that in this research all fields are inserted in a simple landscape structure (tab.XII), the present work confirms the evidences in literature for weed community in the grassy margins but does not confirm them for weed community in the crop field area. This is probably due to the lack of chemical weed control in two of the five conventional fields object of study.

The following chart shows the distribution of weed species number (mean).

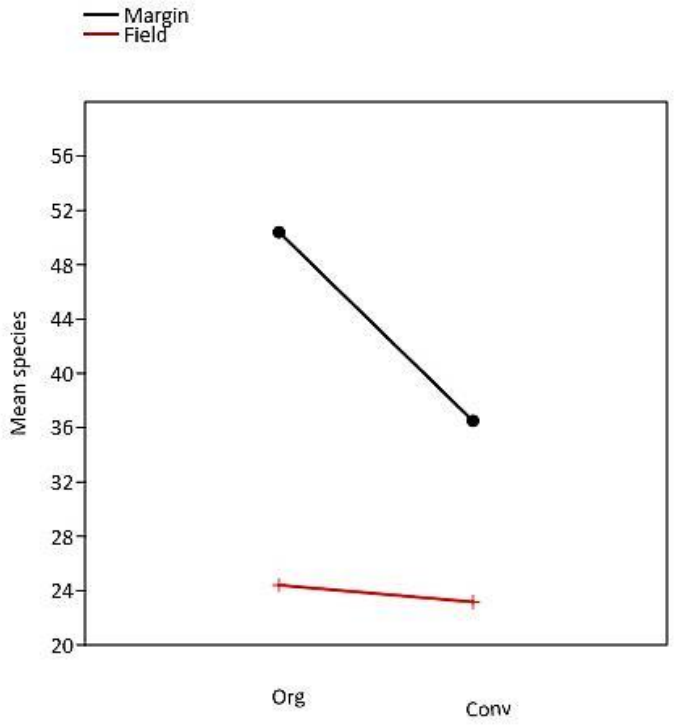


Fig. 66: Plot of the mean number of species according to the management and the habitat.

It is evident how the major difference in species number among the two types of agriculture is more marked in the grassy margin.

Slightly different results were found in other works (José-Maria and Sans, 2011) which pointed out that weed diversity was similar in organic and conventional fields when landscapes were complex, but weed diversity was higher in organic fields in simple landscapes. Moreover, effects of landscape complexity on weed seedbanks in Mediterranean dryland systems were limited and only detected in field edges, and not in field centres. Those authors concluded that the promotion of low-intensity (organic) farming practices regardless of landscape complexity, especially at field edges, would be an effective measure for conservation purposes in Mediterranean agroecosystems. This last trend can be considered true also for the present findings.

Considering the life cycle of the sampled plants it is possible to draw other considerations (tab. XLVI).

	Organic-biodynamic		**Conventional**		**Statistical test** (Two-way ANOVA)		
	Field Margin [Mean (S.E.)]	**Crop field** [Mean (S.E.)]	**Field Margin** [Mean (S.E.)]	**Crop field** [Mean (S.E.)]	**Manag.**	**Hab.**	**Interac.**
Annual (cop/10m^2)	219.2 (44.3)	255.9 (37.9)	354.5 (88.5)	311.1 (168.3)	n.s.	n.s.	n.s.
Biennial (cop/10m^2)	10.7 (1.3)	72.6 (27.6)	4.4 (2.9)	136.2 (113.8)	n.s.	***	n.s.
Perennial (cop/10m^2)	1421.6 (133.1)	48.8 (16.7)	1082.8 (182.0)	47.7 (15.4)	n.s.	***	n.s.

Tab. XLVI: Mean values of abundance in 10 m^2 of plant species with different life cycle. Significance: ***: p value <0.001; n.s.: p value >0.05.

From tab. XLVI it emerges that plant species with perennial life cycle characterize significantly the field margin habitat. This is easily explained due to continuous mechanical practices affecting the cultivated area, which prevent life to those species with longer life cycle. In fact within crop field area plant species with annual life cycle predominate, the only ones that can survive. Also Gago et al. (2007) stressed that tillage destroys in general the annuals established at the moment of the application, but it also creates the favourable conditions for new germinations. This last point is the basic principle of the stale seedbed technique, which is the main weed control technique adopted by organic-biodynamic farmers (see tab. LVI in the appendix).

In order to visualize relationships of similarity among plant community samples in the field margin in a 2D space, a multivariate statistical technique of ordination was performed (fig. 67 a) and by using the recalculated coordinates of each sample points on axis 1 of NMDS plot, a cluster analysis was added to it (fig. 67 b).

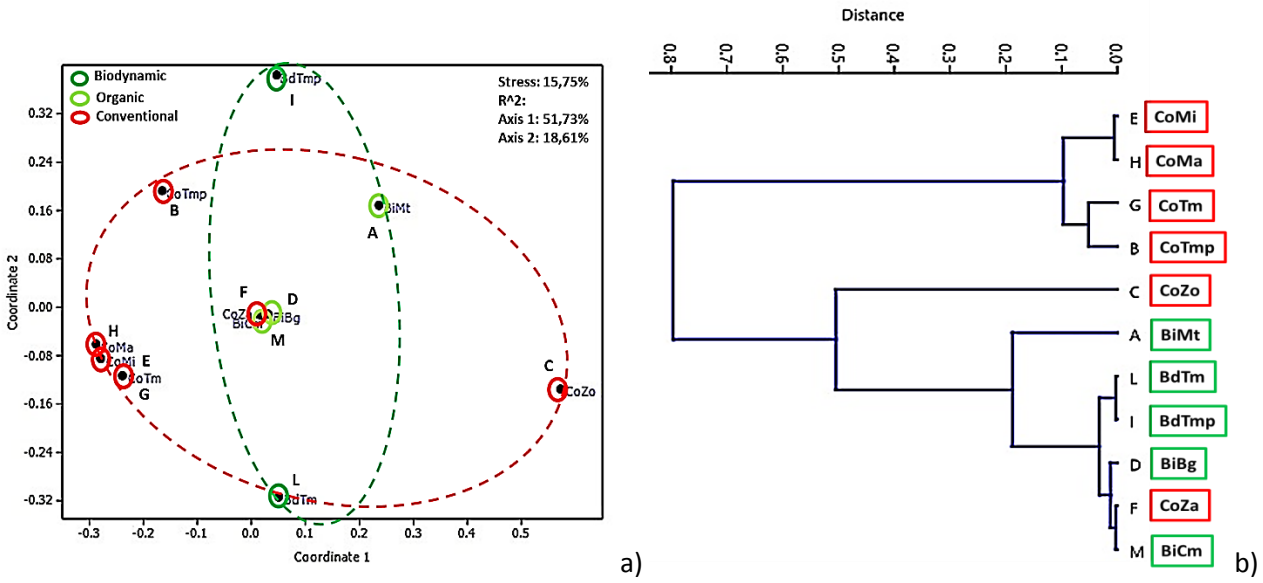


Fig. 67: a) NMDS plot of data concerning plant communities (mean abundance in 10 m^2) in the field margin, Bray-Curtis similarity measure. b) Classical cluster analysis of NMDS scores on axis 1 data of plant communities in the field margin, Ward's method-Euclidean similarity measure.

The cluster diagram underlines how there is not a clear division into two groups according to the management, for the plant communities in the field margin.

In order to visualize relationships of similarity among plant community samples in the crop field in a 2D space, a multivariate statistical technique of ordination was performed (fig. 68 a) and by using the recalculated coordinates of each sample points on axis 1 of NMDS plot, the usual cluster analysis was added to it (fig. 68 b).

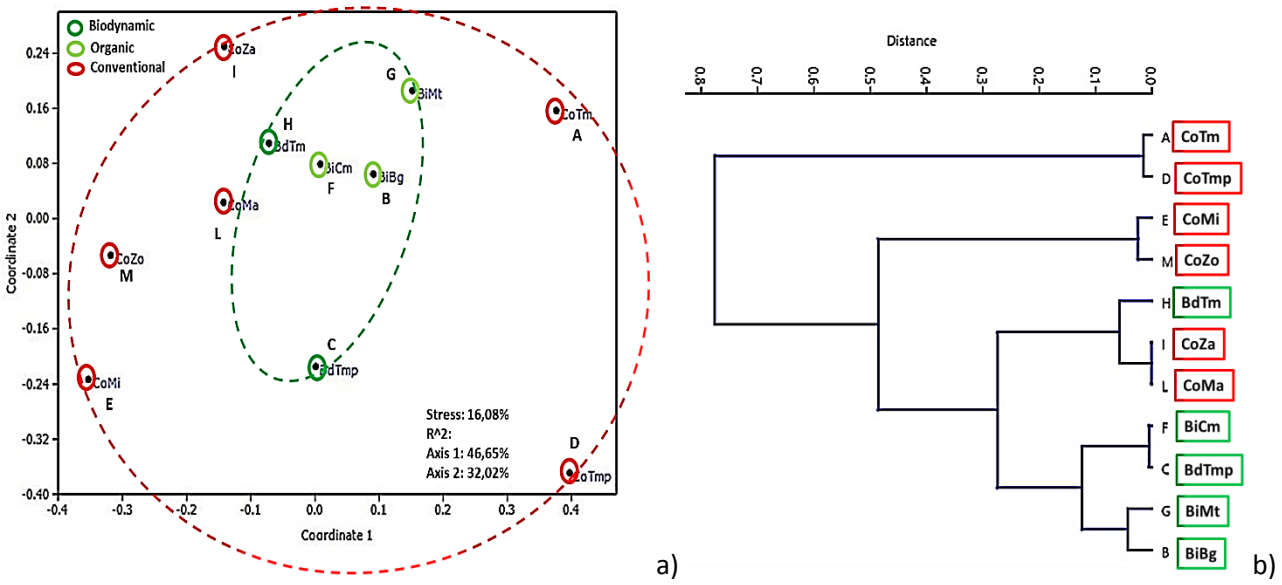


Fig. 68: a) NMDS plot of data concerning plant communities (mean abundance in 10 m^2) in the crop field, Bray-Curtis similarity measure. b) Classical cluster analysis of NMDS scores on axis 1 data of plant communities in the crop field, Ward's method-Euclidean similarity measure.

The same situation of lack of discrimination power between the two types of agriculture of the plant communities living in the crop field area emerges from the cluster diagram in fig. 68 b.

Observing the arrangement of sample points in the NMDS plot (fig. 68 a) it is clear how there are two conventional points (CoTm A and CoTmp D) very far from the others of the same type (marked in red). Probably this difference can be attributed to the fact that they are the only two conventional fields with lack of chemical weed control strategy (see tab. LV in the appendix). This is an important observation that underlines the significance of management practices.

Plant indication features: Ducerf's method

A total of 116 wild plant species was determined, on 86 of which it was possible to attribute a bioindicator value (74,1% of the total) according to the method of the French botanist Gerard Ducerf (Ducerf, 2007). Tab. XLVII shows the overall results on the incidence values of each of three categories.

Wild plant indicators		**Organic-biodynamic** [incidence value (%)]	**Conventional** [incidence value (%)]
Field margin	EQU	652.4 (18.4)	80.8 (2.6)
	REV	1173.8 (33.0)	590 (18.7)
	IRR	1729.3 (48.6)	2490.8 (78.8)
Total		3555.5 (100)	3161.6 (100)
Crop field	EQU	166.8 (22.8)	302.7 (33.6)
	REV	252.3 (34.5)	393.9 (43.7)
	IRR	313.3 (42.8)	204.5 (22.7)
Total		732.3 (100)	901.1 (100)

Tab. XLVII: Incidence values and percentages of the three plant indication categories for the two agroecosystems (organic-biodynamic/conventional) and the two habitats (grassy margin/crop field) considered.

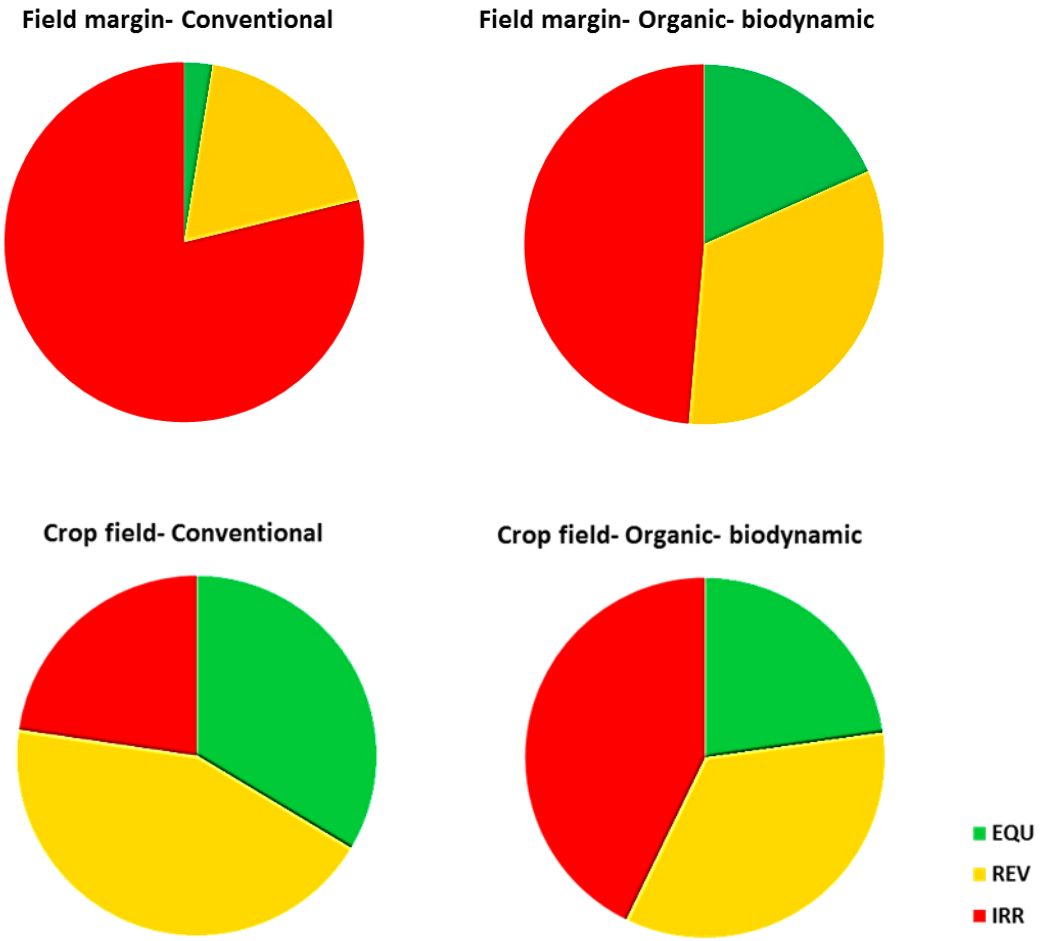


Fig. 69: Pie charts of the percentage of incidence value of the three categories of plant indicators according to Ducerf (2007).

Observing the percentages of the three different plant indicator categories it can be appreciated how overall in organic-biodynamic managed agroecosystem they maintain the same proportions between different habitats (EQU: 18.4 → 22.8; REV: 33.0 → 34.5; IRR: 48.6 → 42.8). On the contrary in conventionally managed agroecosystem comparing different habitats, the percentages of indicator categories change substantially (EQU: 2.6 → 33.6; REV: 18.7 → 43.7; IRR: 78.8 → 22.7). While the field margin can photograph the real situation of this environment, the cropfield, being the crop production site, is more heavily subjected to farmer's practices, as weed control because weeds are competitors with the crop for the resources. Weed control is practiced by using chemical herbicides in the conventional management and with mechanical stale seedbed in the organic-biodynamic one (tabb. LV and LVI in the appendix). The first method is addressed in particular to weeds belonging to the IRR category, while the second method is not so selective. In fact, Gago et al. (2007) underlined that annual weeds can be controlled with properly timed pre-emergent herbicides and in case the plants are already very developed, it is possible to use a contact herbicide. Based on these considerations, it is possible to interpret the strong reduction in conventional management of IRR weeds between the field margin (78.8%) and the cropfield

(22.7%) as due to herbicides use, instead the relative proportions of the three indicator categories maintain similar in organic-biodynamic management due to the less invasive and selective weed control practices.

In this respect, Hawes et al. (2010) pointed out that frequent herbicide use in intensive agroecosystems likely drives reduced weed diversity and abundance. In addition, Hawes et al. (2010) showed that fertilizer use and crop rotations explained as much variation in weed abundance/diversity as farm type across 109 conventional, integrated and organic farms.

In the table below plant species found just in one type of habitat for each management (fidelity value) are listed.

Species	Indicator	Conventional		Organic-biodynamic	
		Grassy margin (fidelity)	**Field** (fidelity)	**Grassy margin** (fidelity)	**Field** (fidelity)
Abutilon theophrasti Medicus	IRR	0.2	1		
Ajuga reptans L.	REV			0.6	
Alopecurus pratensis L.	REV				0.4
Arenaria serpyllifolia L.	IRR	0.2	0.2		
Aristolochia pallida Willd.				0.2	
Avena sativa L.					0.2
Bidens tripartita L.	IRR	0.2	0.2		
Bothriochloa ischaemum (L.)				0.2	
Brachypodium sylvaticum (Hudson) Beauv		0.2			
Bromus hordeaceus L.	REV	0.4			
Cardamine hirsuta L.	REV			0.6	
Carex flacca Schreber				0.2	
Carex spicata Huds.				0.2	
Carex vesicaria L.		0.2			
Centaurium pulchellum (Swartz) Druce				0.2	
Cichorium intybus L.	REV			0.2	
Clinopodium vulgare L.				0.4	
Convolvulus arvensis L.	IRR				0.4
Dactylis glomerata L.	IRR		0.4		
Datura stramonium L.	IRR	0.2	0.4		
Eleusine indica (L.)					0.2
Equisetum arvense L.	REV		0.2		
Erigeron annuus (L.) Pers.	IRR		0.2		
Erodium cicutarium (L.) L'her.	REV			0.2	
Festuca nigriscens Lam.				0.2	
Galinsoga parviflora Cav.				0.2	
Geranium molle L.	REV		0.2		
Geranium rotundifolium L.	IRR	0.2			0.2
Hedera helix L.	IRR			0.2	
Hibiscus trionum L.			0.6		
Hyeracium pilosella L.	IRR			0.2	
Juncus compressus Jacq.				0.2	
Lamium purpureum L.	REV		0.2	0.4	
Leontodon hispidus L.				0.2	
Lysimachia nummularia L.				0.4	
Medicago lupulina L.	REV			0.2	
Medicago sativa L.	REV			0.2	

Mercurialis perennis L.	EQU		0.2		
Oxalis corniculata L.	REV			0.8	
Panicum miliaceum L.					0.2
Papaver rhoeas L.	REV			0.4	
Parietaria officinalis L.	REV		0.2		
Picris hieracioides L.	IRR		0.2		
Ranunculus acris L.	REV		0.2		
Ranunculus repens L.	IRR			0.6	
Rubus caesius L.	IRR	0.2			
Setaria viridis (L.) P. Beauv.	IRR				0.2
Sonchus oleraceus L.	REV			0.2	
Taraxacum officinale Weber (complex)	REV				0.2
Torilis arvensis (Huds.) Link.	REV			0.2	
Torilis nodosa (L.) Gaertner				0.2	
Valerianella locusta (L.) Laterrade	REV	0.2			
Verbascum blattaria L.				0.2	
Veronica chamaedrys L.	REV			0.2	
Veronica peregrina L.				0.2	
Vicia sativa L.	REV			0.4	0.2
Typical species of management		**10**	**14**	**30**	**9**
	EQU		**1**		
	REV	**2**	**5**	**13**	**3**
	IRR	**6**	**7**	**3**	**3**

Tab. XLVIII: List of plant species with a fidelity to one habitat or one management.

The major part of species with fidelity to one habitat/management belonged to reversible (REV) and irreversible (IRR) indicator categories. In the organic-biodynamic grassy margin there were more than twice typical species (30) than in the conventional margin (10) and in the organic crop field (9), while the number of typical species in the two conventional habitats was comparable (10 and 14). Moreover observing the grassy margin in organic-biodynamic management there were more REV species than IRR ones and on the contrary in conventional management the number of IRR species was higher. This situation can be due to a more stable, or at least not irreversible, pedological condition in organic-biodynamic agroecosystems.

Entomophily Index: plant species functionality

From the point of view of insect-pollinated species presence and consequently of pollinator attraction in the agroecosystem, the situation was different in the two sampled environments (tab. XLIX).

	Organic		**Conventional**		**Statistical test** (Two-way ANOVA)		
	Field Margin [Mean (S.E.)]	**Crop field** [Mean (S.E.)]	**Field Margin** [Mean (S.E.)]	**Crop field** [Mean (S.E.)]	**Manag.**	**Hab.**	**Interac.**
E.I.	58.8 (8.3)	14.6 (2.3)	21.6 (6.8)	33.5 (11.8)	n.s.	*	**

Tab. XLIX: Mean values of Entomophily Index (E.I.) calculated on abundance values of entomophilous plant species in the two types of management and habitat. Significance: *: p value <0.05; **: p value <0.01; n.s.: p value >0.05.

From the tab. XLIX it emerges that in the field margin the E.I. was higher than in the crop field and a significant difference was detected between organic and conventional field margins.
This means that in these environments there are more abundance of plant species with resources of pollen and nectar beneficial for pollinators and useful fauna. In this way this useful part of agrobiodiversity is stimulated to visit the field area and there is a higher probability that these insects can pollinate also crop plants.

Pollination, especially crop pollination, is perhaps the best known ES performed by insects. McGregor (1976) estimated that from 15% to 30% of the US diet is a result, either directly or indirectly, of animal-mediated pollination. These products include many fruits, nuts, vegetables and oils, as well as meat and dairy products produced by animals raised on insect-pollinated forage. Conservative estimates suggest that the economic value of pollination provided by wild insect is about $3.07 billion per year in the United States. Therefore attracting and maintaining pollinators in the crop field area is a must to improve crop production, as E.I. indicates. At the smallest scale, for example within field area, some studies (Batary et al., 2013) found higher species richness of forbs of both pollination types (insect and non-insect pollinated) in the edges than in the interior of fields. The authors argued that this is most probably due to the less efficient spraying of pesticides and fertilizers, the higher light availability close to the borders or mass-effects of higher propagule pressure from adjacent habitats. Their results in both agroecosystem types they analysed (meadows and wheat fields) indicated that the organic farming system supports high species richness and cover of entomophilous plants, which is likely to be favourable for the density and diversity of bees and other pollinators (Potts et al., 2009). Therefore organic management contributes not only to biodiversity conservation but also increases resources for functionally important groups such as pollinators (Batary et al., 2013).

Bianchi et al. (2006) reviewed papers concerning pest control in relationships with landscape structure and found that natural enemy populations were higher and pest pressure was lower in complex landscapes versus simple landscapes and highlighted the importance of non-crop habitats for the conservation of a wide range of biota in agricultural landscapes. It is possible to find some evidences of these findings also in this work, because even though there were no differences in landscape structure among the fields considered (all of them are inserted in the same simple landscape dominated by arable land use – tab. XII), upon studying weed community composition, the number of species (tab. XLV) and also the E.I. (tab. XLIX) were significantly higher in organic-biodynamic grassy margins and this can be linked to the improved pest biological control found in the same typology of fields with an higher presence of both predators (tabb. XLI and XLII) and parasitoids (tab. XLIII) and a higher parasitization rate (tab. XLIV). In fact in these marginal environments natural enemies can find alternative food sources and shelters for overwintering when the annual crop has been harvested. These apparently not important environments can be considered as part of a very little scale landscape and their existence can make the difference about natural pest control, as underlined also by other investigations (Bianchi et al., 2006). In fact according to those authors multiple non-crop habitat types may favour natural pest control as grassland, herbaceous and wooded habitats all were associated with enhanced natural enemy populations.

Final considerations on taxa composition of bioindicators and agroecosystem management (1)

To resume all results obtained up to this point in order to answer the first question of the objectives, see tab. L. "Taxa richness" refers to the numerical amount of taxa found in this research for a given bioindicator, while "community composition" refers to the output of ordination and classification analyses made with data of taxa and relative abundance of each bioindicator group.

Functional agrobiodiversity indicator	Taxa richness	Community composition
Soil bacteria	YES	NO
Soil fungi	NO	YES
Mesofauna	NO	YES
Earthworms	YES	NO
Phytophagous agents	Partially	NO
Predators	YES	YES
Carabids	YES	NO
Parasitoids	YES	YES
Weeds (field area)	NO	NO
Weeds (grassy margin)	YES	NO

Tab. L: Summary results on the answer to the question n.1 of the objectives, whether agroecosystem management can change taxa composition of a given bioindicator.

Some spontaneous considerations are that it is not enough to consider only taxa richness in the studies concerning bioindicators, because going into depth with the analysis (and therefore considering also community composition) it is possible to find further results and have a more complete picture; then, coming to the answer to question n.1, according to the present findings, not all bioindicators used were affected by agroecosystem management: there were some more sensitive, such as predators and parasitoids (among the higher trophic levels) and some less sensitive, such as crop pests and weeds.

Crop characterization

Treviso red chicory

There were some difficulties about data collection concerning Treviso red chicory crop nutritional properties especially due to the climate conditions (too dry, see fig. 28) that prevented to sow the crop within the correct period, in particular in the Treviso area. Another problem was the availability of data of two different varieties (early and late) but not for each management. For these two reasons it was not

possible to elaborate statistically Treviso red chicory data, but the detailed data are in the appendix (tabb. LX and LXI).

Crop production and physical properties

To have an idea of the results on production and physical properties see tab. LI. These data cannot be considered comparable for above mentioned reasons and so they have not been elaborated statistically.

Physical properties	Organic-biodynamic		Conventional	
	Early [Mean (S.E.)]	**Late** [Mean (S.E.)]	**Early** [Mean (S.E.)]	**Late** [Mean (SE)]
Weight (g)	307.2 (37.2)	216.5 (27.6)	122.0 (20.6)	220.3 (9.6)
Colour (L)	30.5 (0.4)	34.1 (0.7)	30.8 (0.4)	34.2 (0.8)
Colour (a)	17.5 (2.7)	19.1 (2.5)	7.6 (1.0)	20.3 (1.4)
Colour (b)	2.7 (0.3)	4.3 (0.7)	1.3 (0.3)	3.7 (0.5)

Tab. LI: Mean values of production and physical properties of the two varieties of Treviso red chicory analysed according to the management.

It is evident how conventional early variety is not comparable with the same variety in organic management. This is due almost surely to the slightly different vegetative period: in fact this red chicory was planted with one month of delay with respect to the others.

White cabbage

Detailed data are consultable in tabb. LXII and LXIII in the appendix.

Crop production and physical properties

The same physical properties were object of analysis also for white cabbage. Tab. LII summarises the results.

Physical properties	**Organic-biodynamic** [Mean (S.E)]	**Conventional** [Mean (S.E.)]	**Statistical test** (One-way ANOVA or Kruskal-Wallis)
Inflorescence weight (g)	935.2 (114.9)	1246.3 (81.3)	*
Colour (L)	82.4 (0.3)	81.3 (0.6)	n.s.
Colour (a)	-6.4 (0.2)	-5.7 (0.1)	**
Colour (b)	19.0 (0.6)	18.9 (0.3)	n.s.

Tab. LII: Mean values of production and physical properties of white cabbage according to the management. Significance: **: p value <0.01; *: p value <0.05; n.s.: p value >0.05.

The most important consideration concerns crop production: conventional cabbages weighed significantly more than organic-biodynamic ones. The higher production in conventional agroecosystems in comparison to organic ones is confirmed also in literature (Seufert et al., 2012; Ponisio et al., 2014).

Nutritional properties

Also chemical nutritional properties were analysed in cabbages. Tab. LIII shows the results.

Nutritional properties	**Organic-biodynamic** [Mean (S.E)]	**Conventional** [Mean (S.E.)]	**Statistical test** (One-way ANOVA or Kruskal-Wallis)
d.m. (%)	7.1 (0.2)	7.2 (0.1)	n.s.
FRAP (mg $Fe^{++}E$/kg)	29972.5 (1584.3)	25979.1 (2431.7)	n.s.
Folin (mg GAE/kg)	2393.5 (99.2)	2351.2 (100.2)	n.s.
Ascorbic acid (mg/kg)	7266.3 (744.4)	7488.3 (336.8)	n.s.
N (%)	3.0 (0.04)	3.8 (0.1)	***
Cl^- (mg/kg)	2321.3 (209.8)	2173.0 (105.2)	n.s.
NO_2^- (mg/kg)	41.0 (6.5)	104.9 (26.5)	*
NO_3^- (mg/kg)	326.7 (24.6)	493.9 (127.5)	n.s.
PO_4^{---} (mg/kg)	6928.1 (164.4)	8103.1 (358.6)	**
SO_4^{--} (mg/kg)	5971.5 (207.5)	5346.3 (150.2)	*
Na^+ (mg/kg)	1066.6 (43.2)	1509.1 (77.6)	***
NH_4^+ (mg/kg)	25.0 (1.0)	39.9 (5.3)	**
K^+(mg/kg)	33203.0 (291.4)	34864.7 (1799.3)	n.s.
Mg^{++}(mg/kg)	1237.8 (40.2)	1256.1 (45.7)	n.s.
Ca^{++}(mg/kg)	5028.5 (117.1)	4619.7 (77.1)	*
Chlorogenic acid (mg/kg)	36.0 (2.3)	/	/
Caffeic acid (mg/kg)	20.5 (2.2)	16.4 (1.0)	n.s.
Coumaric acid (mg/kg)	16.0 (0.7)	2.6 (0.4)	***
Ferulic acid (mg/kg)	4.8 (2.1)	2.1 (0.2)	n.s.
Sinapic acid (mg/kg)	18.8 (4.3)	12.9 (0.8)	n.s.
Sulforaphane (mg/kg)	11.2 (2.3)	17.4 (3.5)	n.s.
Glucose (mg/kg)	4907.0 (356.8)	3703.1 (550.1)	n.s.
Fructose (mg/kg)	6925.0 (404.6)	5334.6 (272.7)	**

Tab. LIII: Mean values of nutritional properties of cabbage growing up in conventional and organic fields. Significance: ***: p value <0.001; **: p value <0.01; *: p value <0.05; n.s.: p value >0.05. N.B. Coumaric acid was detected just in cabbages coming from two conventional fields and one organic field, while Chlorogenic acid was detected just in cabbages coming from one organic field.

Quantitative crop elemental analysis

Exploratory investigation with ICP elemental analyzer on the presence of other macro- and micronutrients in crop tissues was performed on cabbage (inflorescence) (tab. LIV).

Elements (mg/kg d.w.)	**Organic-biodynamic** [Mean (SE)]	**Conventional** [Mean (SE)]	**Statistical test** (One-way ANOVA or Kruskal-Wallis)
Al	415.04 (76.04)	502.02 (144.07)	n.s.
B	1632.35 (40.98)	1667.03 (59.60)	n.s.
Ca	377404.9 (17052.8)	305319.73 (9239.04)	**
Cd	11.47 (0.82)	12.33 (0.97)	n.s.
Cl	112357.4 (12838.02)	106109.48 (12199.87)	n.s.
Cr	24.37 (1.32)	34.54 (6.59)	n.s.
Cu	238.74 (6.42)	292.88 (12.96)	***
Fe	3727.01 (90.49)	4576.43 (201.96)	***
Hg	/	/	/
K	2059956.27 (38417.28)	2196458.61 (144961.96)	n.s.
Mg	157006.35 (3608.95)	163763.64 (6784.23)	n.s.
Mn	1805.76 (39.08)	1844.21 (62.65)	n.s.
Mo	136.57 (9.07)	87.72 (5.76)	***
Na	71225.2 (4370.75)	111315.45 (4889.27)	***
Ni	27.65 (1.70)	40.96 (6.32)	*
P	494253.99 (29173.68)	643498.92 (43880.48)	**
Pb	/	/	/
S	599831.23 (20304.21)	620943.36 (28156.33)	n.s.
Sn	/	/	/
Zn	2569.57 (56.76)	3329.96 (128.93)	***

Tab. LIV: Mean values of chemical element abundance (mg/kg d.w.) in organic-biodynamic and conventional cabbages. Significance: ***: p value <0.001; **: p value <0.01; *: p value <0.05; n.s.: p value >0.05. The elements marked in bold and underlined are regulated by law [19].

It is possible to make some considerations about results of cabbage nutritional properties.

The Total Antioxidant Capacity (TAC measured by FRAP) tended to be greater in organic-biodynamic cabbages, although not significantly. This is linked also to the presence of free phenolic acids (chlorogenic, caffeic, coumaric, ferulic, sinapic), which in fact resulted higher in organic-biodynamic cabbages, but only coumaric acid significantly and moreover chlorogenic acid was detected solely in organic cabbages. Phytochemicals, and in particular, phenolic compounds, present in plant foods may be partly responsible for health benefits in humans eating fruits and vegetables (reducing risks for several chronic diseases) (Young et al., 2005). These authors did not find significant differences in phenolic agent contents in vegetables grown up in conventional or organic conditions, but just higher values of Folin in one vegetable probably due to pest attacks. Therefore they concluded that although the organic method alone did not seem to enhance biosynthesis of phytochemicals in vegetables, the organic farming system could provide

[19] Reg. (CE) N. 1881/2006 of 19th December 2006 that define maximum levels of some contaminants in food products (http://www.iss.it/binary/ogmm/cont/Reg1881_06.pdf) and Reg. (UE) N. 488/2014 of 12th May 2014 that modify Reg.(CE) n. 1881/2006 as regard Cd maximum levels in food products (http://eur-lex.europa.eu/legal-content/IT/TXT/PDF/?uri=CELEX:32014R0488&from=IT)

an increased opportunity for insect attack, resulting in a higher level of total phenolic agents. The situation seems similar to that found for this work, especially due to a more intensive use of pesticides in conventional fields (tab. LVII in the appendix). While Sousa et al. (2005) found that tronchuda cabbages from organic farming system presented higher phenolic contents than those from the conventional one. In the present work fructose content was significantly higher in organic-biodynamic cabbages and it also has antioxidant power, making these findings partly in line with evidences in literature.

Na^+ and NH_4^+ contents were significantly higher in conventional cabbages, but this feature is probably linked to soil salinity of the localities, even though an author (Schuphan, 1974) found a link between the use of only mineral fertilization [N:P:K] and the increase in Na^+ in cabbage; moreover as regards mineral fertilization, anhydrous ammonia is often applied as source of N: the ammonia reacts with soil moisture to form ammonium ion, which is held on the mineral and organic exchange complex (Pesek et al., 1989).

N, NO_2^- and PO_4^{---} contents were significantly higher in conventional cabbages (also NO_3^- but not significantly) and these crop features are strictly linked to mineral fertilization [N:P:K] adopted in this type of farming system. NO_3^-, the main form of nitrogen supplied to crops from soil (Magkos et al., 2006) are the major precursor of NO_2^- in the human body (Amr and Hadidi, 2001). Even if NO_2^- are instable, because they tend to link to amines to form nitrosamines, it must be remembered that nitrosamines are carcinogenic and implicated in the genesis of methemoglobinemia (Bruning-Fann and Kaneene, 1993; WHO, 1995). Worthington (2001) reviewing studies concerned with several crop nutritional properties, found that nitrates were significantly lower (-15%) in organic with respect to conventional farming system and this seems to confirm the general trend of also these findings, even though it is possible to appreciate that the variability in nitrate content is much higher in conventional cabbages with respect to organic ones and this probably reflects the different fertilization strategies adopted by conventional farmers. Besides different analyses (Magkos et al., 2006) depicted a complex picture concerning crop nitrate content and underlined how, except for nitrophilic vegetables, there could be many factors, irrelevant to the farming system, and that might affect it, such as soil type, planting and harvesting dates, nitrate in irrigation water, location.

P, Fe, Cu, Zn contents were greater in conventional cabbages. On the contrary to these findings, Worthington (2001) found that Fe, P, Cu, Zn contents were respectively 20%, 10%, 10%, 8% higher in organic cabbages.

Ca^{++} and Mo contents resulted higher in organic-biodynamic cabbages and the same trend was found by Worthington (2001), who in particular pointed out an increase in calcium content of 28% and an increase in molybdenum content of 60% in organic crop in comparison to conventional ones.

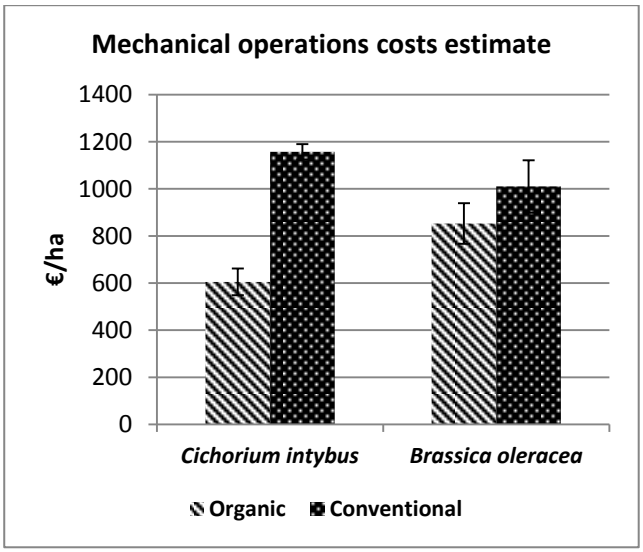
As regards heavy metals (Al, Cd, Hg, Pb) no significant differences in contents were detected between organic and conventional cabbages, even though for Al and Cd a tendency for higher values in conventional cabbages can be seen. For this purpose Worthington (2001) found instead that organic crop contained lower amounts of heavy metals more often than comparable conventional crops. Concerning chemical contaminants in food that result from general environmental pollution, such as Cd, Hg, Cu, Zn, Pb some authors (Magkos et al., 2006) found that their absence, presence and relative amount in organic and conventional food depend mainly on farm location and not so much on management.

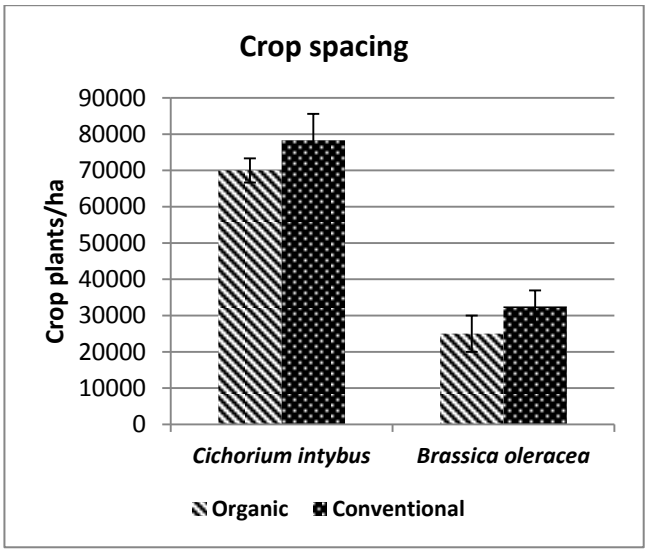
As here briefly described, surely the evaluation of nutritional differences between organic and conventional vegetables is very complex and not always univocal. However an author (Schuphan, 1974) found that generally the effects on mineral contents are variable also depending on soil types. After the

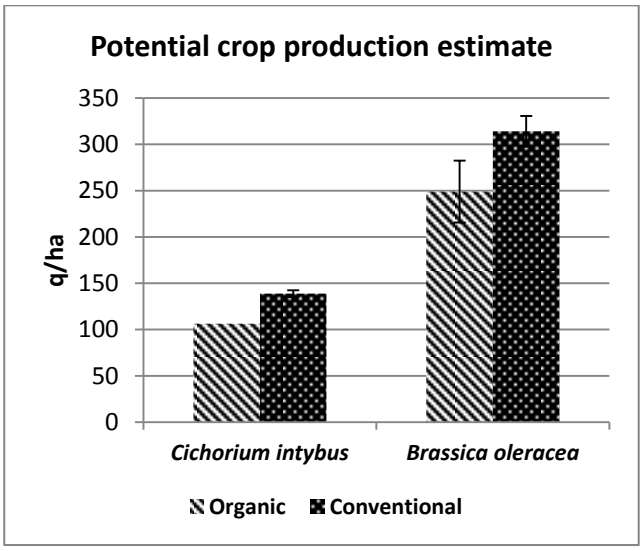
analysis of data from three years of research, also Warman and Havard (1997) underlined some differences in mineral contents but not consistent between cabbages grown up in organic and conventional plots.

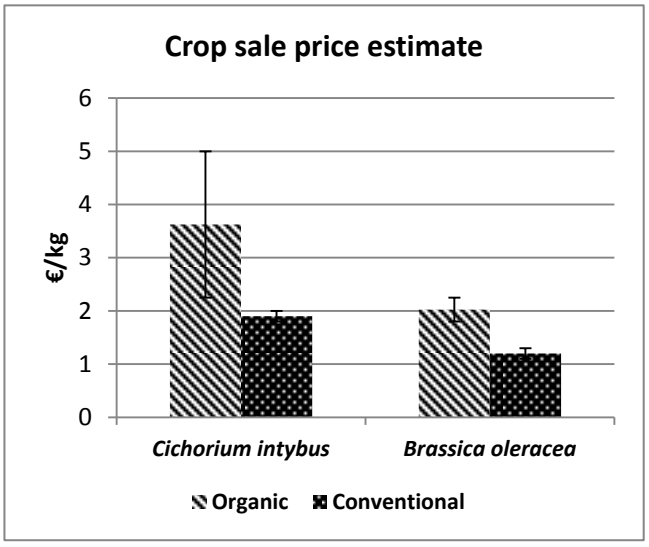
Crop production estimate

In order to complete the crop production overview, some information on costs of management practices, crop production and sale price were collected by farmer interviews and are summarized in the following graphs. It was possible to calculate the mechanical operations costs estimate by checking the price of each management practice in Veneto Region website[20]. All data refer to the production with subsequent retail sale in the farm shop. Since no *ad hoc* survey was carried out with this purpose, the data collected are few, but there was the will to add this point for the completeness of the analysis, the data were not treated with a statistical elaboration.









[20] Data available on: Prezziari agricoli per lavorazioni e sistemazioni agro-forestali (http://www.agrolinker.com/italiano/argomenti/giurestim/prezziarita1.html)

Fig. 70: Economic estimates of crop production and sale for the two horticultural products object of study in this work. Error bars represent standard error.

From these findings it emerges that Treviso red chicory cultivation needed more manpower and mechanical practices in particular in conventional management. In general terms the crop spacing was slightly smaller in conventional management for both the crops. The crop production was higher in conventional fields, while the sale price was generally more expensive for organic vegetables, even though it seemed to be much more variable.

There is a never-ending debate on difference in production between organic and conventional systems. There are studies (Seufert et al., 2012) that by using a comprehensive meta-analysis to examine the relative yield performance of organic and conventional farming systems globally showed that, overall, organic yields are typically lower than conventional yields. However these yield differences are highly contextual, depending on system and site characteristics and range from 5% lower organic yields (rain-fed legumes and perennials on weak-acidic to weak-alkaline soils), 13% lower yields (when best organic practices are used), to 34% lower yields (when the conventional and organic systems are most comparable). Generally there are many evidences in literature that affirm that organic yield are lower than conventional ones (Lotter, 2003; Pimentel et al., 2005; Gomiero et al., 2011). Also Ponisio et al. (2014) with a meta-dataset three times larger than previously used, found that organic yields are only 19.2% (+3.7%) lower than conventional yields, a smaller yield gap than previous estimates. Moreover, they found entirely different effects of crop types and management practices on the yield gap compared with previous studies. For example, they found no significant differences in yields for leguminous versus non-leguminous crops, perennials versus annuals or developed versus developing countries. Instead, they found that two agricultural diversification practices, multi-cropping and crop rotations, substantially reduce the yield gap (to 9 ± 4% and 8 ± 5%, respectively) when the methods were applied only in organic systems. Therefore even though a difference in crop production remains (with conventional one higher than the organic one), the key to decrease this gap appears to rely on management practices.

However it is noteworthy that was pointed out that the assessment of agriculture cannot be limited to crop production alone or account only for farm investment and revenue because practices that achieve high yields may not be ecologically or socioeconomically sustainable (Smith et al., 2000; Gomiero et al., 2011; Gomiero, 2013) as the other results obtained in this work, concerning the environmental point of view, also confirm.

(2) Biodiversity and ecosystem services

In order to answer the question n.2 of the objectives:

Is a higher biodiversity always linked to higher efficiency of ecosystem services in the agroecosystem?

all the biotic and abiotic indicators measured during this work were put together by using radar plot representations. To better characterize the work structure, all the indicators were divided into two main sectors (fig. 71): belowground environment and epigeal environment. The results obtained regarding

biodiversity composition of different groups studied were summarized by using two of the most used in literature diversity indexes (Shannon and Simpson indexes). These results were put in comparison with the ones concerning the functional indicators measured in the sector in which the equivalent biodiversity groups belong to.

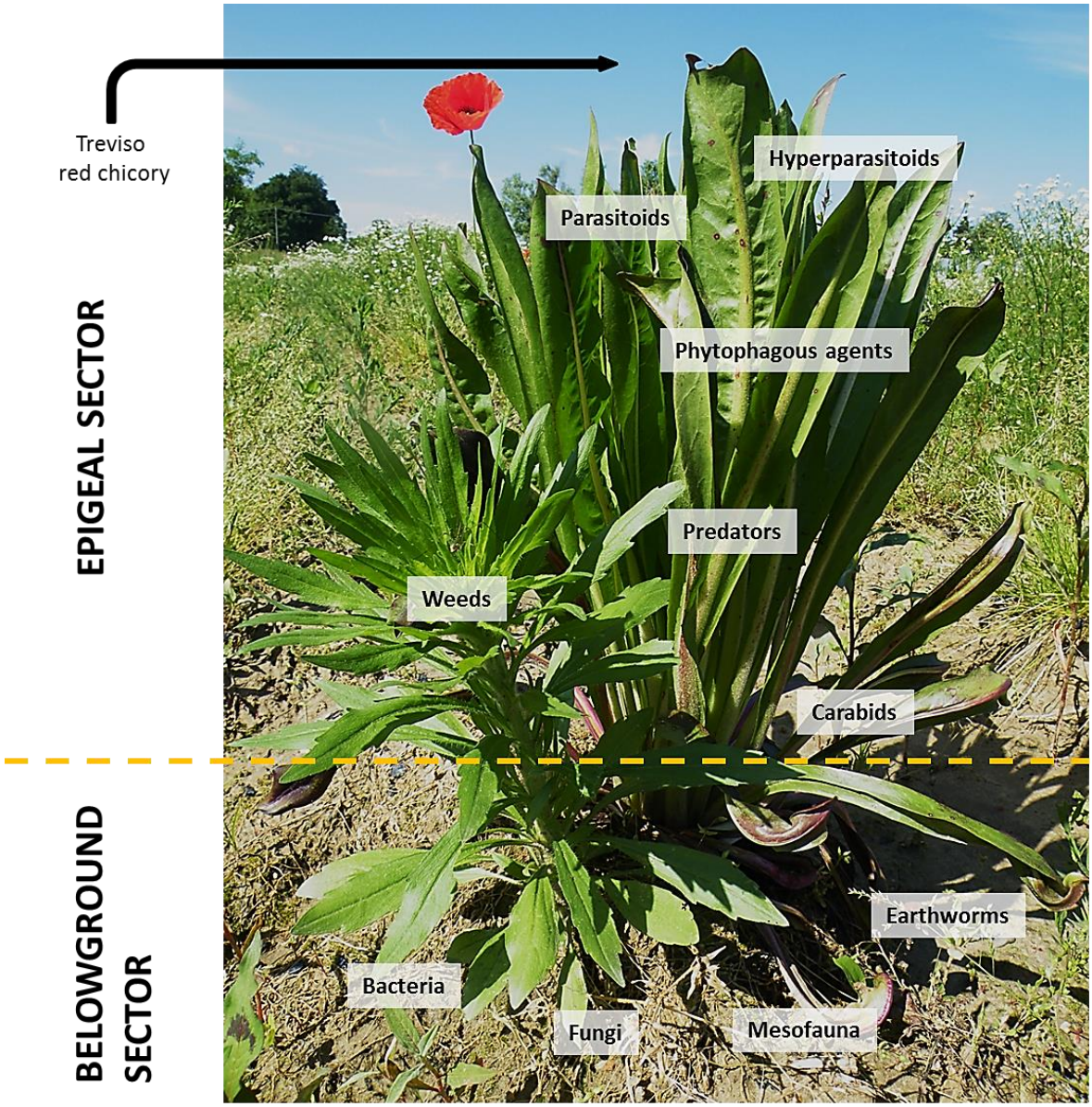


Fig. 71: Representation of the two main sectors in which this work is divided: belowground and epigeal with several bioindicators taken into account (Ph. S. Fusaro).

Belowground sector: diversity

The following radar plot is the summary of results of diversity of the four indicator groups considered: soil bacteria and fungi, mesofauna and earthworms. It was chosen to represent this value by using classical Shannon's and Simpson's diversity indexes, since Shannon's measures both richness (the

number of species) and evenness (how evenly individuals are distributed among species), while Simpson's provides a good estimate of diversity at relatively small sample sizes (Magurran, 2004).

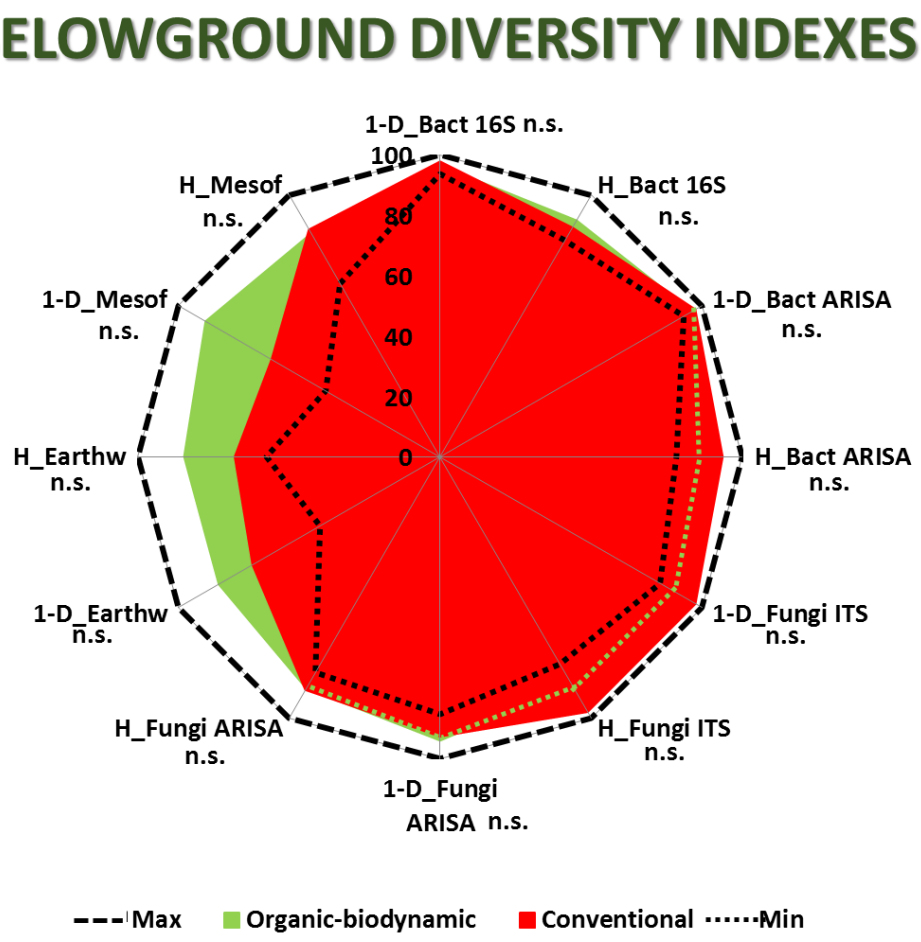


Fig. 72: Mean values calculated for the two agroecosystem managements. LEGEND. 1-D: % Simpson diversity index; H: % Shannon diversity index; Bact 16S: Bacterial community analysed by 16S sequencing; Bact ARISA: Bacterial community analysed by Automated Ribosomal Intergenic Spacer Analysis; Fungi ITS: Fungal community analysed by ITS sequencing; Fungi ARISA: Fungal community analysed by Automated Ribosomal Intergenic Spacer Analysis Earthw: Earthworm community; Mesof: Mesofauna community. Significance: n.s.: p value >0.05

It is noteworthy that no one index is significantly higher in one particular agroecosystem management: it means that biodiversity of these soil indicator groups, described with classical diversity indexes found in literature, was not significantly different according organic-biodynamic or conventional management.

Belowground sector: functionality

The following radar plot shows results on several functional indicators and tests that were performed in order to measure the efficiency of some ES driven by the four indicator groups previously considered (soil bacteria, soil fungi, mesofauna, earthworms).

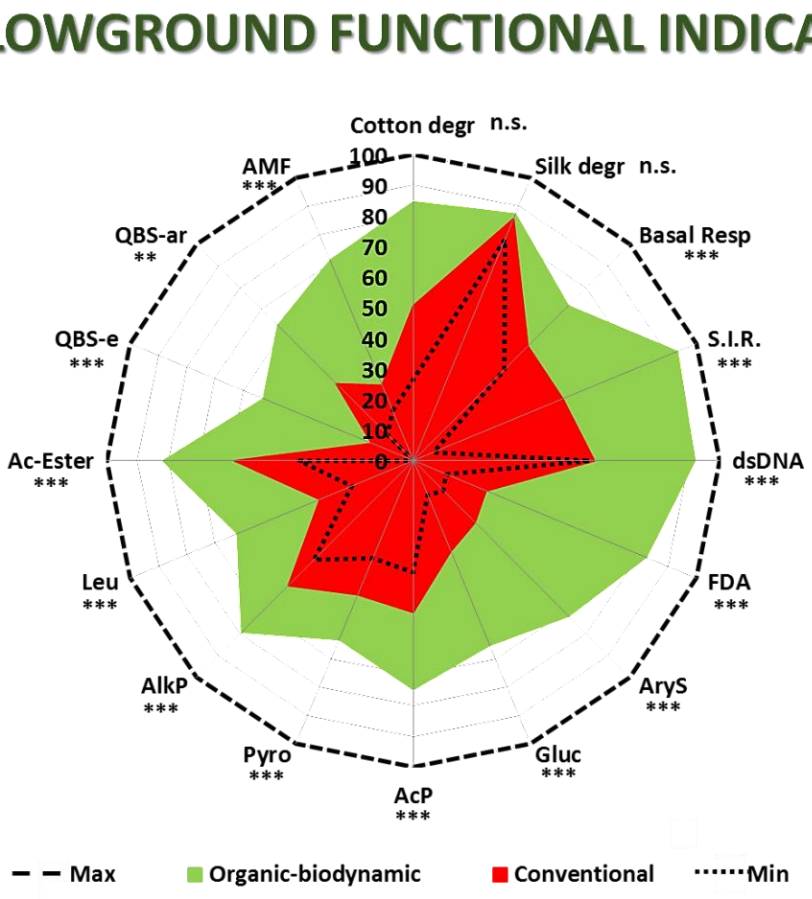


Fig. 73: Mean values calculated for the two agroecosystem managements. LEGEND. Cotton degr: fertimeter % cotton control yarn degradation; Silk degr: fertimeter % silk control yarn degradation; Basal resp: % dH^+ soil dry basal respiration test; S.I.R.: % dH^+ soil Substrate Induced Respiration test; dsDNA: % ug dsDNA/g d.s.; FDA: Fluorescein Diacetate hydrolysis test % µg/g F; Enzymatic activities (in nM/g d.w./h)= AryS: % Arylsulfatase; Gluc: % B-glucosidase; AcP: % Acid phosphomonoesterase; Pyro: % Pyrophosphate-phosphodiesterase; AlkP: % Alkaline phosphomonoesterase; Leu: % Leucine aminopeptidase; Ac-Ester: % Acetate-esterase; QBS-e: % Soil Biological Quality Index based on Earthworms; QBS-ar: % Soil Biological Quality Index based on arthropods; AMF: % n° AMF gene copies/g soil. Significance: **: p value <0.01; ***: p value <0.001; n.s.: p value >0.05.

The situation depicted in this radar plot is completely different from the one in fig. 72. In fact almost all the measured functional indicators had a significantly higher value in organic-biodynamic management. Being the functional test a way to quantify the efficiency of the corresponding ES, it is possible to conclude that in organic-biodynamic soils these ES were more efficient.

Therefore in the belowground sector there does not seem to be a link between biodiversity and ES efficiency or the classical indexes used in literature (Shannon and Simpson) to describe biodiversity are not very suitable for this purpose. In fact the more the sampling effort, the more the rare species one finds and Shannon's Index is calculated from proportions therefore rare species contribute very little and for this reason they can be underestimated (Chao and Shen, 2003; Magurran, 2004), but for other variables as for example soil bacteria in this work it was found that rare species (the ones with abundances lower than 2% and detected only by sequencing) can underline the difference between organic–biodynamic and conventional soils and therefore it is important to consider them in such a biodiversity study.

Epigeal sector: diversity

The following radar plot is the summary of results concerning diversity of the five epigeal indicator groups considered: phytophagous agents, carabids, parasitoids, weeds in margin and in cropfield. It was chosen to represent these values by using classical diversity indexes (Shannon and Simpson), like in the belowground sector. It was not possible to calculate predator and hyperparasitoid diversity indexes for conventional fields due to the scarcity of data available for these two indicator groups.

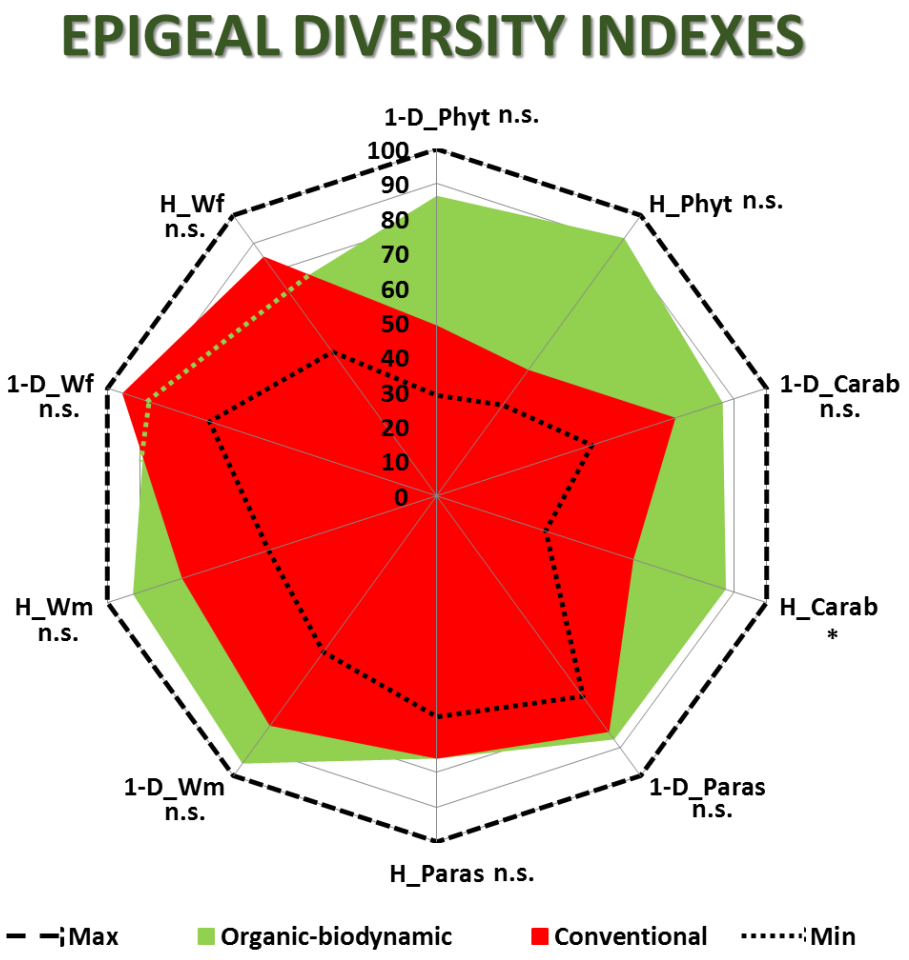


Fig. 74: Mean values calculated for the two agroecosystem managements. LEGEND. 1-D: % Simpson diversity index; H: % Shannon diversity index; Phyt: phytophagous agents community on cabbage; Carab: carabid community; Paras: parasitoid community of P. *xylostella* on cabbage; Wm: weed community in the field margin; Wf: weed community in the field area. Significance: *: p value <0.05; n.s.: p value >0.05

As for fig. 72 in this radar plot almost all diversity indexes are not significantly different between the two types of agriculture considered in this work.

Epigeal sector: functionality

The following radar plot shows results of several functional indicators and tests that were performed in order to measure the efficiency of some ES driven by the five previously considered indicator groups (weeds, phytophagous agents, predators, parasitoids, and hyperparasitoids). The presence of phytophagous agents obviously is not to consider an ES but on the contrary it is a negative element for crop production.

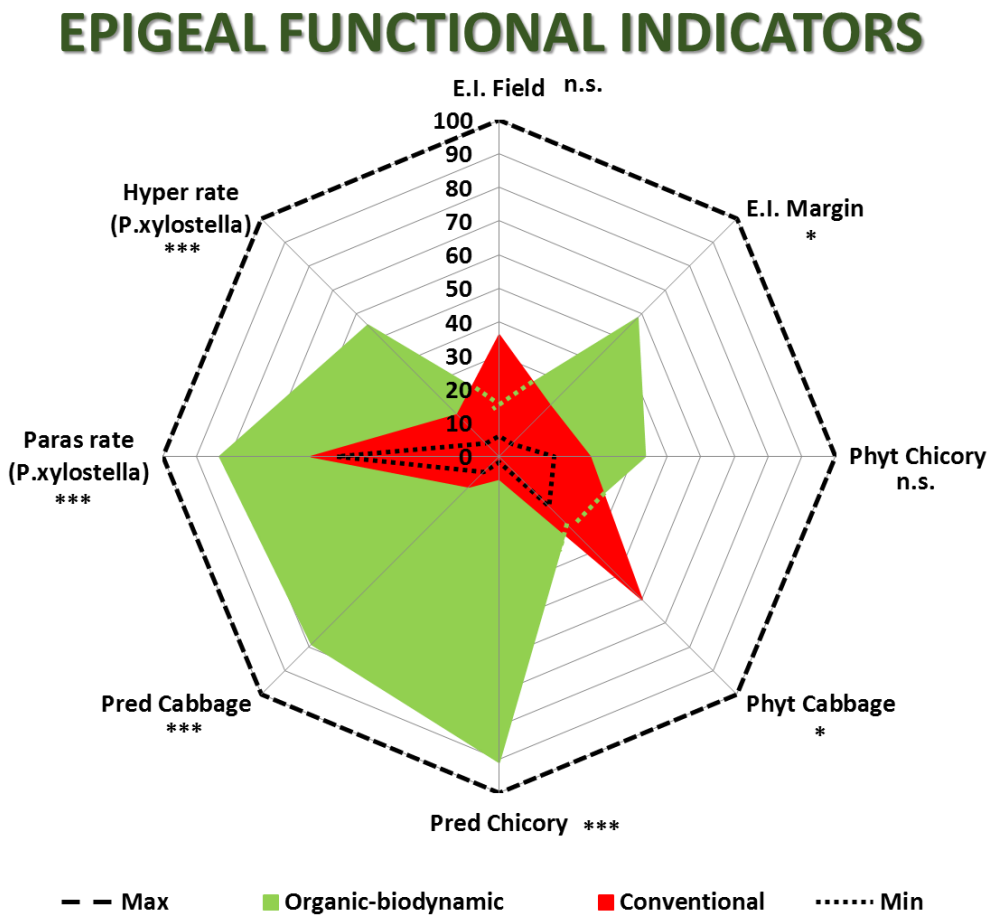


Fig. 75: Mean values calculated for the two agroecosystem managements. LEGEND. E.I. Field: % Entomophily Index calculated within the field area; E.I. Margin: % Entomophily Index calculated in the field margin; Phyt Chicory: % sum of means/4 plants of phytophagous agents on chicory; Phyt Cabbage: % sum of means/4 plants of phytophagous agents on cabbage; Pred Chicory: % sum of means/4 plants of predators on chicory; Pred Cabbage: % sum of means/4 plants of predators on cabbage; Paras rate: % *P. xylostella* parasitization (main phytophagous agent on cabbage); Hyper rate: % *P.xylostella* hyperparasitization. Significance: *: p value <0.05; ***: p value <0.001; n.s.: p value >0.05.

Also in the epigeal sector is the same as for the belowground one: the situation depicted in this radar plot is completely different from the one in fig. 74. In fact almost all measured functional indicators had a significantly higher value in organic-biodynamic management. The phytophagous agents presence on cabbage was significantly more consistent in conventional fields, but, as said before, it is a negative factor

that can reduce crop production. Being the functional test a way to quantify the efficiency of the corresponding ES, it is possible to conclude that in organic-biodynamic soils these ES were more efficient.

Therefore also in the epigeal sector there does not seem to be a link between biodiversity and ES efficiency, or another explanation is that again the classical indexes used in literature (Shannon and Simpson) to describe biodiversity are not suitable for this purpose, possibly due to the scarce importance given to rare species. If biodiversity is not significantly different in organic-biodynamic and conventional agroecosystems, but functionality is more efficient in the former, probably in these environments almost the same diversity amount involves groups that are better interacting among each others and the result is an overall improved efficiency of ES.

Also in literature it is possible to find some evidences about this phenomenon. For example Tscharntke et al. (2005) stressed how biodiversity may enhance functioning when species add to the function via a unique (complementary) occupation of the total niche. In fact each species or species group may focus on different resource parts (resource partitioning) or promote positive intraguild interactions, thereby improving the ecological functioning. Redundancy, meaning that a positive relation between diversity and functioning holds only for few species and additional species do not increase function, but plateau at higher diversity levels, is important in the most commonly studied case of biodiversity–ES (Tscharntke et al., 2005). Therefore increasing species diversity appears to enhance ecosystem functioning only up to a saturation point (Tscharntke et al., 2005). In a simple environment, like the annual agroecosystems studied in this thesis, the sampled agrobiodiversity can likely have almost reached the saturation point in both the two types of agriculture (organic-biodynamic and conventional) and therefore it is possible to try and interpret the results obtained: there is no link between the amount of agrobiodiversity (apparently equal in the two types of management) and the ES functioning (significantly higher in organic-biodynamic management), possibly because ES depends idiosyncratically on the involved species and management may select species combinations minimizing negative interactions within functional groups (Tscharntke et al., 2005). Even others (Albrecht et al., 2007) revealed that community and interaction structures might not be detected in studies that focus simply on species richness and abundance, since their findings demonstrated that interaction diversity declines more rapidly than species diversity. However other reports (Cardinale et al., 2012) pointed out that for many ES, there are insufficient data to evaluate the relationship between biodiversity and the service and for a small number of ES, current evidence for the impact of biodiversity runs counter to expectations, like in this study.

(3) Ecosystem services and agroecosystem management

The present chapter aims at answering the question n.3 of the objectives:

Which ecosystem services are more efficient in each of the two agroecosystem management types (organic vs. conventional)?

The following radar plot includes all functional tests that were performed during this work, both in the epigeal and belowground sectors.

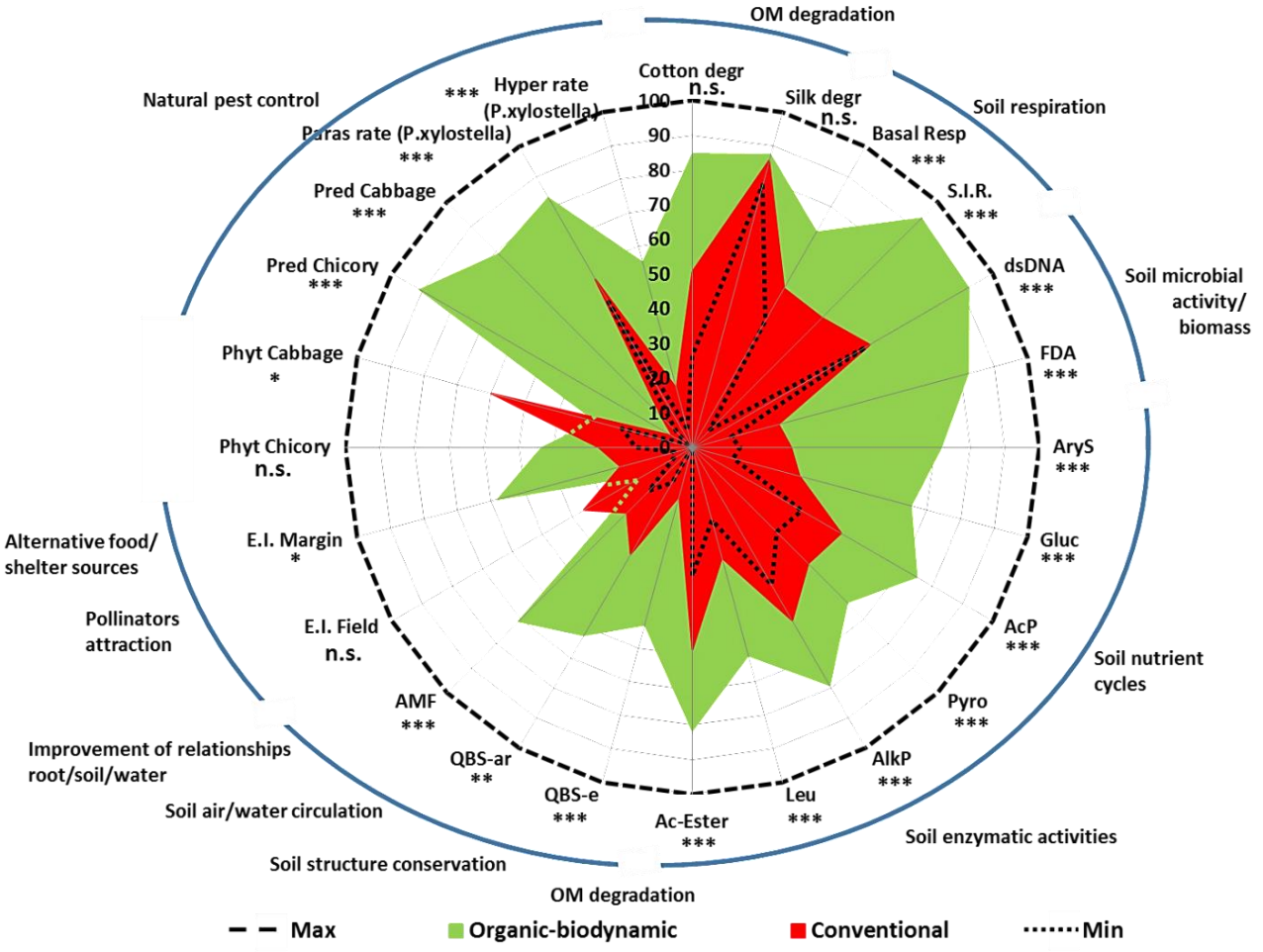


Fig. 76: Mean values calculated for the two agroecosystem managements. LEGEND. Cotton degr: fertimeter % cotton control yarn degradation; Silk degr: fertimeter % silk control yarn degradation; Basal resp: % dH^+ soil dry basal respiration test; S.I.R.: % dH^+ soil Substrate Induced Respiration test; dsDNA: % ug dsDNA/g d.s.; FDA: Fluorescein Diacetate hydrolysis test % µg/g F; Enzymatic activities (in nM/g d.w./h)= AryS: % Arylsulfatase; Gluc: % B-glucosidase; AcP: % Acid phosphomonoesterase; Pyro: % Pyrophosphate-phosphodiesterase; AlkP: % Alkaline phosphomonoesterase; Leu: % Leucine aminopeptidase; Ac-Ester: % Acetate-esterase; QBS-e: % Soil Biological Quality Index based on Earthworms; QBS-ar: % Soil Biological Quality Index based on arthropods; AMF: % n° AMF gene copies/g soil; E.I. Field: % Entomophily Index calculated within the field area; E.I. Margin: % Entomophily Index calculated in the field margin; Phyt Chicory: % sum of means/4 plants of phytophagous agents on chicory; Phyt Cabbage: % sum of means/4 plants of phytophagous agents on cabbage; Pred Chicory: % sum of means/4 plants of predators on chicory; Pred Cabbage: % sum of means/4 plants of predators on cabbage; Paras rate: % *P. xylostella* parasitization (main phytophagous agent on cabbage); Hyper rate: % *P.xylostella* hyperparasitization. Significance: **: p value <0.01; ***: p value <0.001; n.s.: p value >0.05.

In fig. 76 the ES corresponding to the several functional indicators measured are marked in blue. Organic matter degradation is measured by fertimeters degradation, key soil enzymatic activities, QBS-ar and QBS-e; soil respiration rate is represented by two respiration tests (the basal one and the Substrate-Induced Respiration test); overall soil microbial activity is measured by Fluorescein Diacetate Hydrolysis test, while overall soil microbial biomass is measured by dsDNA quantification essay; soil nutrients cycles are measured by the key enzymatic activities; soil structure conservation and soil water and air circulation are

characterized by QBS-e and QBS-ar indexes; improvement of relationships among roots, water and soil is guaranteed by AMF; attraction for pollinators and alternative food and shelters sources are measured by Entomophily Index and natural pest control comprehends the presence of predators, parasitization rate and hyperparasitization rate.

Almost all the measured functional indicators were significantly higher in organic-biodynamic agroecosystems (except for the presence of phytophagous agents on cabbage that was higher in conventional fields, but as said before, it is not an ES, on the contrary is a negative element for crop production). This means that the ES considered seem to be more efficient in this type of agriculture, and for this reason it can be defined as more environmentally sustainable, saving external inputs.

(4) Correlations

This part of the thesis concerns the answer to the question n.4 of the objectives:

Are there correlations between different functional indicators? Are some indicators more informative and representative of the overall on-going phenomena? Can we choose one single indicator and spare monitoring analysis costs?

It is suitable to the development of a methodological toolkit that can be useful in terms of future agroecological researches and agroecosystem monitoring, and above all in a perspective of reducing costs.
By performing a Pearson's correlation statistical analysis or a Spearman's correlation when one of the two interacting variables had not normal distribution, it was possible to extrapolate significant correlation coefficients. Even though with this statistical analysis it is not possible to get information about cause-effect relationships between two variables, it is useful to know the type of trend (direct or indirect) of changing of one variable at the change of the other one, in order to reduce the costs of monitoring analysis. To get more details on the correlation coefficient values, see the complete list in the appendix (tab. LXIV).
A scheme of the total amount of the analysed data is shown in fig. 77.

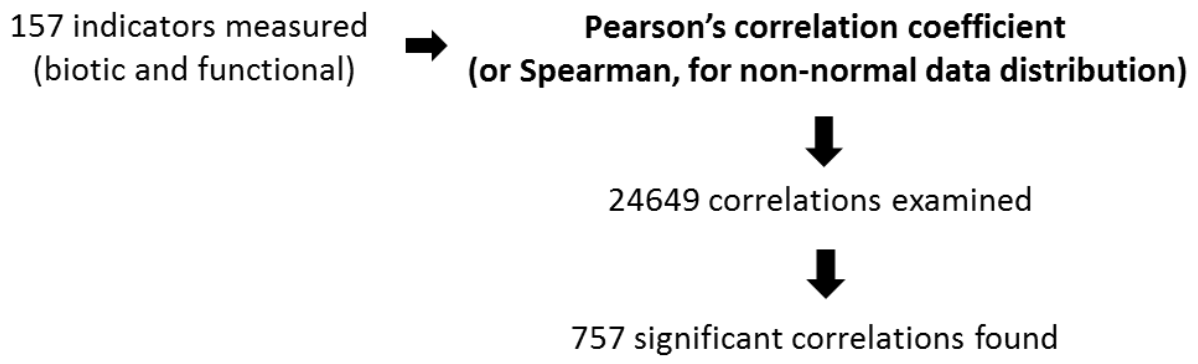


Fig. 77: Total amount of data examined to answer the question n.4 of the objectives, whether there were correlations between all indicators considered in this work.

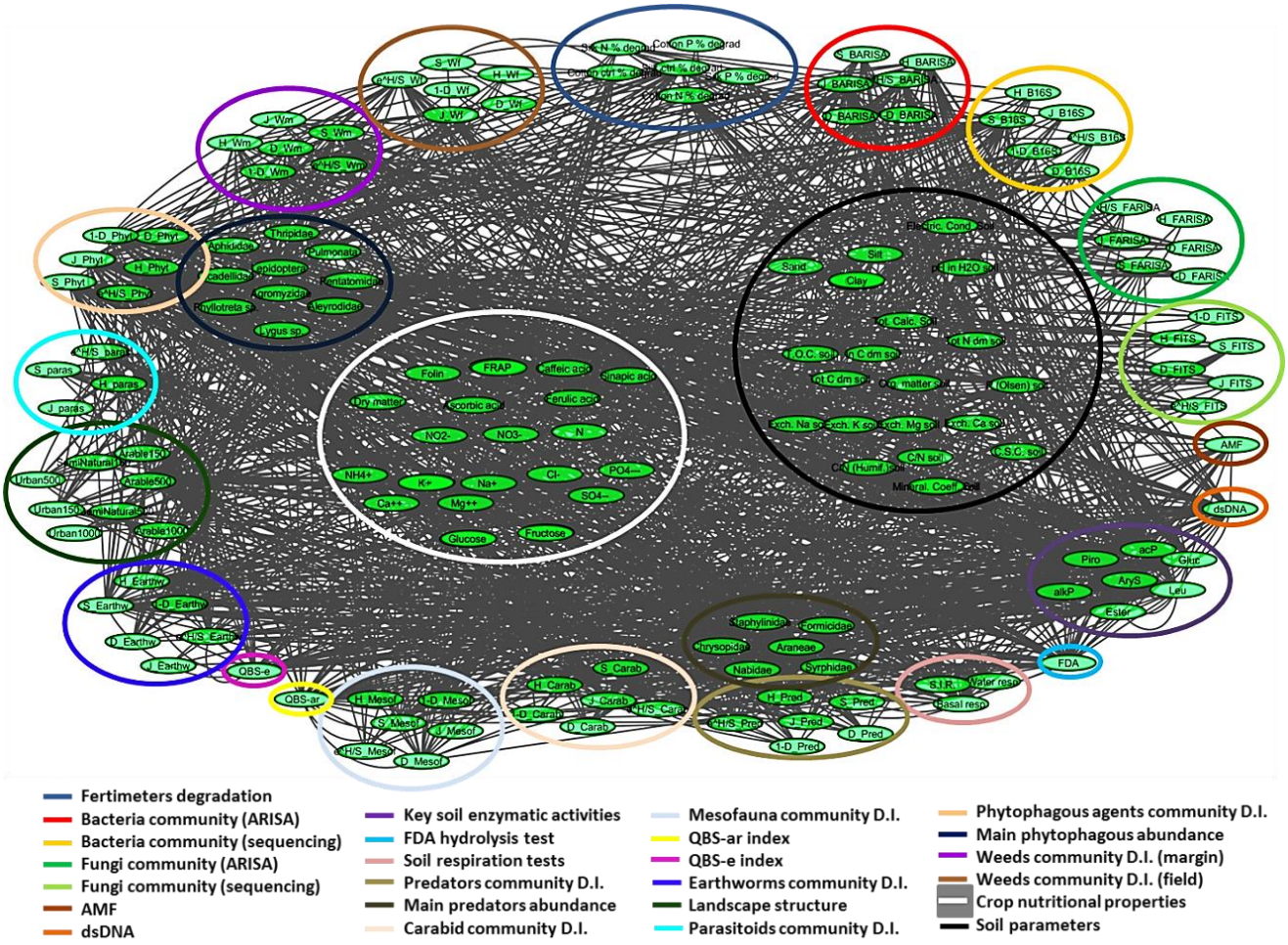


Fig. 78: Overview of significant correlation relationships found between all the measured indicators in this work. All these relationships are significant with p value <0.05. D.I. : diversity indexes.

This scheme represents the complexity of the overview of just the significant correlations found between all the analysed variables. It underlines the concept that every factor is linked with many others and the correct way to consider each one is in relationship with the others. A take-home message emerging from this figure is the importance of contextualization of each topic in agroecological research.

From now on every topic will be briefly discussed.

Fertimeter

In the following picture (fig. 79) significant correlations between fertimeter results and other indicators are highlighted.

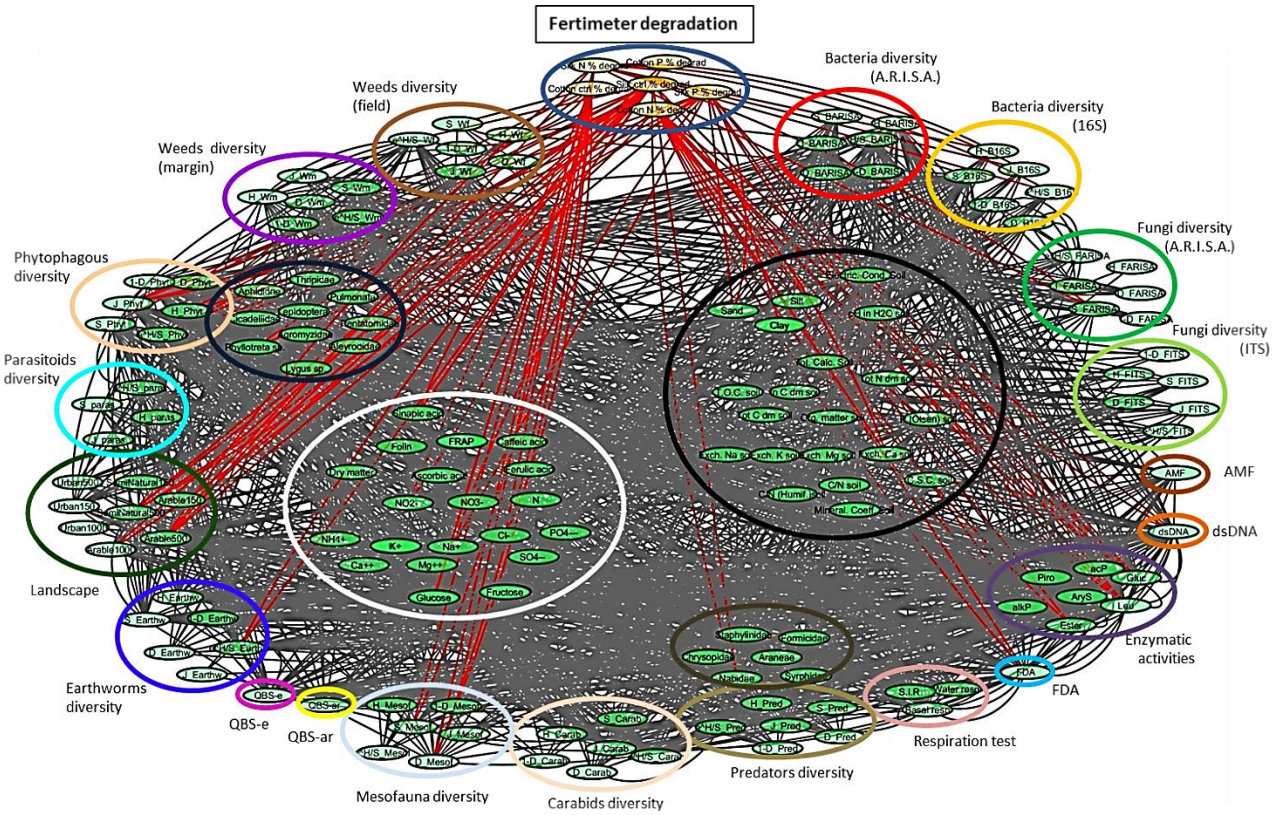


Fig. 79: Focus on the correlation relationships between fertimeter yarn degradation (%) and other indicators. All these relationships are significant with p value <0.05.

Some correlations are noteworthy such as between fertimeters degradation and key soil enzymatic activities, bacteria and fungi communities, FDA hydrolysis test, dsDNA test, but also with mesofauna diversity indexes. Some of them can be explained because for example β-glucosidase activity interests the cellulose degradation (Karaca et al., 2011), that is to say the cotton yarn in fertimeter, and more the link between fertimeter degradation and mesofauna diversity is supposedly due to the fact that not exclusively microbiological actors have their influence on yarns degradation, but also other soil inhabitants such as mesofauna components also important in OM degradation. Probably the correlations that concern fertimeter degradation rate and mesofauna or key soil enzymatic activities can contribute to elucidate the link found by some authors (Stevanato et al., 2014) between higher productivity in vineyards and higher mineralization of OM determined by fertimeter.

In essence it means that by using the fertimeters essay, a very cheap method to measure soil fertility, it is possible to have also information about the trend of many other different indicators.

Bacterial communities

A.R.I.S.A.

The following picture (fig. 80) regards the significant correlations found between data of soil bacterial communities analysed by A.R.I.S.A. technique and other indicators.

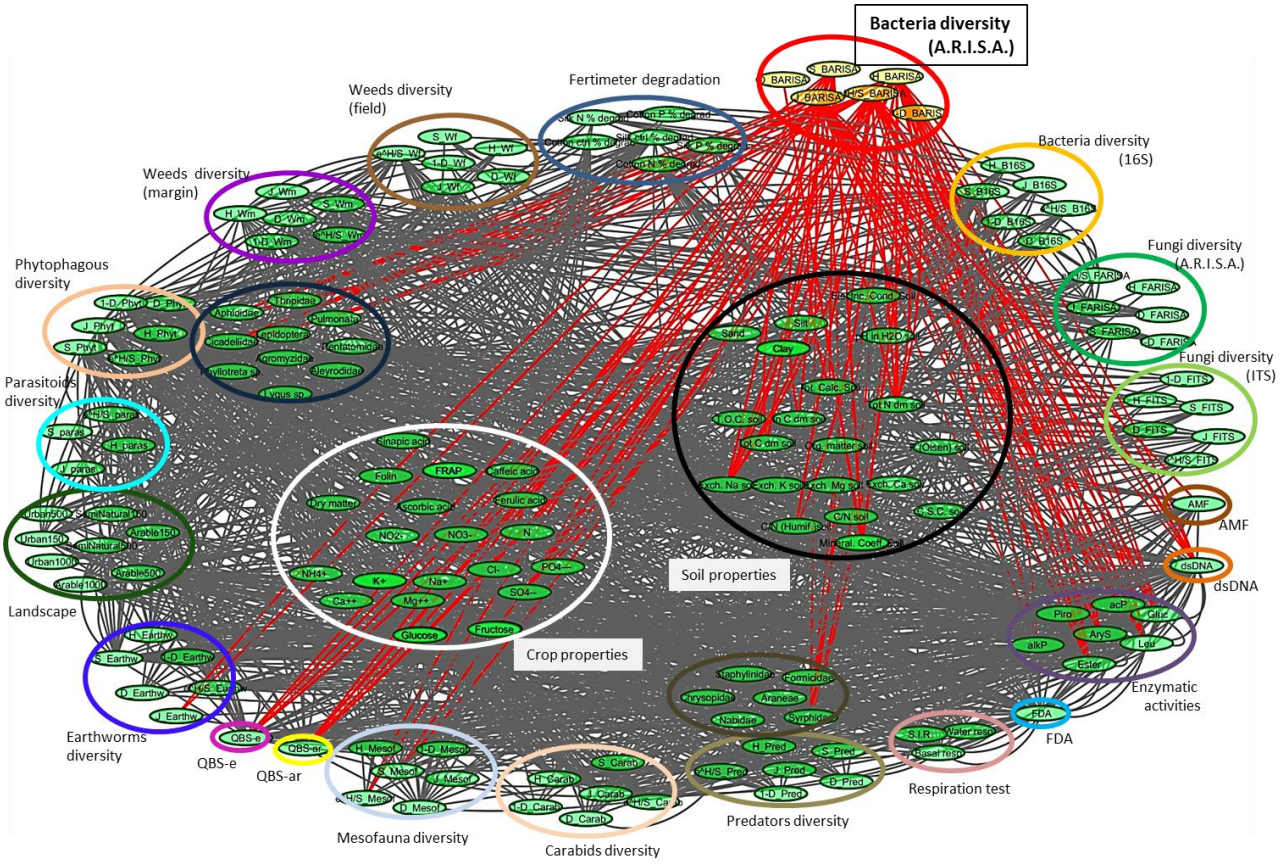


Fig. 80: Focus on the correlation relationships between soil bacterial community (analysed by the A.R.I.S.A. technique) diversity indexes and other indicators. All these relationships are significant with p value <0.05.

It is interesting to notice strong relationships between soil bacteria communities analysed with A.R.I.S.A. technique (a low-detail but not expensive screening technique- tab. XVIII) and the total amount of soil DNA (dsDNA), various enzymatic activities, soil chemical-physical properties, but also mesofauna and QBS-ar and earthworms and QBS-e. These correlations underline the fact that the most abundant and easily detectable bacterial strains have a great impact and strong influences not only with their environment of life (the soil) but also with other two among the most important soil decomposers and detritivores (mesofauna and earthworms). Moreover in support of this consideration, the symbiotic link between earthworms and bacteria living in their gut has been extensively demonstrated, which helps to make casts richer in macronutrients (Le Bayon and Milliret, 2009; Bernard et al., 2010; Aira and Dominguez, 2014) and to improve humic substances into the soil (Dell'Agnola and Nardi, 1987) and for this reason earthworms have a great impact also in natural fertilization of soils, while regarding mesofauna some authors (Renker et al., 2005) demonstrated that mites can disperse microorganisms on their body.

In particular concerning the interactions with soil enzymatic activities Sinsabaugh et al. (2014) showed that heterotrophic microbial communities converge towards a common steady state functional organization in relation to resources availability by regulating extracellular enzyme expression to optimize the short-term

responsiveness of carbon and nutrient acquisition. This homeostatic mechanism directly connects the stoichiometries of OM composition and eco-enzymatic activities.

16S sequencing

The following picture (fig. 81) regards the significant correlations found between data of soil bacterial communities analysed by 16S sequencing, NGS technique, and other indicators.

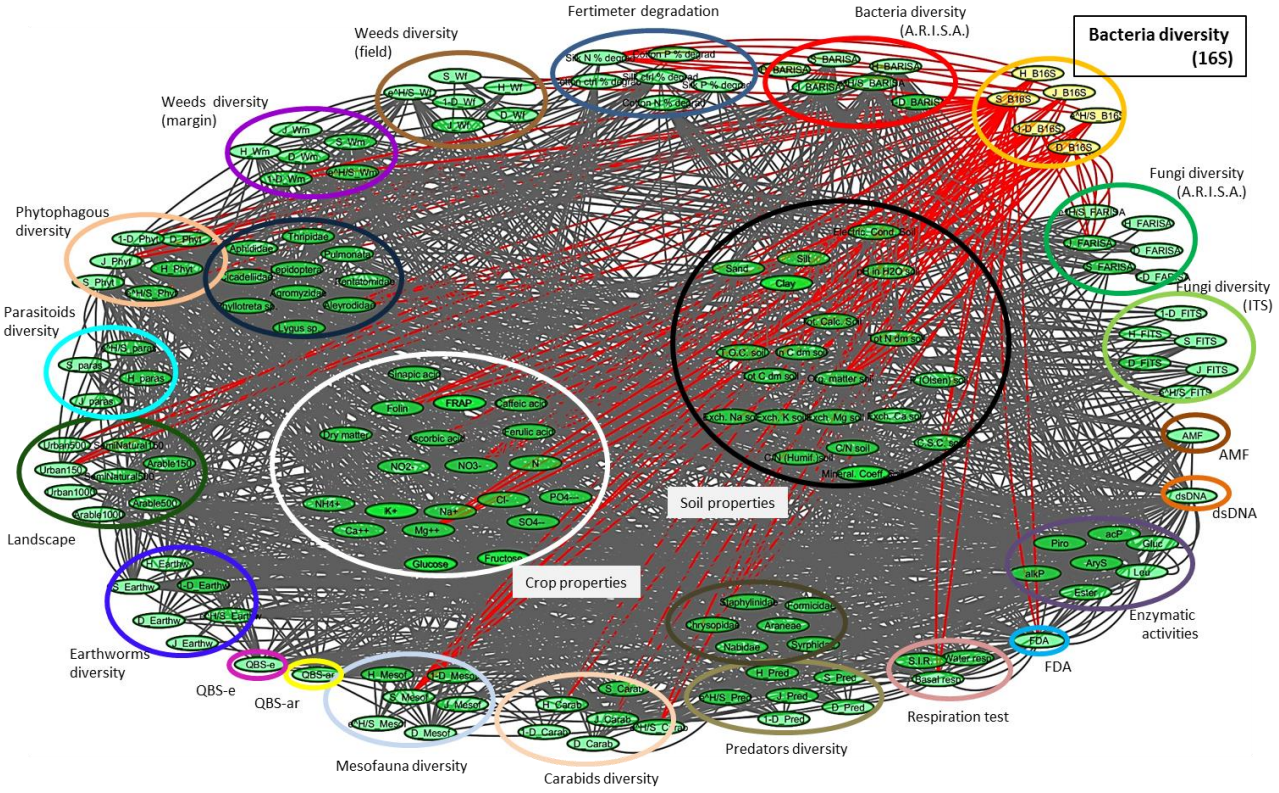


Fig. 81: Focus on the correlation relationships between soil bacterial community (analysed by 16S sequencing) diversity indexes and other indicators. All these relationships are significant with p value <0.05.

Analysing soil bacteria communities by using NGS technique such as 16S amplicon sequencing, it is possible to have information also about the trend of other indicators, such as the fertimeter degradation, the composition of fungal communities, weed communities, mesofauna communities, carabid communities, but also the soil respiration rate and FDA hydrolysis test. Recalling that for the number of bacterial strains detected with A.R.I.S.A. technique there were no significant differences between organic and conventional soils (tab. XIV), while for the ones detected with 16S amplicon sequencing there were and especially concerning three of the less abundant bacterial phyla (Fibrobacteres, WS2 and GNO2- fig. 34) that resulted to be more represented in organically managed soils, here it is interesting to notice that there are strong interactions between better detected bacterial communities and fertimeter degradation probably due to the detection of also the less abundant phyla which can have an important function in cellulose (and in

general OM) degradation (Ransom-Jones et al., 2012). Another consideration that can be done regards relationships between bacterial communities and weed communities found here. In this respect Kremer and Li (2003) demonstrated that weed rhizospheres had greater proportions of bacterial isolates characterized as "growth suppressive" to green foxtail (*Setaria viridis*) and field bindweed (*Convolvulus arvensis*): 15% and 10% respectively, and this suggests that bacteria can affect weed communities in such a way.

Fungal communities

A.R.I.S.A.

The following diagram (fig. 82) regards the significant correlations found between data of soil fungal communities analysed by the A.R.I.S.A. technique and other indicators.

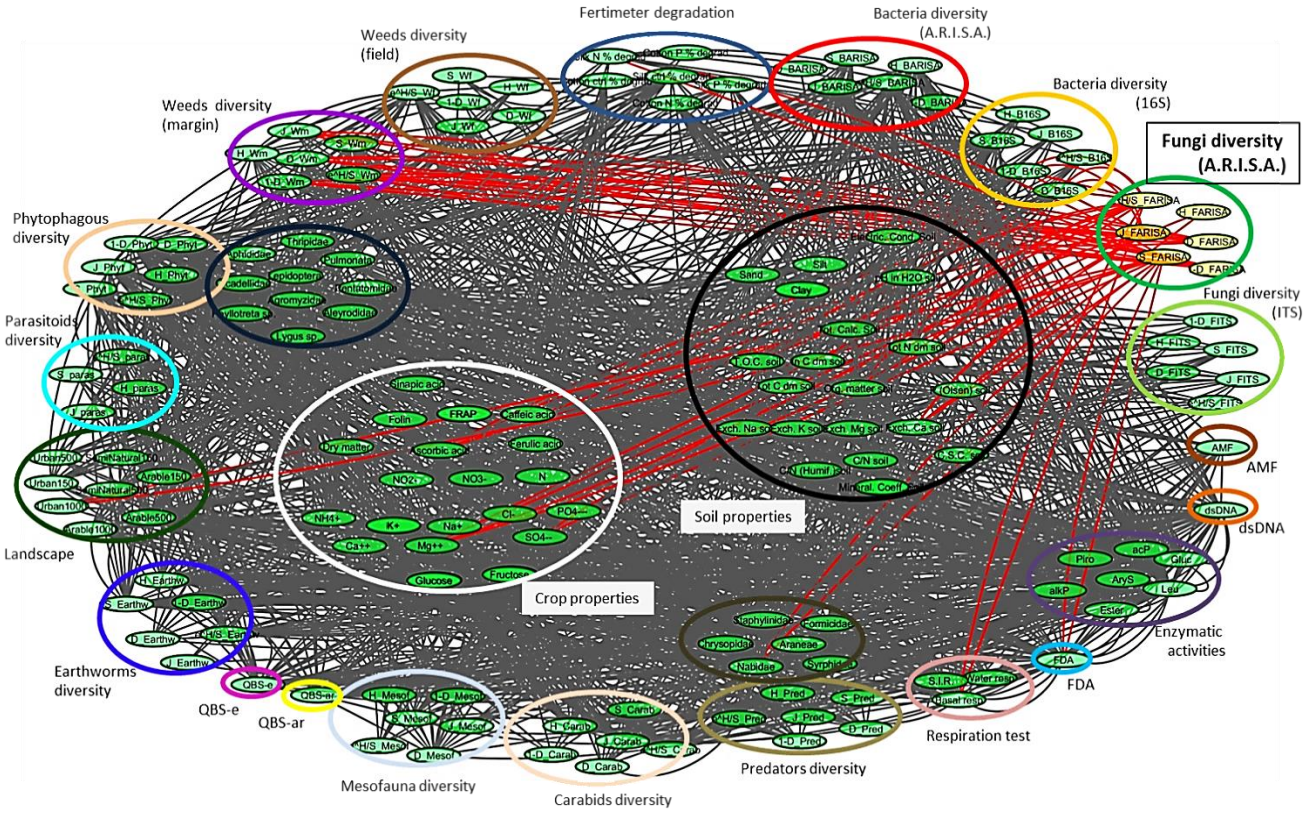


Fig. 82: Focus on the correlation relationships between fungal community (analysed by the A.R.I.S.A. technique) diversity indexes and other indicators. All these relationships are significant with p value <0.05.

In this part significant correlations were found between soil fungal communities analysed by the A.R.I.S.A. technique and FDA hydrolysis test, respiration rate, fertimeter degradation, but also with weed communities and crop nutritional properties. Some considerations can be done on these last two topics. Among soil fungi there are some species that can interact with plants in a negative (parasitic or saprophytic fungi) or in a positive way (mycorrhizal fungi) and therefore they can be among the responsible of weed community composition and of the crop nutritional properties caused by plant absorption capability modified by the fungal presence (van der Heijden et al., 2008; Daisog et al., 2011). But the correspondence between soil fungi and weeds is not a one-way relationship: Mouhmadou et al. (2013), by studying microcosms in which two weed species were grown under artificial conditions, were able to dissociate soil effects from plant effects and thence they succeeded in demonstrating that also plant species exert a key control on soil fungi: in fact plant species identity was the main determinant of soil fungal communities. Moreover van der Heijden et al. (2008) reviewed interactions among soil microbes and plant diversity and found that plants may influence soil fungi through species-specific interactions.

ITS sequencing

The following picture (fig. 83) regards the significant correlations found between data of soil fungal communities analysed by ITS sequencing, NGS technique, and other indicators.

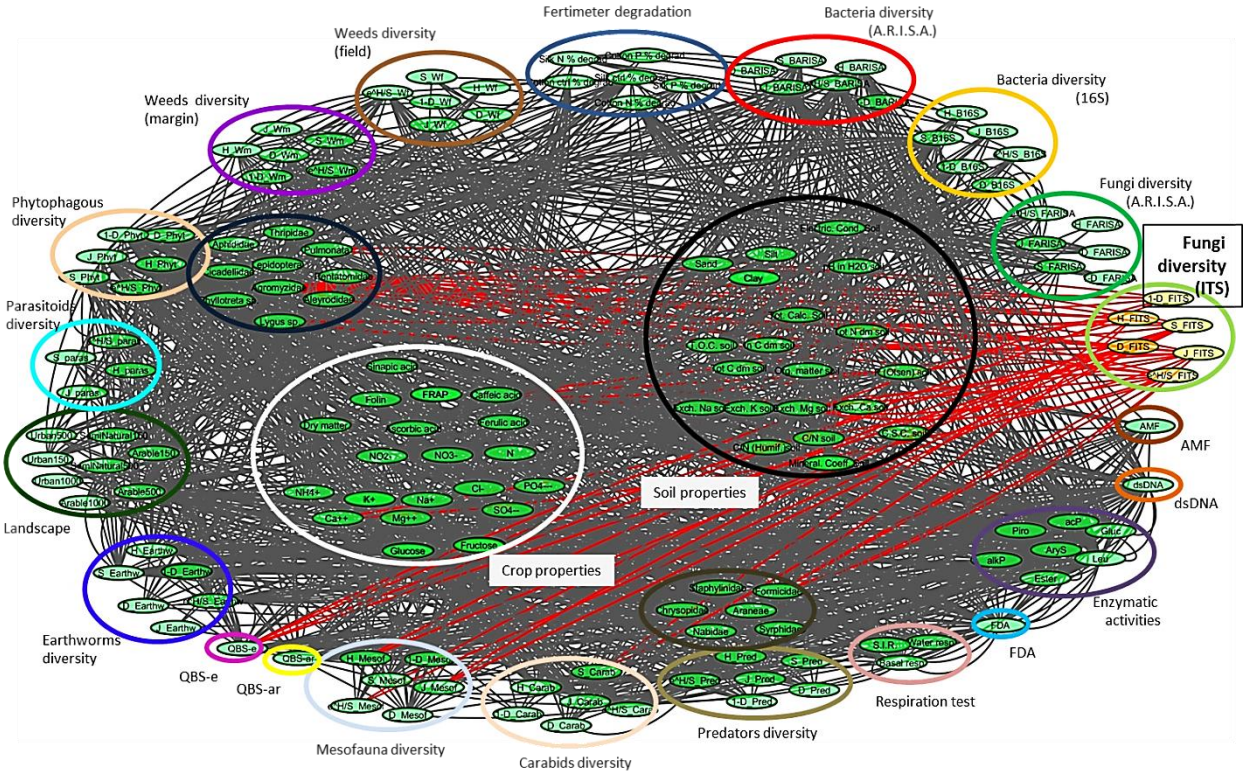


Fig. 83: Focus on the correlation relationships between fungal community (analysed by ITS gene sequencing) diversity indexes and other indicators. All these relationships are significant with p value <0.05.

This picture underlines how fungal communities analysed by ITS gene sequencing seem to be correlated with mesofaunal, earthworm (QBS-e) and phytophagous agent communities. It is a more detailed analysis technique with respect to A.R.I.S.A. able to detect also less abundant taxa and possibly only these taxa could be important as food for some mesofauna taxa and therefore more fungal taxa can allow the existence of some fungivorous mites or springtails. At this purpose for example de Vries et al. (2013) found an interesting link between dissolved organic carbon into the soil and fungal-feeding collembolans and according to these authors it suggests that this functional group by using soil fungi might be a sensitive indicator for changes in labile C availability. While the link between earthworms, through QBS-e index, and soil fungi community could be due to the interaction between them that happens in earthworms' gut that makes their casts different in mineral and microbial composition in comparison to the soil (Le Bayon and Milliret, 2009; Aira and Dominguez, 2014). Moreover Aira and Dominguez (2014) studied this effect particularly for endogeic earthworms, which are the most represented ecological category found in this work and therefore the one that mainly contribute to the QBS-e index value. Another consideration concerns a connexion between a situation of disequilibrium in soil fungi community (with high values of dominance index) and an increase in abundance of several phytophagous agent taxa and vice versa. Therefore put together the considerations about soil fungi and earthworms and soil fungi and phytophagous agents, the plot exhibits a framework similar to the one demonstrated with microcosms experiment by Trouvé and coworkers (2014). They found that slug herbivory was affected by soil organisms via altered plant nutrient availability and plant quality and, in particular, that earthworms significantly increased average AMF colonization of plant roots and reduced total slug herbivory (Trouvé et al., 2014). This confirms the close relationship between aboveground and belowground realities.

AMF

The following diagram (fig. 84) regards the significant correlations found between quantitative data of AMF analysed by qRT-PCR experiment and other indicators.

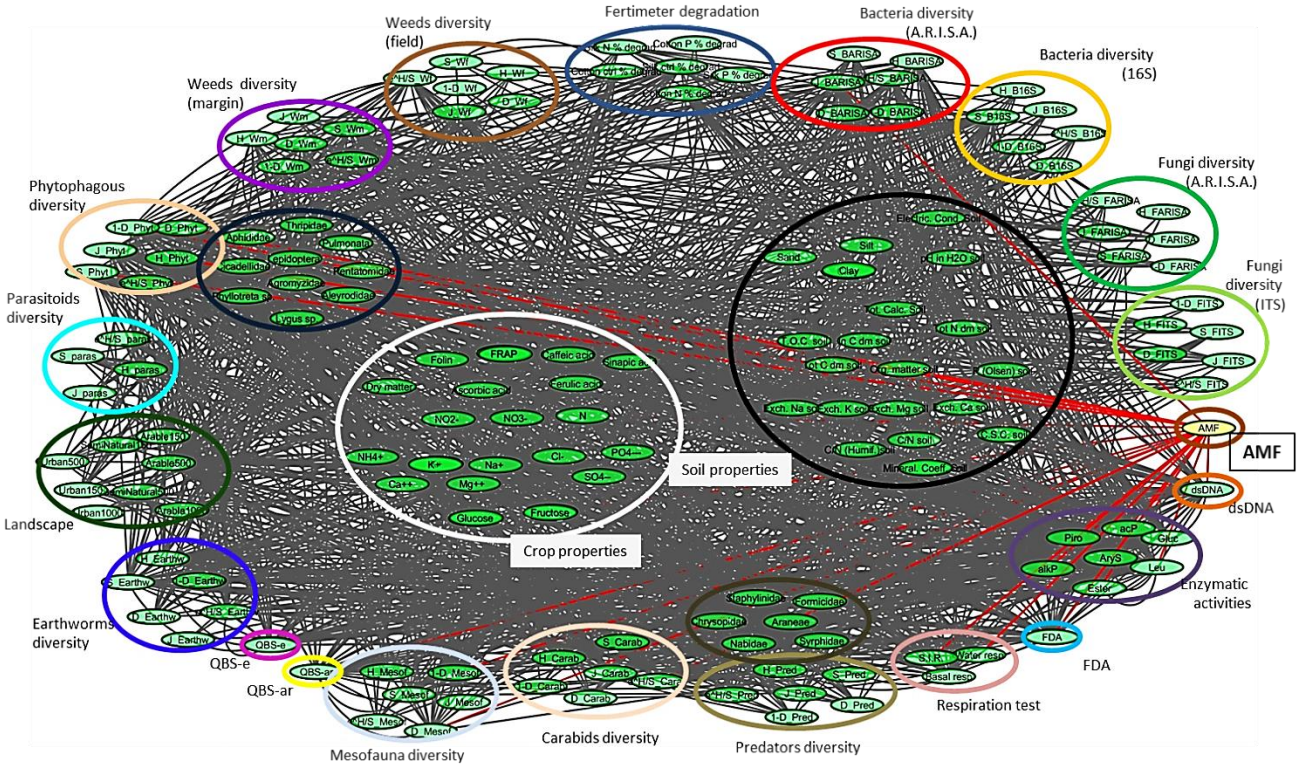


Fig. 84: Focus on the correlations relationships between AMF abundance into the soil and other indicators. All these relationships are significant with p value <0.05.

By studying the abundance of Arbuscular Mycorrhizal Fungi, one can have indirect information on the trend of some other indicators, such as for example the equitability of bacterial community, the dsDNA soil quantity, some key soil enzymatic activities, the soil respiration rate but also on mesofauna and phytophagous agent community. Some of these correlations can be explained also in literature, for example Joner and Jakobsen (1995) with a microcosm experiment demonstrated that AMF can stimulate the release of acid phosphomonoesterase (acP) from roots of subterranean clover (*Trifolium subterraneum*) and in particular that extracellular phosphatases are not produced by extraradical hyphae of the AMF symbioses, but the influence of AMF hyphae on these enzymatic activities in root-free soil seem to be indirect and driven through interactions also with other microorganisms (Jansa et al., 2011). The dependence of the AMF on the host plant for organic carbon can be affected by environmental conditions such as for example availability of CO_2 (Jansa et al., 2011) that is strictly linked to soil respiration rate, as this study confirms.

Moreover from these findings a connexion arises between the increased amount of AMF and a more balanced phytophagous agent community (with high values of Shannon and evenness and lower values of dominance indexes). This confirms data in literature concerning the fact that AMF colonize plant roots, resulting from expansion and/or complementation of the root function, and enhance plant productivity by facilitating plant nutrient uptake, mainly of elements with low mobility in the soil (for example P, Zn, Cu), as well as conferring plant resistance or tolerance to biotic and abiotic stresses (such as pests, pathogens, drought) (van der Heijden et al., 2008; Jansa et al., 2011; Mouhmadou et al., 2013).

dsDNA content

The following image (fig. 85) regards the significant correlations found between quantitative data of dsDNA into the soil and other indicators.

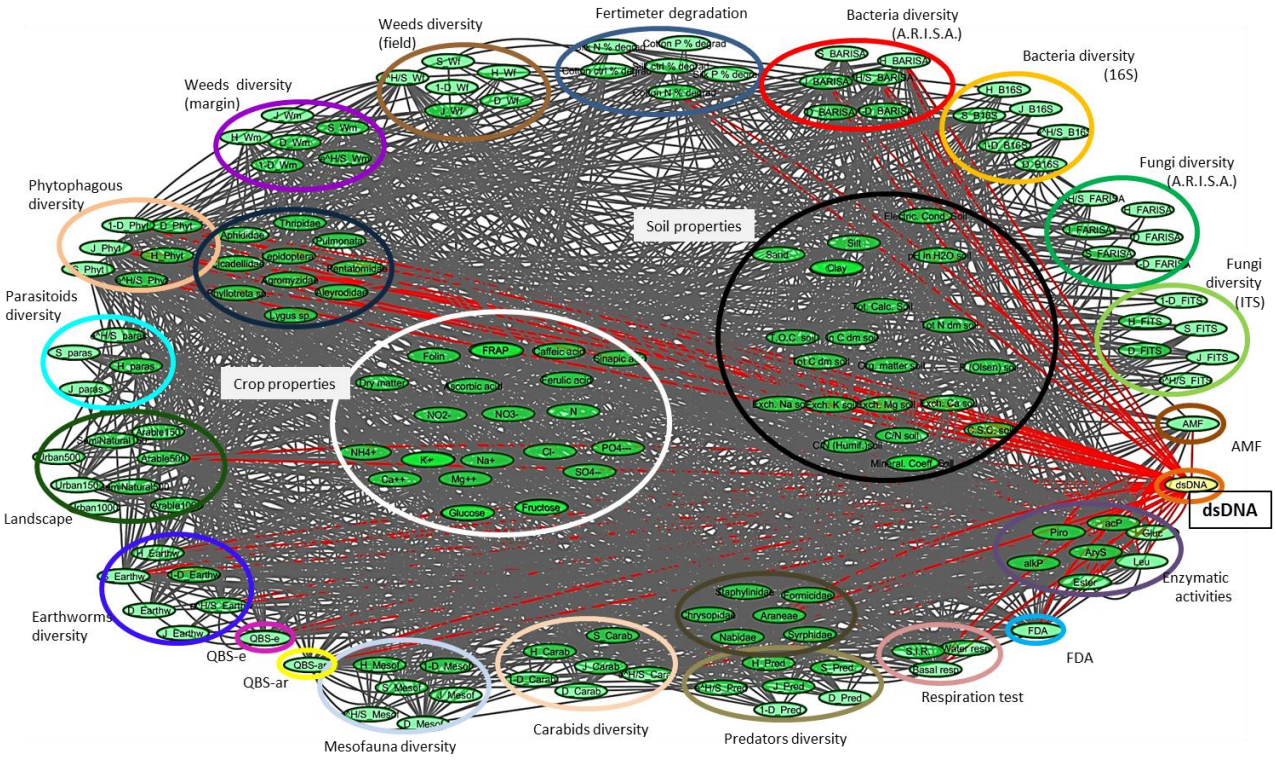


Fig. 85: Focus on the correlation relationships between dsDNA quantification into the soil and other indicators. All these relationships are significant with p value <0.05.

Double-stranded DNA quantification results to be associated, among others, with the trend of AMF presence, some key soil enzymatic activities, soil respiration rate, fertimeter degradation, but also with bacterial community analysed by A.R.I.S.A. technique. Given that dsDNA is a measure of microbial biomass (Sandaa et al., 1998; Gangneux et al., 2011; Cowie et al., 2013), Ekenler and Tabatabai (2003) demonstrated that most of the enzymatic activities were significantly and positively correlated with soil microbial biomass. Also in this study it emerges that dsDNA content is positively correlated with all soil enzymatic activities measured (AryS, AcP, AlkP, Leu, Gluc, Ester, Piro) (see tab. LXIV in the appendix). This fact is not surprising because microbial biomass is the most important source of soil enzymes. dsDNA content does not comprise only microbial contribution, but also plant contribution for a little part: Gangneux et al. (2011) found that plant dsDNA never exceed 2.6% of total dsDNA. The overall sum of plant, bacterial and fungal dsDNA represented 50% of total soil dsDNA (Gangneux et al., 2011); this means that the remaining 50% represents other important soil inhabitants, such as archaea, algae and protozoa. The big part of dsDNA due to bacteria can explain the correlations found in this work between the dsDNA quantification and bacterial community diversity indexes: the amount of dsDNA is probably composed mainly by a few

dominant bacterial phyla and so when bacterial community exhibits a higher diversity value with also less abundant phyla, the dsDNA decreases.

Key soil enzymatic activities

The following picture (fig. 86) regards the significant correlations found between quantitative data of seven key soil enzymatic activities and other indicators.

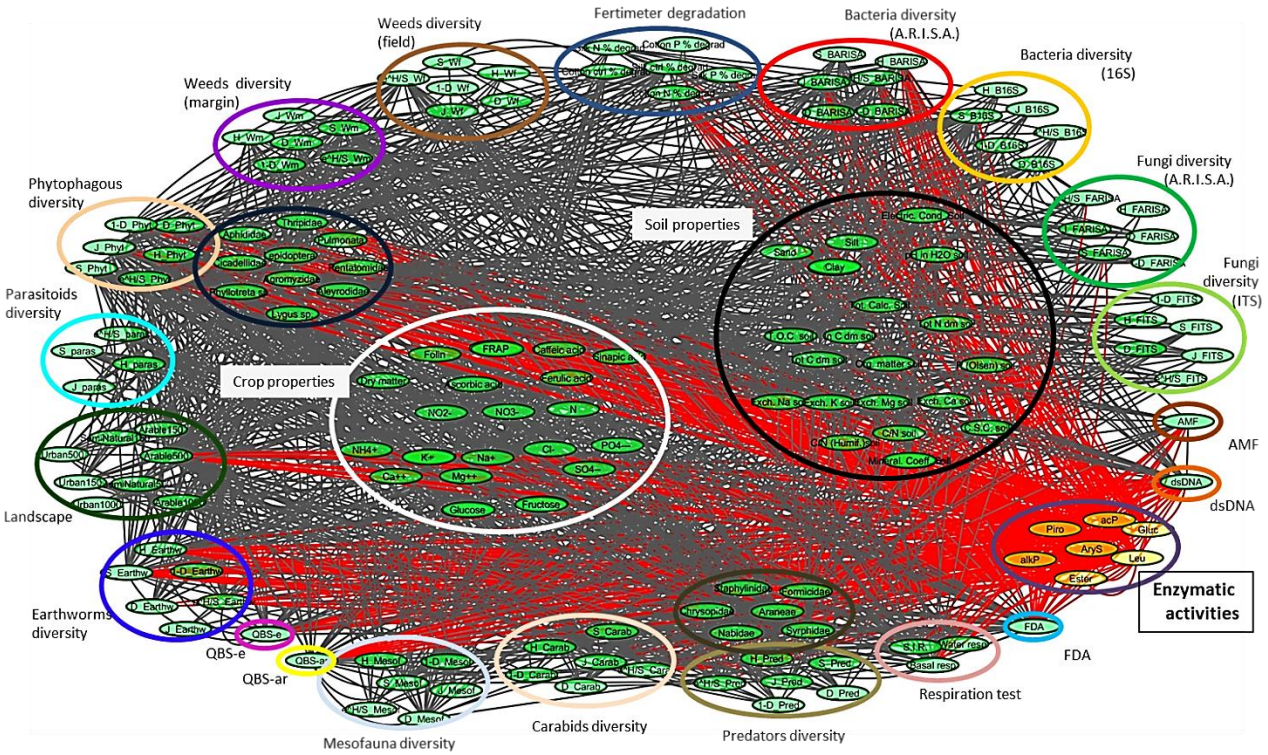


Fig. 86: Focus on the correlations relationships between some key soil enzymatic activities and other indicators. All these relationships are significant with p value <0.05.

The quantity of correlations between enzymatic activities and many different indicators is evident: for example FDA hydrolysis test, dsDNA content, AMF abundance, soil respiration rate, QBS-ar, QBS-e, earthworm community, phytophagous agent community, fertimeter degradation, bacterial community analysed by A.R.I.S.A. technique are noteworthy. Many confirmations of these results can be found in literature.

To characterize the overall situation and confirming the huge amount of correlations found in this work concerning enzymatic activities, Karaca et al. (2011) asserted in their review that soil enzymes are powerful tools applied in the assessment of short- or long-term changes in soil and especially in agroecological monitoring, agricultural practices such as OM applications, irrigation, fertilization and tillage change soil aggregation processes, nutrient recycling and also soil biological activities governing soil enzymatic production. Also others (Alkorta et al., 2003) showed that among the various biological indicators that have

been proposed to monitor soil health, soil enzyme activities have great potential to provide a unique integrative biological assessment of soil and the possibility of assessing the health of the soil biota, even though it is better to consider them in conjunction with other biological and physicochemical measurements. In fact these findings show how enzymatic activities are strictly related to many soil inhabitants, such as earthworms, mesofauna, bacteria, carabids, but also, perhaps less directly, with other agroecosystem inhabitants, such as phytophagous agents and predators. The connection between these two last indicators and soil enzymes can be explained by invoking the improvement of crop plant growth environment (with higher enzymatic activities), that makes the crop plant more resistant to pest attacks. Making a more detailed example, in this study several strong correlations were found between some diversity indexes of earthworm community (such as dominance, Shannon, Simpson indexes and number of taxa) and acetate-esterase activity (Ester). In general, earthworms accelerate the degradation of organic compounds, although the mechanism by which this is achieved is not entirely clear. However, it seems likely that this is a combination of increased aeration of the soil, stimulation of the microbial population, which in turn degrades the contaminants and metabolism of the contaminants by the earthworms themselves (Blouin et al., 2013). Since esterase activity was demonstrated to be involved in biodegradation of synthetic polymers (Sakai et al., 2002), maybe this can justify a positive interaction between earthworms and esterase activity found in this analysis.

FDA hydrolysis test

The following diagram (fig. 87) regards the significant correlations found between data of Fluorescein Diacetate hydrolysis test and other indicators.

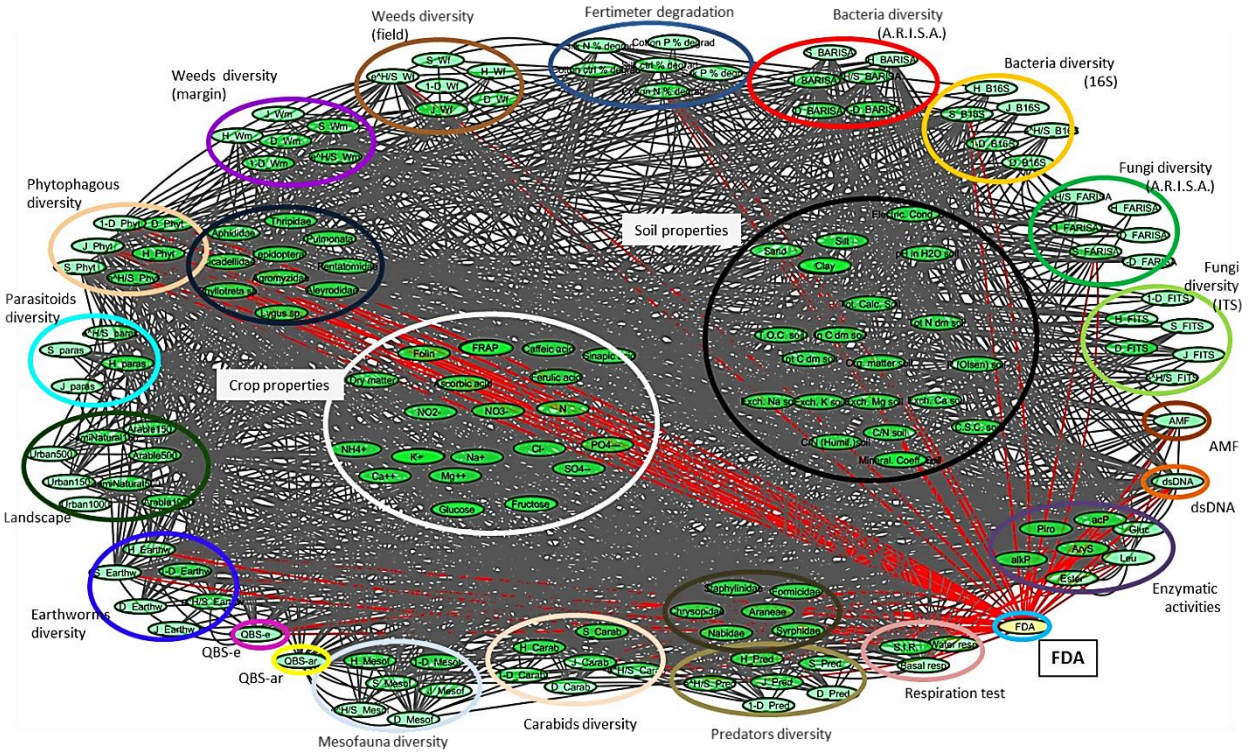


Fig. 87: Focus on the correlations relationships between fluorescein resulted from FDA hydrolysis and other indicators. All these relationships are significant with p value <0.05.

By performing FDA hydrolysis test it is possible to have information on the trends of AMF abundance, dsDNA content, some key soil enzymatic activities, fungal community analysed by A.R.I.S.A. technique, bacterial community analysed by 16S sequencing, fertimeter degradation percentage, the evenness of weed community into the field, phytophagous communities and earthworm communities. Some researchers (Schnurer and Rosswall, 1982) demonstrated that FDA hydrolysis could be used as an overall indicator of microbial activity and it was correlated with microbial respiration: significant positive correlations between FDA hydrolysis test and two of the three soil respiration tests (the dry basal one and S.I.R.) found in this work, confirm it. Other studies (Das and Varma, 2011) underlined the correlation between soil enzymatic activities and microbial one (such as FDA hydrolytic activities). With greater detail, these results show that there are positive strong correlations between FDA hydrolysis test and the enzymatic activities of β-glucosidase, arylsulfatase, leucine aminopeptidase and acid phosphomonoesterase. Generally Dick (1997) affirmed that the FDA test was a simple, non-specific, but sensitive technique that can be used to estimate relative levels of microbial activity in soils, and it was recommended as a useful parameter for a rapid assessment of soil quality.

Soil respiration tests

The following image (fig. 88) regards the significant correlations found between data of soil respiration rate and other indicators.

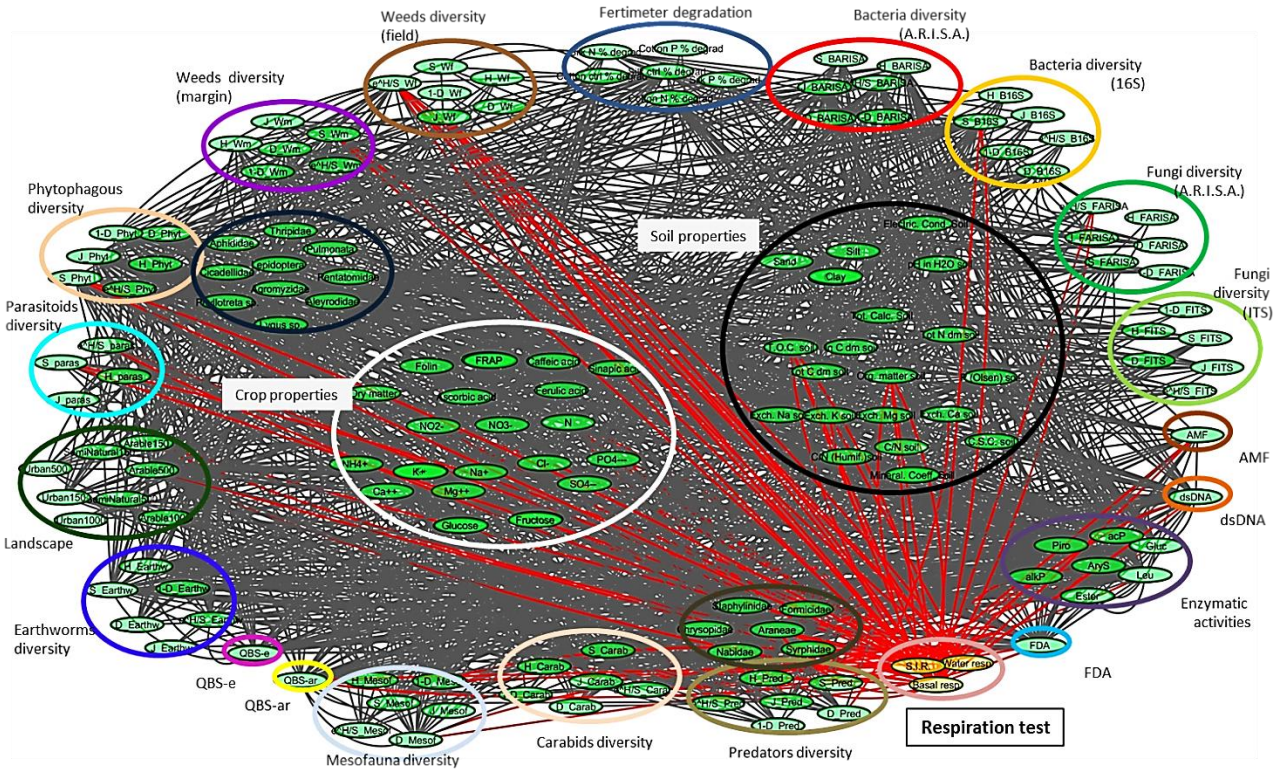


Fig. 88: Focus on the correlations relationships between soil respiration rate and other indicators. All these relationships are significant with p value <0.05.

The soil respiration rate is strictly linked with FDA hydrolysis test, dsDNA content, AMF abundance, soil OM percentage, total organic carbon percentage into the soil, the evenness of fungal community analysed by A.R.I.S.A., the number of bacterial taxa analysed by 16S sequencing, weed community into the field, phytophagous agent, parasitoid and mesofauna communities. CO_2 production is equivalent to evaluate total microbial activity, that is to say microbial capacity of soil OM decomposition, in fact some authors (Komilis et al., 2011) used the respiration assay compared with the FDA hydrolysis assay to assess compost stability and maturity. Also in this work strong positive correlations were found between dry basal and S.I.R. respiration tests and soil OM and T.O.C. quantity.

CO_2 results from several sources, not only microbial but also from plant root and faunal respiration. During OM decomposition, organic nutrients contained in OM (organic P, N and S) are converted to inorganic forms that are available for plant uptake. This conversion is known as mineralization and soil respiration is also known as carbon mineralization. This indicator reflects the capacity of soil to support soil life including crops, soil animals and microorganisms (Parkin et al., 1996). In fact in this thesis several correlations were found between this overall indicator and many others soil actors, such as bacteria, fungi, weeds, mesofauna, carabids and phytophagous agents.

Stated that production of CO_2 measured in situ is a measure of soil heterotrophic activity and root respiration and it forms a pathway of C loss from soil, with an across-Europe study de Vries et al. (2013) demonstrated that production of CO_2 was greatest in the permanent grassland, which is consistent with these soils having the greatest C content. Moreover these authors underlined how production of CO_2 was also positively related to the biomass of earthworms, which were most abundant in the permanent grassland. Several field-based experiments showed significant impacts of earthworms on C and N cycling, but evidence for impacts of earthworms on respiration in the field is still scarce (de Vries et al., 2013). Despite this last cited study, also in this work no evidence was found of correlation between earthworms and soil respiration rate.

Predator community

The following picture (fig. 89) regards the significant correlations found between data of predator community and other indicators.

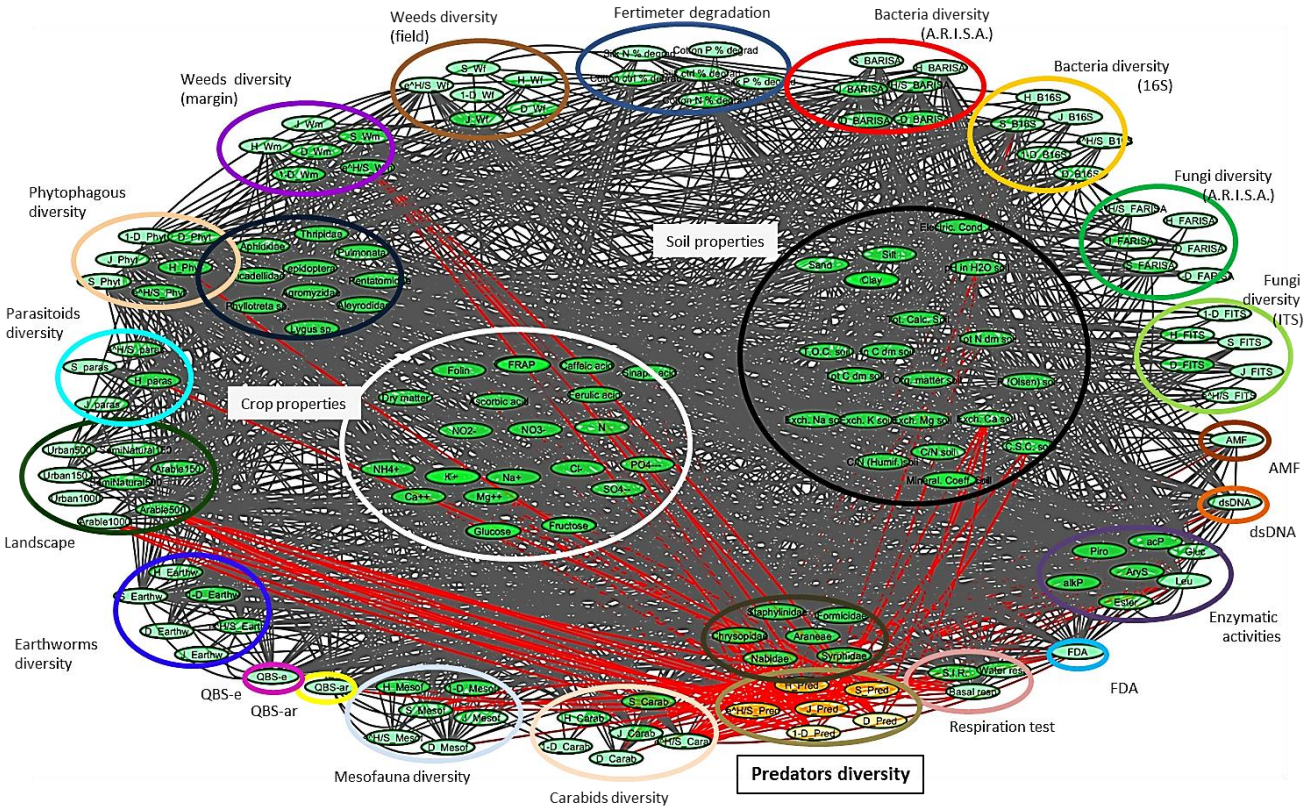


Fig. 89: Focus on the correlations relationships between predator community diversity indexes and other indicators. All these relationships are significant with p value <0.05.

Among other considerations it is noteworthy to notice how predator community is correlated with some soil properties, with weed community composition in the field margin, with phytophagous agent and parasitoid community and also with the landscape structure. A first simple and direct consideration can be

on the strong and positive correlation between the taxa diversity of predators and the diversity in phytophagous agent community: it is comprehensible how more different preys can sustain a higher diversity of predators. Burgio et al. (2006) showed the key role of ecological infrastructures like hedgerows within rural landscape in northern Italy, demonstrating that age and maturity of the hedgerows appear to influence the abundance and distribution of predator families in the adjacent grassy margins. Also in this study several strong correlations were found between predator community and weed community in the grassy margin, but it seems that a more diverse predator community corresponds to a less diverse weed community. Possibly this is due to the presence of some dominant phytophagous that prefer just some key species of weeds and that can sustain a more various generalist predator community. Moreover these authors considered also the shrubby and arboreal species forming the hedgerows as well as the age, while in this work only the diversity of grassy weed community in the field margin was considered. Concerning the relationships between the predator community and the landscape structure in this study several strong correlations were found between arable land use percentage and the composition of predator community. There is a recurrent tendency: if arable land use increases in the surroundings of the field, the predator community tends to be dominated by few generalist species. The 2012 was a year with a very dry weather (fig. 28) and this drought was the cause of some agronomic phenomena, such as a general and widespread death of corn before harvest. This fact caused a forced migration of corn pests, such as for example *Ostrinia nubilalis* on other crops to complete their life cycle and this interested also Treviso red chicory studied in this research[21]. Therefore it is possible to interpret this phenomenon because generalist predators could follow the migration of crop pests from one crop field to another, but specialist predators (which make predator community more diverse) need the availability of particular preys and maybe of a more complex landscape with a higher presence of seminatural areas. In fact generally in literature it is demonstrated that in agroecosystems the diversity and abundance of natural enemies that provides biological control in crop fields are influenced in a positive way by the structure and composition of the surrounding landscape (Marino and Landis, 1996; Thies et al., 2003; Tscharntke et al., 2005; Gardiner et al., 2009). Another important consideration regards intraguild competition between predator community and carabid community and between predator community and parasitoid community that emerges from this study. If the dominance of carabid community increases, the evenness of predator community decreases. It can be due to the fact that among carabids predator (zoophagous) species were found but also spermophagous species (tab.XL) and therefore if the formers dominate, also enter in competition with other generalist predators for space and prey-resources. Obviously crop pest-prey abundance is enhanced when intraguild predation (IGP) between predator and predator occurs and this can decrease crop pest biological control (Rosenheim et al., 1995; Muller and Brodeur, 2002), but the reality of these interactions seems to be so complex that relatively few natural predator-prey systems exhibit the rigid specialization assumed in the predator-prey IGP model (Borer et al., 2007). On the other hand, if the number of predators taxa increases, the Shannon's index of parasitoid community decreases. This can be explained because an increasing variety of predators can prey a higher number of crop pests and these are not available anymore as food resource for parasitoid life cycle fulfilment. This phenomenon is explained also in literature. In fact at this purpose Rosenheim et al. (1995) recognized two types of IGP: first, predators may prey directly on parasitoids, feeding either on immature stages developing externally on the host or on free-living parasitoid

[21] Squizzato Angelo (2012) "Radicchi "stressati" dal caldo e dall'esplosione di parassiti" Ortogiornale www.ortoveneto.it (http://www.ortoveneto.it/index.php?pagename=ConsumatoriNews&categoryId=9&docId=770)

adults (and only when the predator also attacks the host of the parasitoid can be defined as IGP), and second, predators may prey on parasitized hosts, consuming both the host and indirectly an associated immature parasitoid.

Carabid community

The following image (fig. 90) regards the significant correlations found between data of carabid community and other indicators.

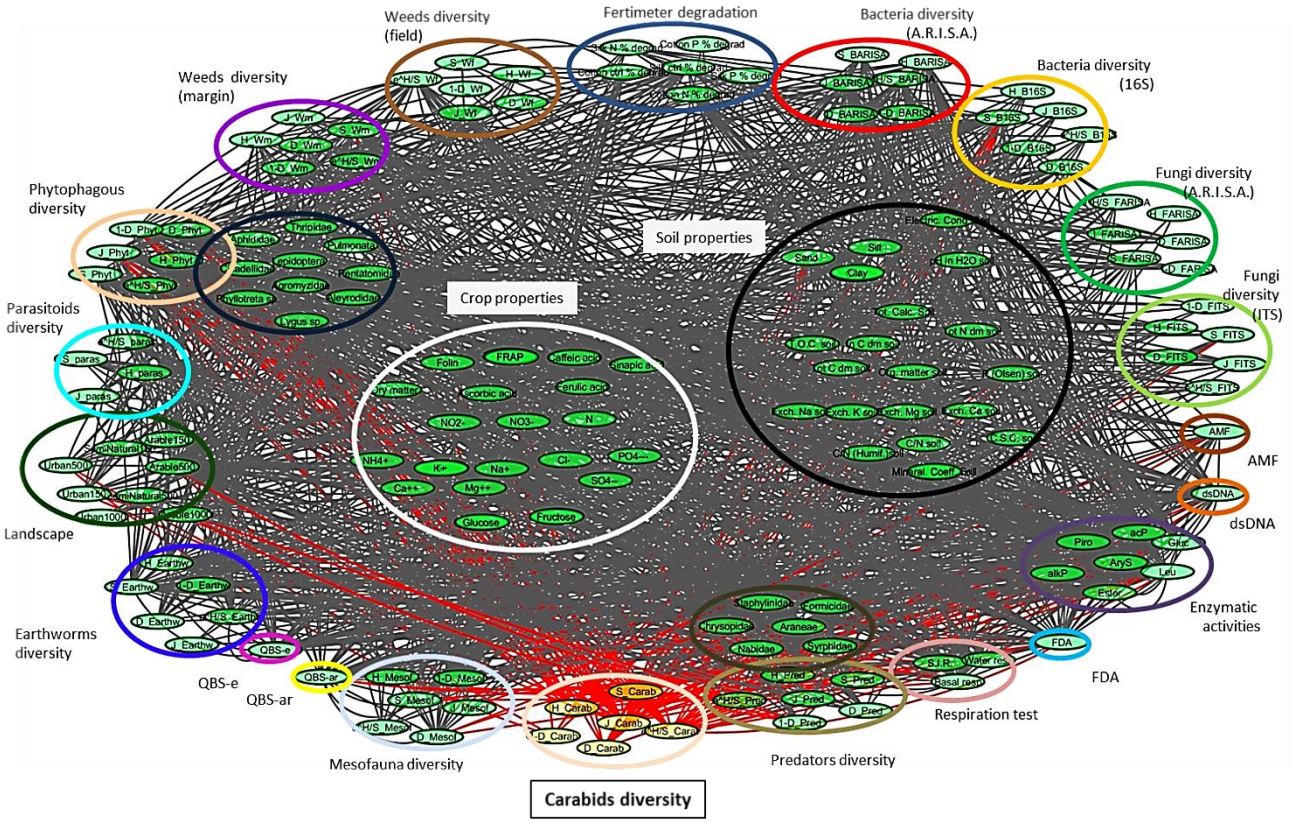


Fig. 90: Focus on the correlations relationships between carabid community diversity indexes and other indicators. All these relationships are significant with p value <0.05.

Some interesting correlations concerning carabids are regards phytophagous agent, weed communities and landscape structure. In detail a more diverse phytophagous agent community seems to sustain a more diverse carabid community and this can be logically interpreted considering that most carabids are polyphagous and they have been implicated as the predators of many pests, including aphids, lepidopteran larvae and slugs (Lovei and Sunderland, 1996; Kromp, 1999; Gongalsky and Cividanes, 2008) and this can justify the key role of carabids in agroecosystem biological control. This important role was underlined by several lines of research, one of which (Menalled et al., 1999) demonstrated that in annual crops generalist natural enemies like carabids have the potential to maintain a variety of pests below outbreak levels. Also Clark et al. (1994) found that the most common potential predators in corn fields included carabids.

Another concern is on the relationships between the increase in number of weed taxa in the field margin and the decrease in dominance in the carabid community. In some studies (Kromp, 1999) it was reported that boundary strips, like weed strips, generally enhance total carabid diversity and in certain species also population densities in cultivated land. Ranjha and Irmler (2014) by studying the process of colonization of carabids from field margins to crop fields under organic management found that grassy strips do not affect the dispersal of typical arable field species, but the species that prefer grass vegetation can only bypass the barriers of arable fields by grassy strips. Results in this work can be interpreted since if the weed species variety is higher, it is more probable to have also a more diverse carabid community (with decreased dominance) due to dispersion facility. Another implication of this correlation can be that some carabids are primarily seed feeders (Rainio and Niemela, 2003; Gongalsky and Cividanes, 2008) and so they can have a control on weed community composition.

The other important consideration is on the link between carabids and landscape structure. Some strong correlations were found with urban and arable land use and in particular negative with the former and positive with the latter. In literature it is possible to find many evidences of these relationships. Some studies (Fournier and Loreau, 2001) found that carabid faunas in forest patch remnants differed weakly from those found in hedges and crops and it was concluded that small forest remnants do not behave as "climax" habitats in intensive agricultural landscape, maybe because of their small size and strong isolation. While recent hedges appear to have a key role for the maintenance of carabid diversity. Gobbi and Fontaneto (2008), by analysing a database of carabid communities collected in representative habitats of Po lowland, demonstrated how residual patches of lowland wood host poor species communities, but stenoecious (with restricted ecological requirements). Also fields in this study are inserted in an intensive agricultural landscape and no strong correlations between carabids and seminatural land use percentage were found, which can be explained with these references.

Mesofauna community

The following picture (fig. 91) regards the significant correlations found between data of mesofauna community and other indicators.

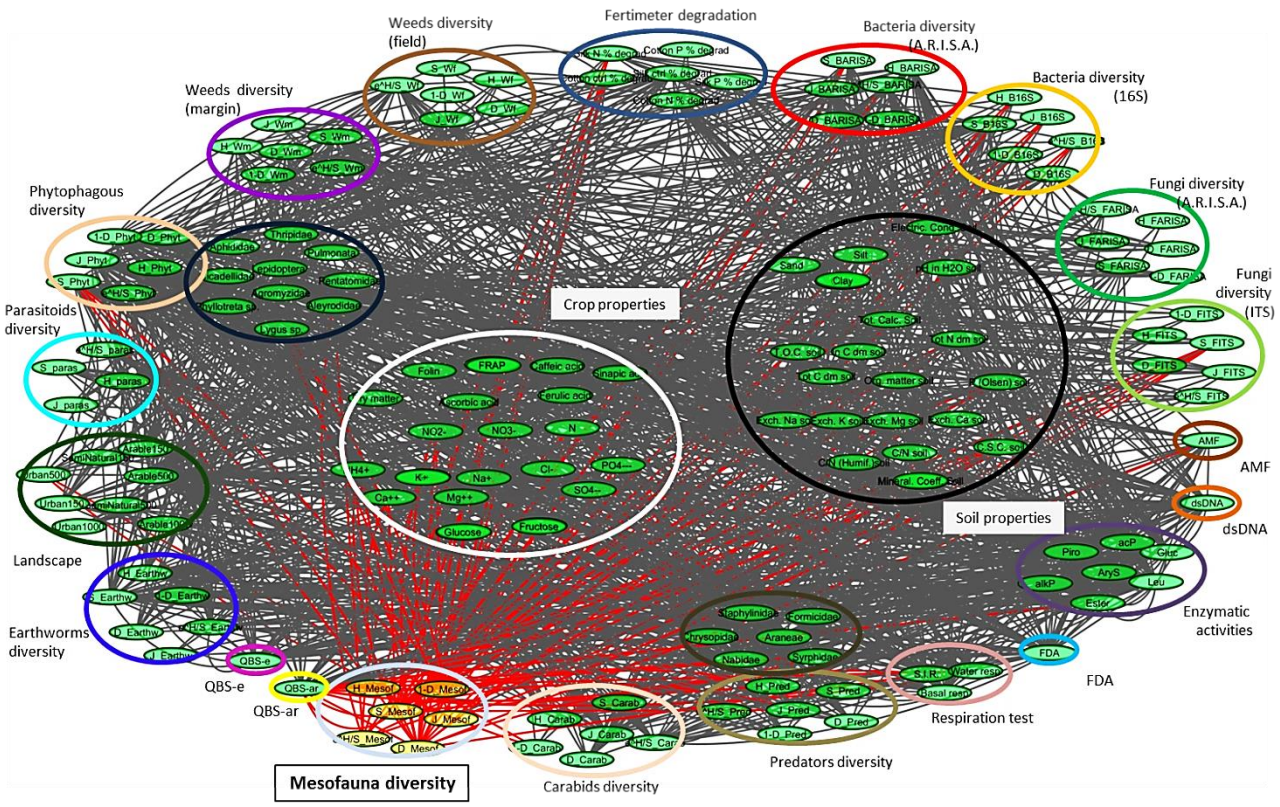


Fig. 91: Focus on the correlations relationships between mesofauna community diversity indexes and other indicators. All these relationships are significant with p value <0.05.

Among others, mesofauna community composition resulted to be linked to bacterial, fungal and predator communities but also to soil respiration rate. Considering the first correlations it is possible to reconstruct a simple agroecosystem food web. In fact soil fungal and bacterial diversity can sustain a wide range of mesofauna taxa, fungivorous and bacterivorous species (de Vries et al., 2013), meanwhile in turn mesofauna diversity can be a valid food source to sustain generalist predator community. Evidences in literature about the polyhedric role of mesofauna into the soil food web were presented (Behan-Pelletier, 1999; Gulvik, 2007). Moreover Renker et al. (2005) demonstrated that mites can disperse microorganisms such as fungal propagules on their body and they affect growth and species composition of fungi by selective grazing (Schneider et al., 2005), so contributing to determine the distribution pattern of microbial communities.

The positive correlation found here between soil respiration rate and mesofauna community diversity probably can be explained with the key role of mesofauna in OM decomposition (Gulvik, 2007) and this action is fundamental for OM mineralisation that can be measured with respiration rate (Parkin et al., 1996).

QBS-ar

The following picture (fig. 92) regards the significant correlations found between data of QBS-ar index based on arthropods and other indicators.

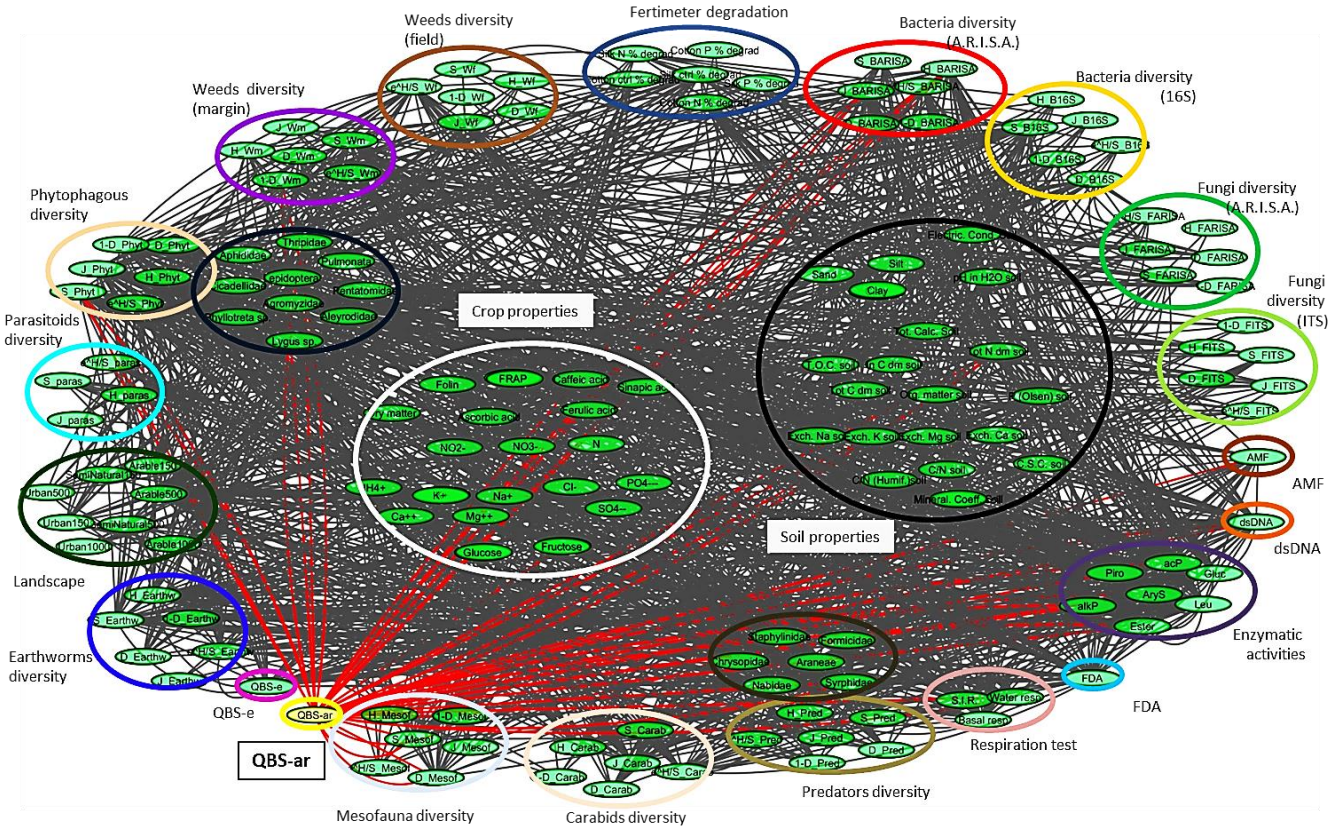


Fig. 92: Focus on the correlations relationships between QBS-ar index value and other indicators. All these relationships are significant with p value <0.05.

Looking at this representation (in comparison to the previous one about mesofauna community) it is remarkable how the use of an overall index in the study of biodiversity implies some consequences.

Among the advantages, the more practical use with no need of taxonomic expertise about each involved group must be considered, but among the disadvantages there is the tendency to simplify a complex reality unavoidably loosing details: it is a balance between costs and benefits.

Despite this consideration, the soil biological quality index based on arthropods resulted to be associated to weed community composition in the field margin, bacterial communities (analysed by the A.R.I.S.A. technique) and also to some soil properties, such as AMF abundance, dsDNA content, soil respiration rate and some key soil enzymatic activities.

Earthworm community

The following image (fig. 93) concerns the significant correlations found between data of earthworm community and other indicators.

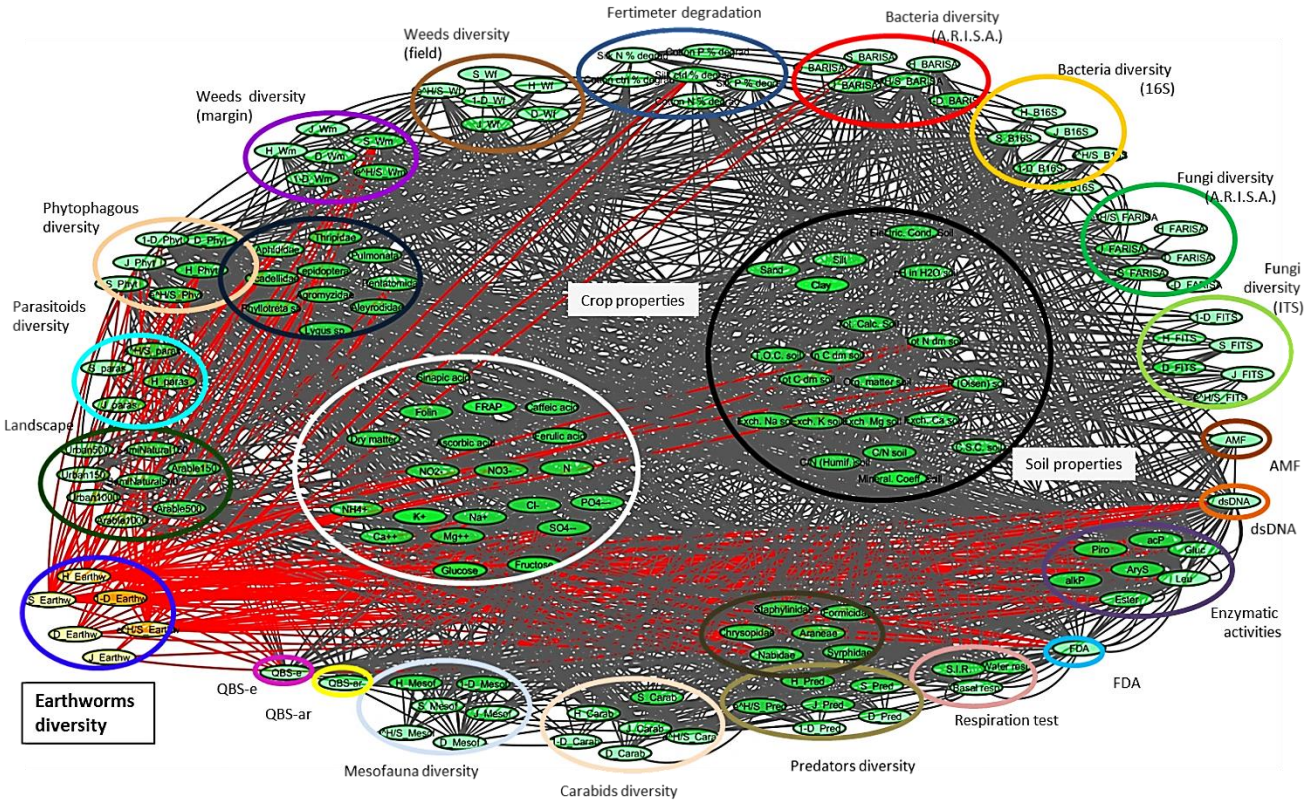


Fig. 93: Focus on the correlations relationships between earthworm community diversity indexes and other indicators. All these relationships are significant with p value <0.05.

Earthworm community composition is correlated mainly with dsDNA content, FDA hydrolysis, some key soil enzymatic activities and some soil properties. In particular it was suggested that earthworms increase P availability in their casts (Le Bayon and Milliret, 2009; van Groeningen, et al., 2014), in fact in this work a strong positive correlation between Shannon's index of earthworm community and the amount of P available for plant growth was found (analysed by the Olsen method). Moreover at community level, the ecological categories of earthworms appear to be predominant in the soil P transformation and storage (Le Bayon and Milliret, 2009). For this purpose, some studies (Coulis et al., 2014) recognised the key role of endogeic earthworms (the most abundant ones also in this research) in reducing the competition for nutrients (soil phosphorus) in plant-plant interactions. Also Zaller et al. (2013), with a mesocosm experiment, demonstrated that earthworms, with their big amount of cast production that enriches in nutrients the soil, can create a heterogeneity which plays a role in structuring plant communities. This can be linked to other correlations found in this analysis, such as for example between the increase in diversity of earthworm community and the increase in diversity of weed community. As concerning strong and positive correlations found between a more diverse earthworm community and higher enzymatic activities, these confirm evidences in literature according to which earthworms accelerate organic compounds degradation, having a stimulating effect on nutrient turnover by increasing the available surface area of OM through comminution (Blouin et al., 2013). In greater detail Tao et al. (2009) demonstrated that the presence of earthworms significantly increased alkaline phosphatase activity in agroecosystems with

rotation (also found in these results), and moreover all enzymatic activities studied by these authors in earthworm casts were significantly higher than those in the surrounding soil. So the overall presence of earthworms strongly affected soil enzymatic activities and the enhanced enzymatic activities of casts probably acted as a trigger and contributed to the surrounding soil enzyme activities.

QBS-e

The following diagram (fig. 94) regards the significant correlations found between data of QBS-e index based on earthworms and other indicators.

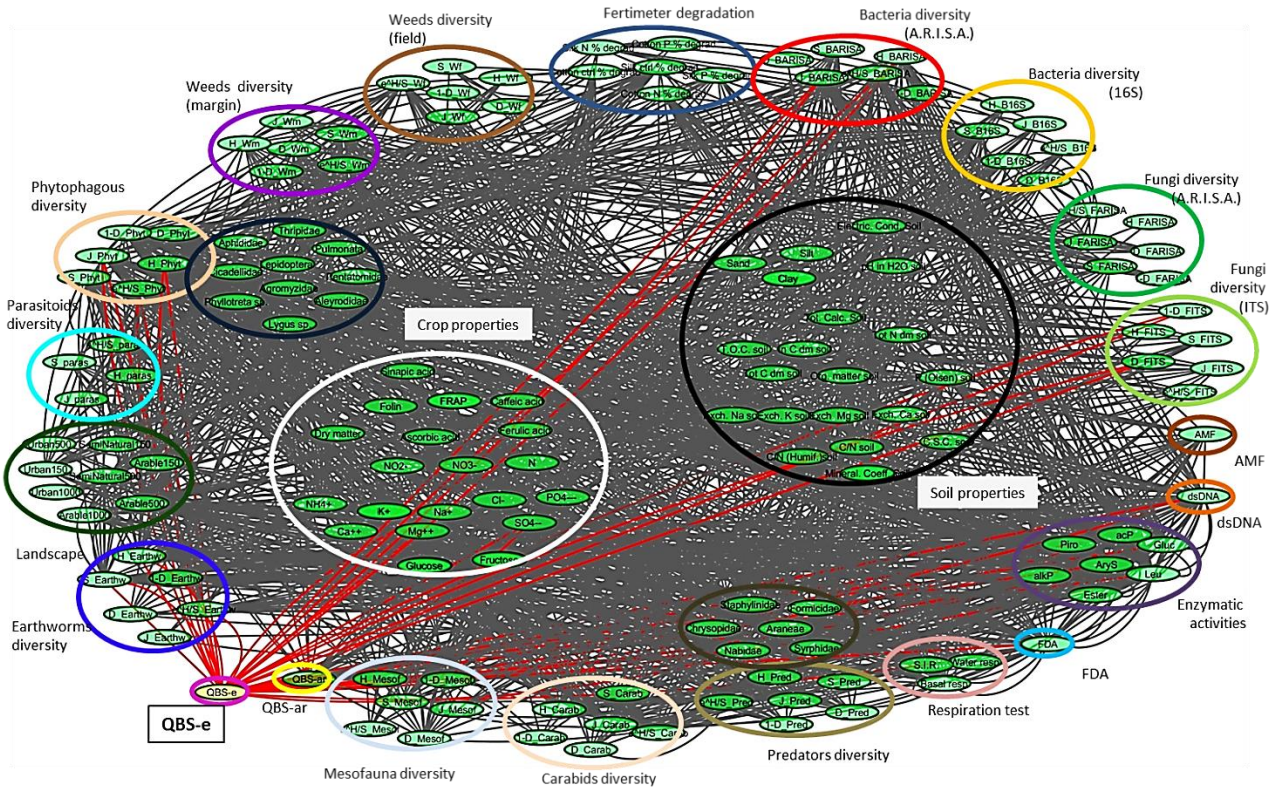


Fig. 94: Focus on the correlations relationships between QBS-e index value and other indicators. All these relationships are significant with p value <0.05.

Being valid the same consideration made for QBS-ar index upon the advantages and disadvantages that arise by using indexes instead of making a complete survey of each taxonomic unit of the chosen bioindicator (see above), it is remarkable that with the application of QBS-e index some new strong correlations emerged between the value of this index and soil fungal community, which had not arisen just from the analysis of the earthworm community (fig. 93). In particular high values of QBS-e index, which represent a good presence and abundance of earthworms, are correlated to a fungal community dominated by some fungal strains. On this respect, results obtained by Zaller et al. (2013) suggested that

subsurface casts provide microsites from which for example root AMF colonization can start, therefore it appears that physiological activity of earthworms affects also fungal community.

Parasitoid community

The following image (fig. 95) regards the significant correlations found between data of parasitoid community and other indicators.

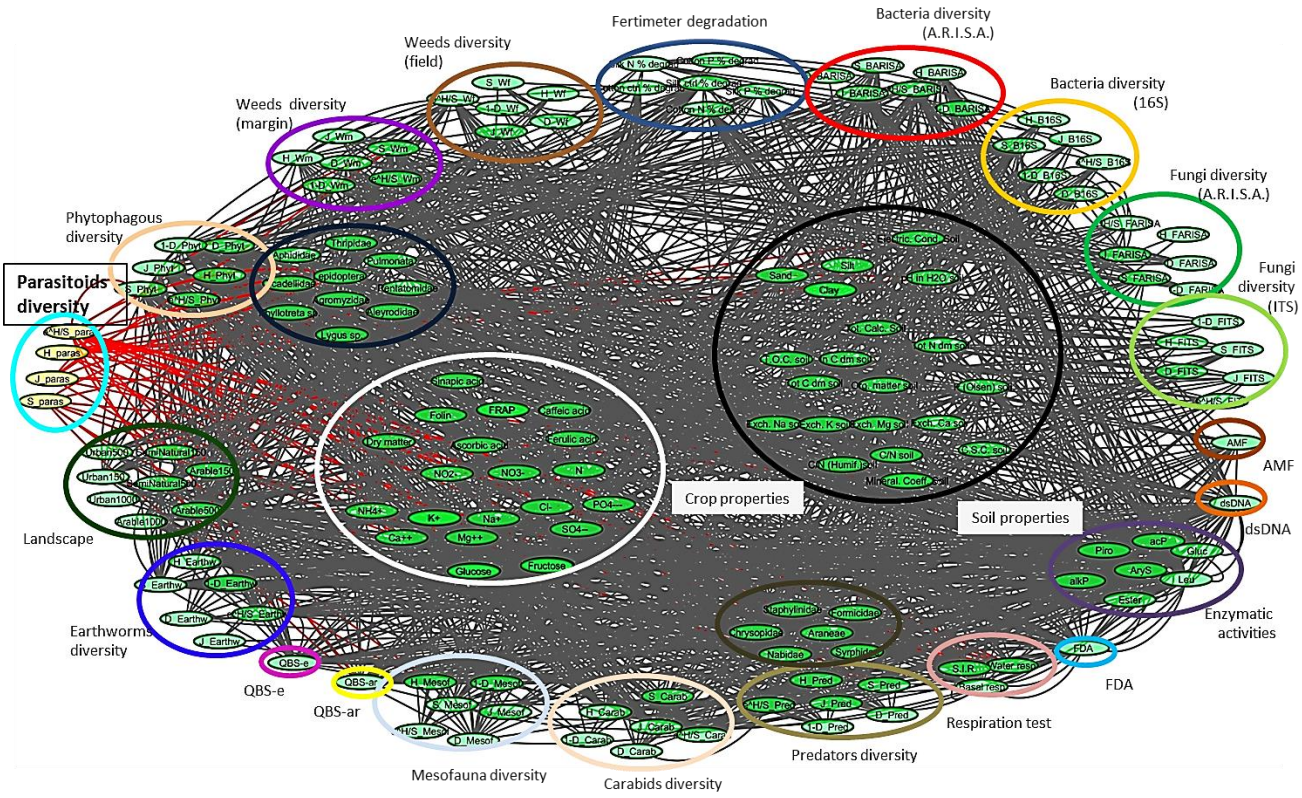


Fig. 95: Focus on the correlations relationships between parasitoid community diversity indexes and other indicators. All these relationships are significant with p value <0.05.

Among all correlations found that interest parasitoid community, some of them are remarkable. For example, a strong and positive correlation was found between the increase in taxa of phytophagous community and the increase of evenness of parasitoid community. It is easy to explain because a wide variety of preys can enhance the biodiversity of parasitoid community, due to a higher probability to complete their lifecycle, since many parasitoids can develop in many different hosts. In the section of this thesis dedicated to parasitoid overview it is clear that a more diverse community of phytophagous agents was able to sustain also a more diverse parasitoid community in organic agroecosystem (fig. 58 and tab. XLIII). Another concern is upon the positive correlation found between the number of taxa of weeds in the field margin and the equitability of parasitoid community. From literature it is known that parasitoids (and other natural enemies) need alternative food sources like pollen, nectar, alternative preys when the ones on the crop are not available (post-harvest) and shelters for overwintering (Landis et al., 2000; Vollhardt et

al., 2010; Géneau et al., 2012; Balzan et al., 2014). Therefore with the increase in the biodiversity in the grassy margin, it is more probable that there are resources to sustain a more diverse parasitoid community. Also other studies (Tscharntke et al., 2007) underlined that many species of natural enemies benefit from frequent movement between crop and non-crop habitats, even within a generation or growing season. For example, parasitoids (Hymenopteran but also Diptera, such as Tachinidae) and hoverflies require herbivorous insects as hosts for their larvae, but feeding on floral resources as adults increases their longevity and potential fecundity (Tooker et al., 2006). These correlations that tie weeds, phytophagous agents and parasitoids can overall represent the tritrophic interaction among plants, herbivores as host and parasitoids like their natural enemies (Buchori et al., 2008).

About parasitoid community and landscape structure there are many evidences in literature (Gardiner et al., 2009; Tscharntke et al., 2007). Boccaccio and Petacchi (2009) found significant effects of landscape on parasitization rates: connectivity at a large scale (landscape configuration) may favour parasitoids more than the abundance of woodland and semi-natural areas (landscape composition). Inclan et al. (2014) with a study about tachinids, one of the most diverse and abundant groups of non-hymenopteran parasitoids, found that abundance and species richness were negatively affected by habitat loss in highly fragmented landscapes, but the effect was less evident in landscapes with relatively high habitat connectivity. From these references it seems that the most important factor is not landscape structure (results in this thesis highlight strong correlations between parasitoid community and the percentage of arable land use in the surroundings of the field), but landscape configuration or habitat connectivity, that was not considered in this work (the arrangement and connection among hedgerows for example).

Another important consideration is that hymenopteran parasitoids, among the most common parasitoids agents found also in this study, are potential bioindicators that provide a useful means to assess the wider biodiversity of arthropod populations in agroecosystems (Anderson et al., 2011). In fact these authors found that both abundance and taxon richness of hymenopteran parasitoids had stronger relationships with overall arthropod taxon richness than any other arthropod group they investigated (Anderson et al., 2011). In this respect, also in the present study correlations were found between parasitoid community and soil mesofauna and abundance of some predator groups.

Phytophagous agent community

The following diagram (fig. 96) regards the significant correlations found between data of phytophagous agent community and other indicators.

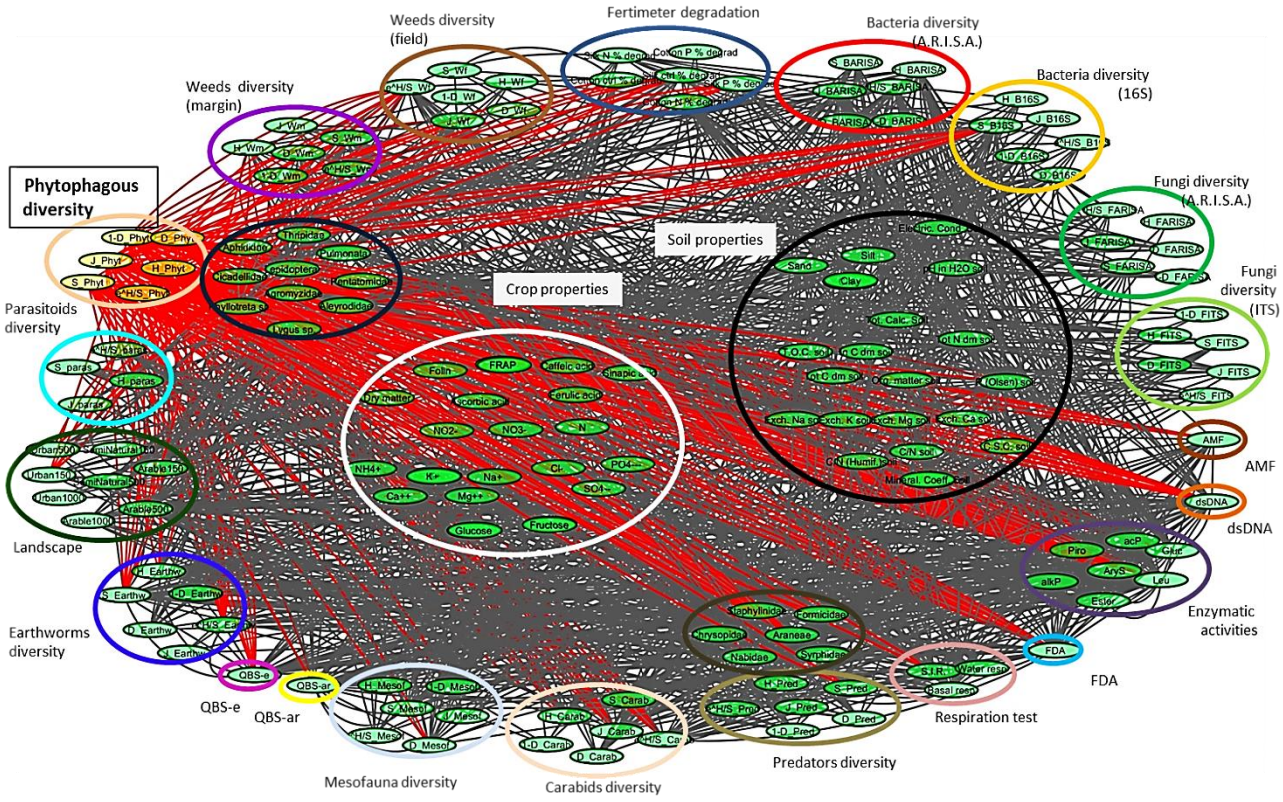


Fig. 96: Focus on the correlations relationships between phytophagous agent community diversity indexes and other indicators. All these relationships are significant with p value <0.05.

Probably of more direct interpretation are some of the many correlations found here between phytophagous agent community and, for example, weed community in the crop field area. At the increasing in diversity of the weed community corresponds a decreasing in diversity of the herbivore community. This fact can be due to the presence of non-selective herbivores that can consume a wide variety of plant species (polyphagous) and can cause severe damage to crop production in case of their outbreaks, while they can survive eating weeds when the crop species is not available anymore (post-harvest) (Winkler et al., 2009; Géneau et al., 2012). For this reason, to improve the effectiveness of agroecosystem management, Géneau et al. (2012) moreover stressed the importance of plant screening to achieve plant selectivity in order to maximize biological control and not to enhance the fitness of the crop pests.

Phytophagous community is also linked to several soil indicators such as AMF abundance, FDA hydrolysis, dsDNA content, enzymatic activities, respiration rate and fertimeter degradation percentage. Considering almost all of these indicators there is a positive correlation with a more diverse phytophagous community, while the correlation becomes negative if it refers to dominance index of phytophagous community. This could mean that if there are good soil conditions in terms of fertility, respiration rate, enzymatic activities, AMF colonization, these have effect on the crop plant and affect indirectly also crop pest community. Altieri and Nicholls (2003) discussed about the potential links between soil fertility and crop protection and suggested that plant resistance is linked directly to the physiology of the plant and thus any factor that affects the physiology of the plant may lead to changes in resistance to crop pests. These considerations

mean that by measuring the functional indicators found to be linked to crop pest community, it is possible to have information about the potential crop resistance or tolerance to pests.
Continuing with the considerations on agroecosystem trophic web, several strong correlations between phytophagous community and carabid community are noteworthy, because being carabids generalist predators (polyphagous natural enemies) (Sunderland, 1975; Sunderland et al., 1987), they take advantage from a more diverse phytophagous community.

Weed community in grassy field margin

The following image (fig. 97) concerns the significant correlations found between data of weed community in grassy field margin and other indicators.

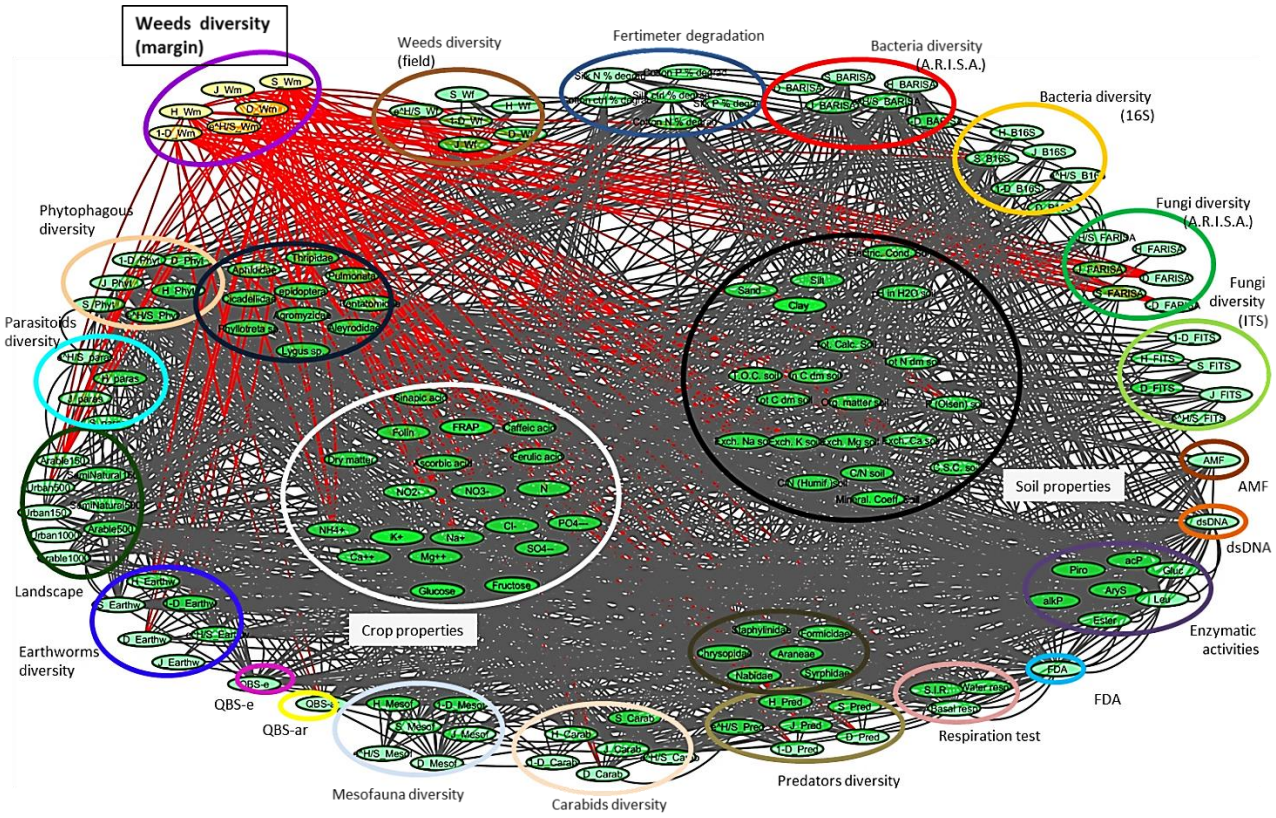


Fig. 97: Focus on the correlations relationships between weed community in the field margin diversity indexes and other indicators. All these relationships are significant with p value <0.05.

An interesting note that can be done regards the relationships between weed community in the margin and weed community in the crop field area: if weed diversity increases in the grassy margin, it decreases in the crop field area (the latter is characterized by the dominance of just few species). The situation on the margin reflects more the real situation of the soil affected by less management practices (just few mowings

per year) with respect to the crop field area interested by ploughing, rotary tillage and many other mechanical practices (see tabb. LV and LVI in the appendix). In this respect, see again fig. 69 comparing the difference in weed community according to Ducerf's method. In practice contextualizing this concern, having more species in the grassy margin is the starting point for the colonization also of the crop field area, but here the environment is not so suitable for all species due to hard human impact and only few ones can prosper (the most ruderal and opportunist). Being the grassy margin less disturbed, it can have more durable relationships with fungal community, like the ones found in this analysis, since it was demonstrated that for example AMF communities can be shaped by tillage practices as well as by N-fertilization (Avio et al., 2013). In this respect, it is interesting to notice that there are no relationships between weed community in the crop field and fungal community (fig. 98). Another concern is on correlations between the increase in diversity of weed community and the decrease in abundance of some crop pests, such as for example lepidoptera. This tendency is confirmed by Cardinale et al. (2012) which affirmed that plant diversity is often negatively associated with the abundance of herbivorous pests. This phenomenon can be interpreted as the base of agronomic principle according to which monoculture (with zero plant diversity) can encourage the outbreaks of one or few crop pests. Another interesting correlation concerns the increasing abundance of spiders (the most abundant generalist group found in the present work tabb. XLI and XLII) associated to the increasing taxa diversity in weedy margins. In this respect Nentwig (1998) found that a tall and diverse vegetation with sufficient interspaces was likely to enhance the presence of most web-building spiders, and these findings could explain also the correlation found in the present work.

Weed community in the crop field area

The following diagram (fig. 98) regards the significant correlations found between data of weed community in the area of crop field and other indicators.

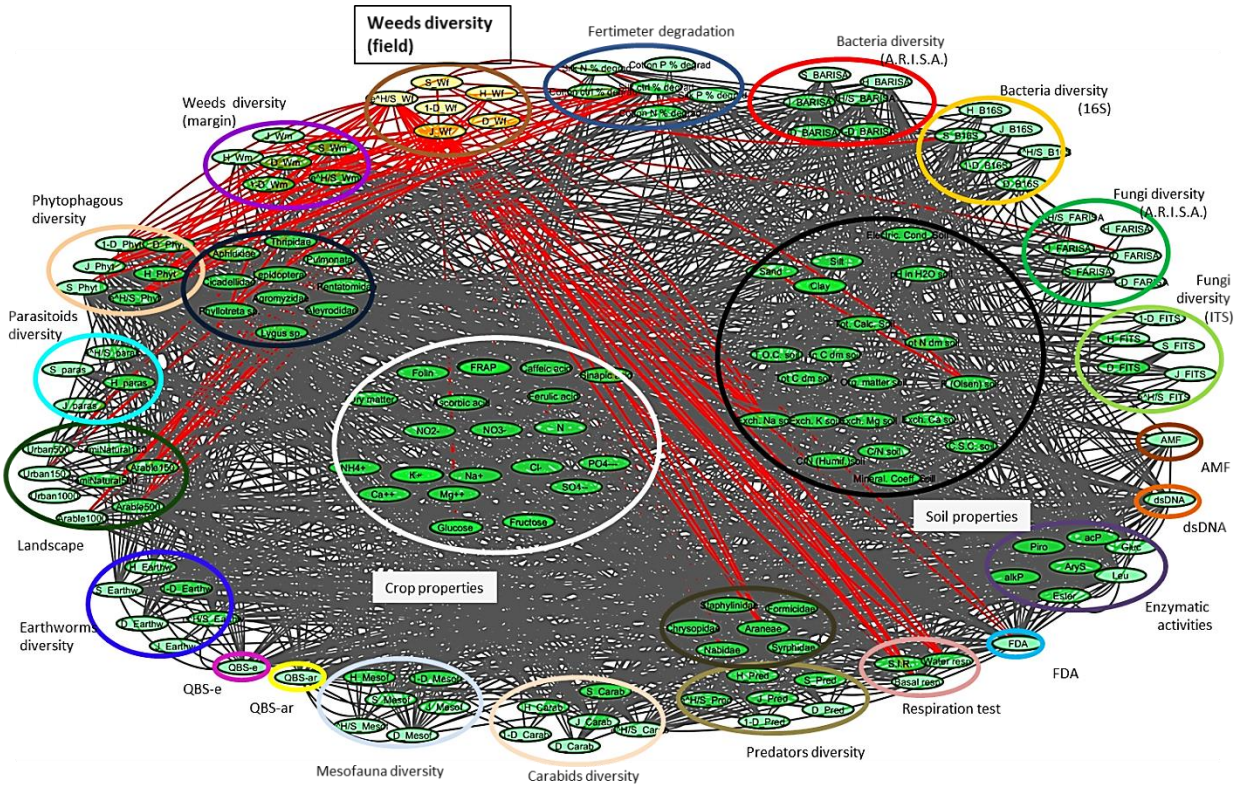


Fig. 98: Focus on the correlations relationships between weed community in the crop field diversity indexes and other indicators. All these relationships are significant with p value <0.05.

A consideration that can be done concerns the correlations found between weed community in the crop field area and the landscape structure, in particular between the decreasing in weed biodiversity at the increasing of percentage of the arable land use in the surrounding of the field. Some evidences of this phenomenon were studied by others (Gonzalez-Moreno et al., 2013) which demonstrated that the most opportunist or alien species richness was more affected by the surrounding landscape. Roschewitz et al. (2005) verified that increasing landscape complexity was positively associated with weed species diversity more strongly in the vegetation of conventional than organic fields, to the extent that diversity was similar in both farming systems when the landscape was complex. In the case of this research, arable land use, which is associated to simple landscape, can select and promote the opportunist and ruderal species that in this way can spread also in the surroundings and become the dominant ones in weed community.

Landscape structure

The following picture (fig. 99) regards the significant correlations found between the categories of landscape structure and other indicators.

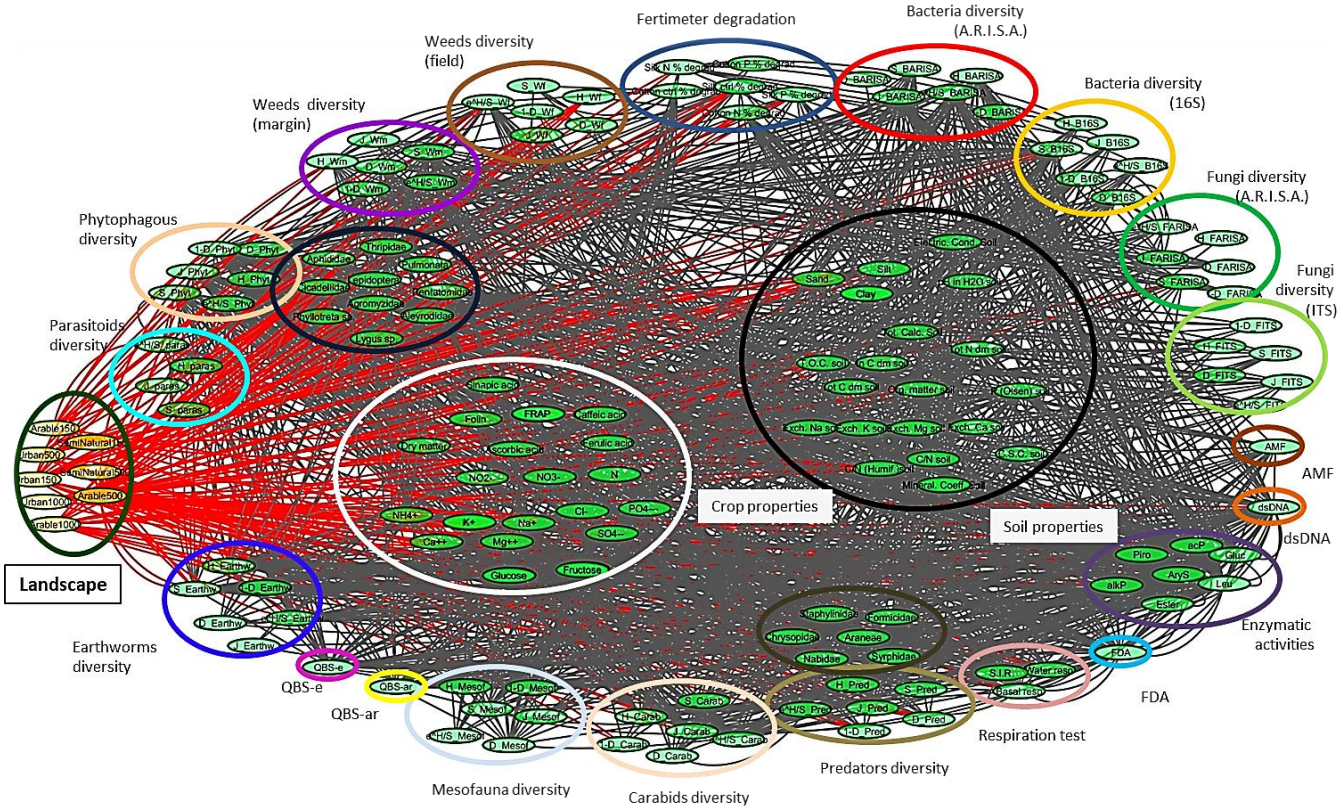


Fig. 99: Focus on the correlations relationships between landscape structure categories (urban, arable, seminatural) and other indicators. All these relationships are significant with p value <0.05.

The category of landscape that predominates in this simple landscape structure is the arable land use, followed by the urban land use (tab. XII) and the major part of correlations found regard just these two categories. Considering arable land use percentage correlations are of more direct interpretation some of them, for example those relating to more mobile life forms, such as generalist predators, parasitoids, carabids, phytophagous agents and weeds (that are mobile due to the seed dispersion phase) (Benvenuti, 2007; Elzinga et al., 2007; Gongalsky and Cividanes, 2008; Sivakoff et al., 2012). Moreover there are many species of all these bioindicators strongly associated to cultivated environments, which are the most ruderal and opportunistic and can contribute to species community composition.

Earthworms have lower dispersal abilities in comparison to winged insects like parasitoids (Elzinga et al., 2007) or crop pests and generalist predators (Sivakoff et al., 2012), which can move a few kilometres, but Mathieu et al. (2010) demonstrated that they present high capacities of habitat selection in particular due to soil quality and presence/absence of litter and they resulted from this work more strictly linked to seminatural environments, where it is expected to have a better soil quality than in agroecosystem environments.

The second more spread environment in the surrounding of the fields object of study is the urban one. This is obviously related to anthropic species. In this respect it is possible to do a consideration regarding urban land use and weed community: the weed community in the crop field area seems to benefit, in term of biodiversity, from the proximity to anthropic environments, while on the contrary the typical ones of the

field margin seem not. Perhaps this is due to the fact that weed community in the cropfield is shaped by more intensive agronomical practices, while the one in the margin represents a more natural situation (fig. 69).

Soil chemical-physical parameters

The following diagram (fig. 100) regards the significant correlations found between some soil properties and other indicators.

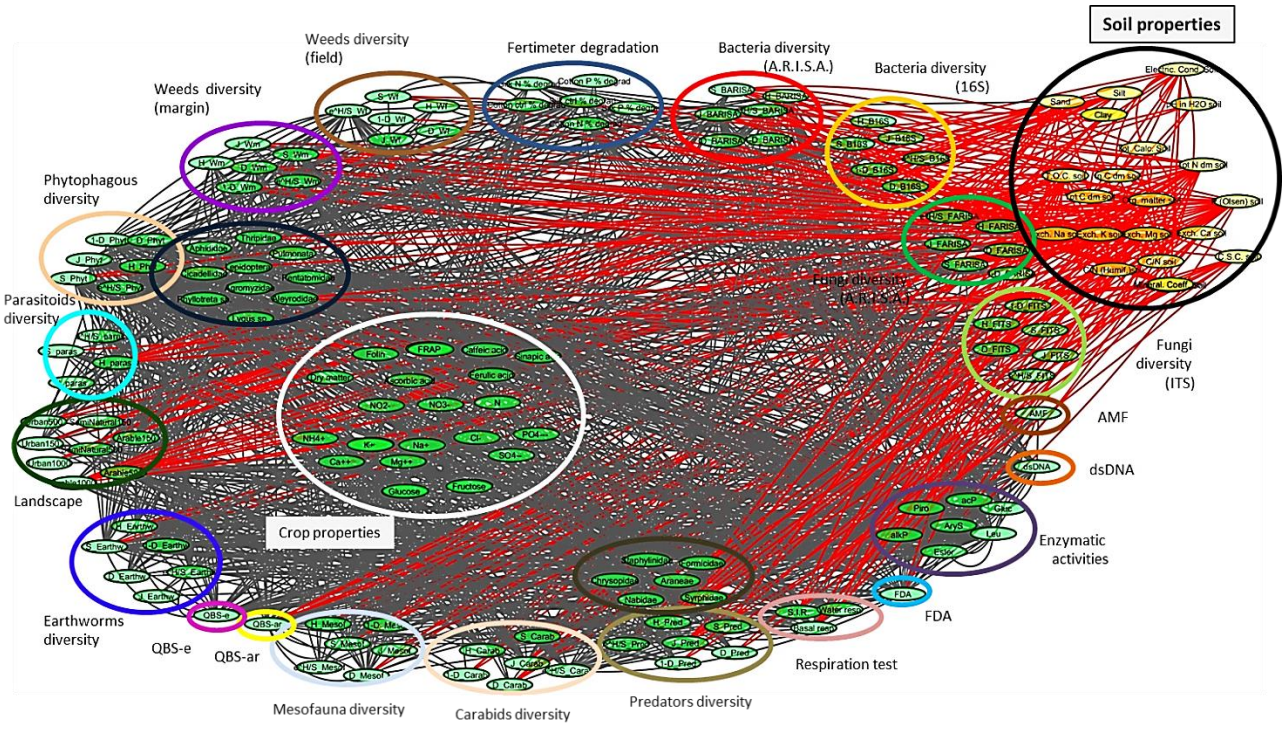


Fig. 100: Focus on the correlations relationships between some soil chemical-physical properties and other indicators. All these relationships are significant with p value <0.05.

The numerous correlations regarding soil properties demonstrate and highlight that soil is considered a very complex "organism" that interacts and runs with all life forms living in it (de Vries et al., 2013). In fact strong correlations were found between several soil parameters and bacteria, fungi, mesofauna, carabid, predator, weed, earthworm communities. This means that all of them can be considered good bioindicators, since the definition of bioindicator says "*a bioindicator is a living organism, with precise ecological requirements, which by its presence provides the operator with important information on the environmental conditions in which it lives. It can be defined as a species or assemblage of species that is particularly well matched to specific features of the landscape and/or reacts to impacts and changes*" (Paoletti and Bressan, 1996; van Straalen, 1997).

Moreover there are several correlations also with other functional indicators measured, such as respiration rate, enzymatic activities and FDA hydrolysis. Indeed both biotic indicators and functional ones give us information about several soil properties and they can be very useful to monitor the state of an agroecosystem and its soil if there is not the possibility to proceed with specific laboratory analyses.

Crop nutritional properties

The following image (fig. 101) regards the significant correlations found between some crop nutritional properties and other indicators.

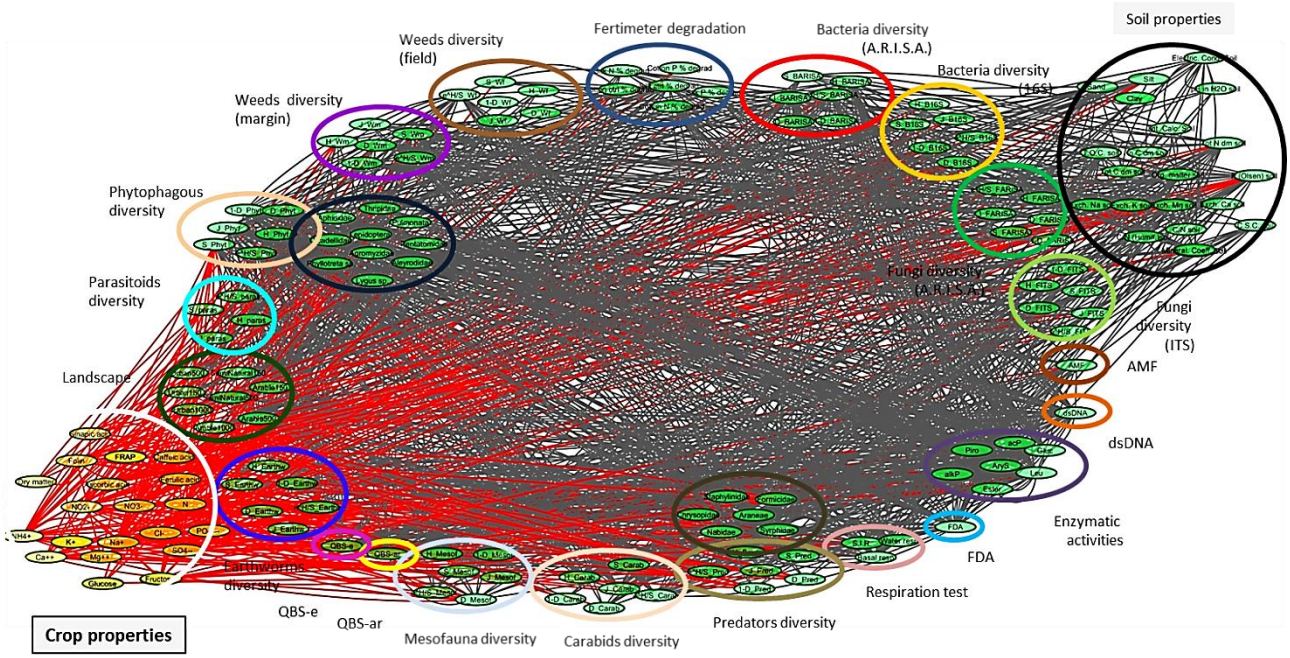


Fig. 101: Focus on the correlations relationships between some crop nutritional properties and other indicators. All these relationships are significant with p value <0.05.

From this correlation analysis it emerges that crop nutritional properties are strictly associated to many other indicators and characteristics of the agroecosystem in which the crop grows. First of all they are correlated with some soil properties, but also with biodiversity groups living in the same environment, such as phytophagous agents, weeds, bacteria, fungi and AMF, predators, mesofauna and earthworms. Secondly, by performing analyses, as for example those of fertimeter degradation, of some key soil enzymatic activities, or of soil respiration rate it is possible to have indirectly information about the trend of some crop nutritional properties.

This means that crop plants are strongly dependent on the environment in which they live, in fact local specificity plays an important role in determining the performance of a farming system (Gomiero, 2013) and this does not include just merely climate and soil aspects, but all the life forms living in contact or next to crop plant. Since every life form is adapted by evolution to its environment, but also climate and soil are

characteristic of a particular area, crop plants are affected by these factors. This can explain the existence of PDO (Protected Designation of Origin) and PGI (Protected Geographical Indication) brands attributed to several crop plants, especially in Italy. In fact Italy is at the first place in Europe for denominated agricultural products with 68 certified products (for a total of 215 in all over Europe)[22]. It seems not just a coincidence that Italy is among the biodiversity hotspots at global scale (fig. 102).

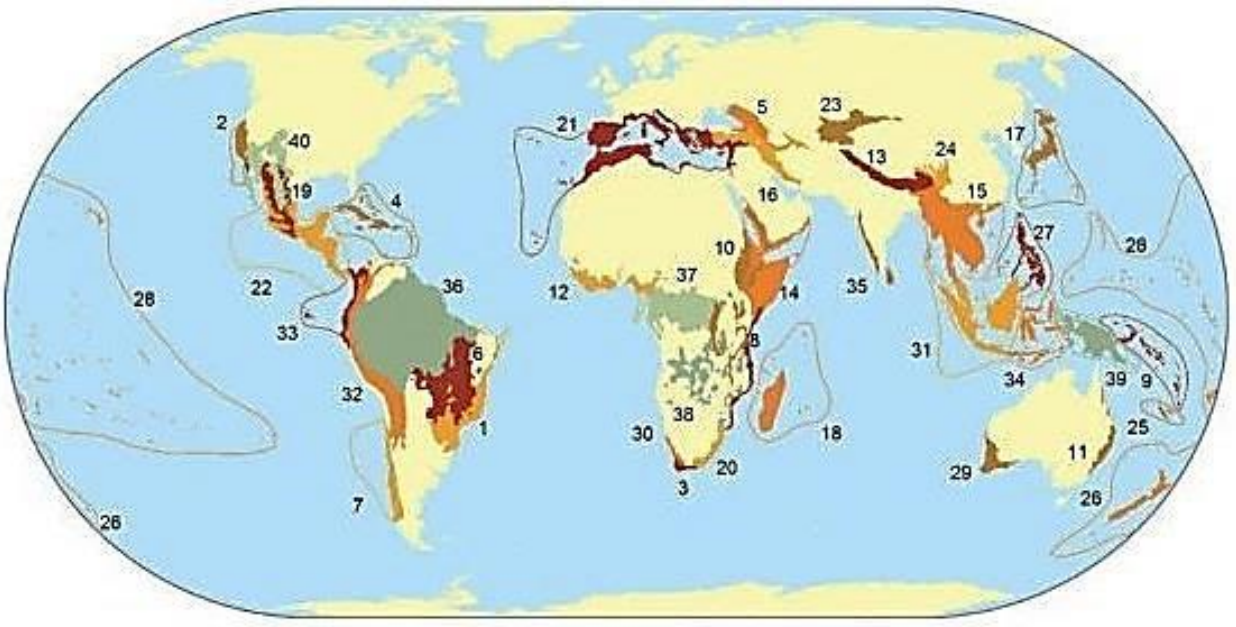


Fig. 102: The planet's biodiversity hotspots (regions 1–35) and high biodiversity wilderness areas (regions 36–40) (© Proceedings of the National Academy of Sciences)[23].

Possibly also this high concentration of biodiversity contributes to have a high number of typical agricultural products. Concluding, as for wines the concept of *terroir* is known that is concerned with the relationship between the characteristics of an agricultural product (quality, taste, style) and its geographic origin, which might influence these characteristics (Van Leeuwen and Seguin, 2006), also for other crops it could probably be defined to give more importance to typicity.

Examples of correlations useful for the optimization of monitoring analyses

In order to see how these correlations can be useful for the optimization of monitoring analyses in agroecosystems, see the following examples (figg. 103 and 104).

[22] Agricultural products and foodstuffs - PDO and PGI - Reg. (EC) No 510/2006
Fru., veg., cereals. Available on the website: http://ec.europa.eu/agriculture/external-studies/2012/value-gi/sectors-fruit-veg-cereals_en.pdf
[23] See more at: http://blog.conservation.org/2012/05/language-diversity-is-highest-in-biodiversity-hotspots/#sthash.RfVOpapl.dpuf

Variable A	Variable B	Corr coeff	P value	Test	Significance	
F (µg/g) FDA	AMF	**0,79098**	0,034156	Pearson	*	→ Mycorrhizae
F (µg/g) FDA	Gluc	**0,99664**	0,00023391	Pearson	***	Enzymatic activities
F (µg/g) FDA	AryS	**0,98527**	0,0021404	Pearson	**	
F (µg/g) FDA	Leu	**0,97781**	0,003956	Pearson	**	
F (µg/g) FDA	acP	**0,88405**	0,046561	Pearson	*	
F (µg/g) FDA	dsDNA	**0,94268**	0,016332	Pearson	*	→ Soil DNA content
F (µg/g) FDA	Basal resp.	**0,76587**	0,044703	Pearson	*	Soil respiration
F (µg/g) FDA	S.I.R.	**0,75918**	0,047777	Pearson	*	
F (µg/g) FDA	Taxa_S_FARISA	**0,71399**	0,046663	Pearson	*	→ Fungi
F (µg/g) FDA	Taxa_S_B16S	**0,84187**	0,017507	Pearson	*	→ Bacteria
F (µg/g) FDA	Sand	**0,7728**	0,024551	Pearson	*	→ Soil texture
F (µg/g) FDA	Cotton N % degrad	**0,89286**	0,012302	Spearman	*	→ Soil fertility
F (µg/g) FDA	Evenness_e^H/S_Wf	**-0,8045**	0,029123	Pearson	*	→ Weeds
F (µg/g) FDA	QBS-e	**0,91101**	0,0043228	Pearson	**	Earthworms
F (µg/g) FDA	Taxa_S_Earthw	**0,87548**	0,0098159	Pearson	**	
F (µg/g) FDA	Shannon_H_Earthw	**0,7842**	0,036848	Pearson	*	
F (µg/g) FDA	Evenness_e^H/S_Phyt	**0,98733**	0,00023965	Pearson	***	Classical diversity indexes for crop pests
F (µg/g) FDA	Equitability_J_Phyt	**0,97332**	0,0010581	Pearson	**	
F (µg/g) FDA	Shannon_H_Phyt	**0,95765**	0,0026527	Pearson	**	
F (µg/g) FDA	Dominance_D_Phyt	**-0,92375**	0,0084996	Pearson	**	
F (µg/g) FDA	Simpson_1-D_Phyt	**0,92375**	0,0084996	Pearson	**	
F (µg/g) FDA	*Phyllotreta* sp.	**-0,83845**	0,037041	Pearson	*	→ Flea beetles abundance
F (µg/g) FDA	Nabidae	**0,92839**	0,0075074	Pearson	**	Predators abundance
F (µg/g) FDA	Araneae	**0,83062**	0,040603	Pearson	*	
F (µg/g) FDA	Evenness_e^H/S_Carab	**0,88542**	0,018942	Pearson	*	Classical diversity indexes for carabids
F (µg/g) FDA	Shannon_H_Carab	**0,8637**	0,0266	Pearson	*	
F (µg/g) FDA	Equitability_J_Carab	**0,85105**	0,031629	Pearson	*	

1 indicator correlated to → **27 indicators**

Fig. 103: All the significant correlations found in the present work between the value of fluorescein found with FDA hydrolysis test and other 27 indicators measured.

The table in fig. 103 shows how by performing FDA hydrolysis test on soils of a particular area, it is possible to have information about the trend of other 27 indicators referring to the same area.

Another example is in the following figure.

Variable A	Variable B	Corr coeff	P value	Test	Significance
QBS-e	Leu	**0,94235**	0,0048895	Pearson	**
QBS-e	Gluc	**0,92617**	0,0079741	Pearson	**
QBS-e	AryS	**0,843**	0,03504	Pearson	*
QBS-e	acP	**0,82606**	0,042751	Pearson	*
QBS-e	dsDNA	**0,81156**	0,049918	Pearson	*
QBS-e	F (µg/g) FDA	**0,91101**	0,0043228	Pearson	**
QBS-e	Shannon_H_BARISA	**-0,66093**	0,037463	Pearson	*
QBS-e	Equitability_J_BARISA	**-0,68949**	0,02739	Pearson	*
QBS-e	Dominance_D_FITS	**0,72937**	0,040039	Pearson	*
QBS-e	Simpson_1-D_FITS	**-0,72937**	0,040039	Pearson	*
QBS-e	Taxa_S_Earthw	**0,92916**	0,00010107	Pearson	***
QBS-e	Evenness_e^H/S_Earthw	**-0,66683**	0,035203	Pearson	*
QBS-e	Shannon_H_Earthw	**0,66608**	0,035486	Pearson	*
QBS-e	Evenness_e^H/S_Phyt	**0,8691**	0,011082	Pearson	*
QBS-e	Equitability_J_Phyt	**0,81736**	0,024751	Pearson	*
QBS-e	Shannon_H_Phyt	**0,78869**	0,035056	Pearson	*
QBS-e	Nabidae	**0,77929**	0,03887	Pearson	*
QBS-e	SO4--	**0,81237**	0,026401	Pearson	*
QBS-e	Na+	**-0,80473**	0,029043	Pearson	*

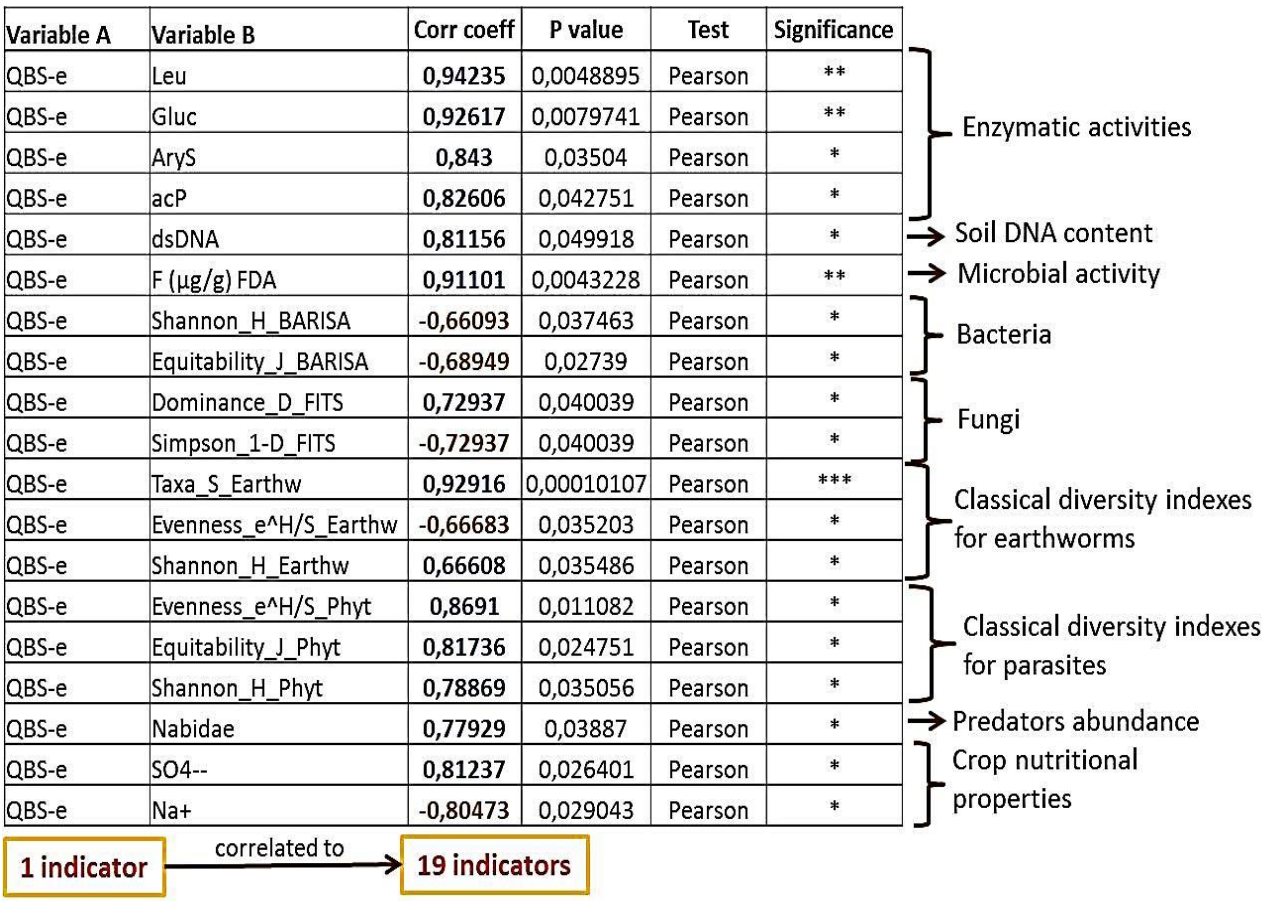


Fig. 104: All the significant correlations found in the present work between the value of QBS-e index and other 19 indicators measured.

The same considerations can be done for fig. 104: by calculating QBS-e index on earthworms sampled in a particular soil, it is possible to have information on the trend of other 19 indicators referring to the same agroecosystem.
Other details on correlations found in this work can be found in tab. LXIV in the appendix.

These considerations can be useful for the optimization of the costs of monitoring analyses within an agroecosystem context: based on the aim of the analysis, it would be possible to choose to apply those indicators that are more representative of the overall on-going phenomena, that is to say the ones involved in a considerable number of correlations.

CONCLUSIVE REMARKS

This work of research has allowed to answer the initial specific questions:

(1) *Can different agroecosystem managements (organic/conventional) change taxa composition of the different bioindicator groups in horticultural crops?*

Taxa composition of a bioindicator group does not always change according to different agroecosystem managements. It depends on the type of bioindicator, in fact it seems that there are more sensitive bioindicators to management practices, such as predators and parasitoids, than others, like phytophagous agents and weeds. It has been discussed that probably it is reductive to consider just the number of species or taxa composition and it is better to take in consideration also some functional and ecological traits, as for the case of earthworms.

(2) Is a higher biodiversity always linked to higher efficiency of ecosystem services in the agroecosystem?

Biodiversity *per se* described by classical diversity indexes seems not at all to be linked to the functionality of ecosystem services. In fact at equal biodiversity in the belowground and epigeal sectors, the ES functionality is higher in organic-biodynamic fields. By studying only the relationships between biodiversity and biological control ecosystem service Crowder and Jabbour (2014) reached the same conclusion. Even though biodiversity remains a sort of insurance for the future, since there is mounting evidence that biodiversity increases the stability of ecosystem functions through time (Cardinale et al., 2012), perhaps the answer has to be searched in functional agrobiodiversity, not in overall biodiversity and above all within the interactions among different biodiversity groups. In fact, functional agrobiodiversity emphasizes the application and development of informed management practices that specifically enhance and exploit elements of biodiversity for their role in providing ES (ELN-FAB, 2012).

(3) Which ecosystem services are more efficient in each of the two agroecosystem management types (organic vs. conventional)?

Among all ecosystem services measured by functional indicators in this thesis, almost all were better performing in agroecosystems with organic-biodynamic management. This means that this type of agriculture is more environmentally sustainable, because the process of crop production can be practiced with less impoverishing of natural resources such as soil, fertility, biodiversity, water and using less external inputs. Linking to the above-mentioned concept of functional agrobiodiversity, a guiding principle is to use external inputs in a rational way, building on biological regulation where possible (ELN-FAB, 2012). However the sustainability of the food system has to be addressed from many different perspectives, in a

holistic way and with a long term perspective in mind; given the crucial role that food production plays in our life, our major concern should be to secure that farming practice guarantees the resilience of our food production system (Gomiero, 2013).

(4) *Are there correlations between different functional indicators? Are some indicators more informative and representative of the overall on-going phenomena? Can we choose one single indicator and spare monitoring analysis costs?*

With the methodological part of this analysis many correlations were found among functional and biotic indicators and many of them emerged as more informative in comparison with others. Surely this information can be useful to improve planning strategies of monitoring analyses according to the availability of resources, such as money, time, competences and purposes. For instance for a farmer, it would be useful to monitor in his farm soil fertility by using fertimeter along with application of QBS-e index and pay attention to biological control evidences, such as crop pests outbreaks and above all predators and parasitoids presence, and control the diversity of weed community; while for an operator for the control of the agricultural sector, with the possibility to use a laboratory of analysis it would be recommended for sure to proceed with enzymatic activities assays and in particular with arylsulfatase, β-glucosidase and leucine-aminopeptidase activities (which resulted to be the ones correlated with most others indicators) as solid proxy of belowground sector health, and the analysis of higher trophic levels such as phytophagous agents and predators/parasitoids to quantify the efficiency of natural pest control.

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APPENDIX

A- Management practices on Treviso red chicory

Management practices Treviso red chicory crop- 2012										
Fields	**CoMa**	**CoZo**	**CoMi**	**CoTm**	**CoTmp**	**BiCm**	**BiMt**	**BiBg**	**BdTm**	**BdTmp**
Agriculture type	monoculture	monoculture	monoculture	monoculture	polyculture	polyculture	polyculture	polyculture	monoculture	polyculture
Variety	Late	Late	Late	Early	Early	Early	Early	Late	Early	Early
Transplanting period	19/7	17/7 (sowing)	15-16/7	25/8	3-4/9	24/7	10/8	17-18/7	1/8	10-12/9
Planting layout (plants/m^2)	6,5	9	6	6	6	6,5	7,5	8	6	6
Ploughing	√	√	√ (40cm)							
Subsoiling				√ (50cm)			√	√ (60cm)		
Digging								√ (25cm)		
Rotary tillage (pre)	√ (x3)	√ (x3)	√ (x4)	√	√	√			√	√
Harrowing				√	√		√	√	√	√
Weeding	√	√ (x2)	√				√			
Rotary tillage (post)	√ (x3)	√					√	√		
Hoeing			√			√ (x5)	√	√		
Rotating lifting spinner		√ (x3)								
Fertilization	Nitrophoska [12:12:17] (3q/ha)- Manure (200q/ha)	Agriorto special [3:6:18] – (400kg/ha) - YaraMila [12:6:18]- (1,5q/ha)	D-Coder [6:8:18] (5q/ha)				Stillage [3:0:5]- (25q/ha)	Fomet stable manure [3:3:3]- (50q/ha)		
Green manure						Crop residues	Sudan Grass	Barley - vetch		

Extra fertilization	Nitrophoska (3q/ha)		Pinus, algae, humic acids, extract						501 Prep.	501 Prep.
Weed control	Stomp Aqua (2,5l/ha)	Bonalan (2,5l/ha) + Kerb (2,5l/ha)	Stomp Aqua (2l/ha) - Agil vs. Graminaceae: (1-1,2l/ha)							
Irrigation	Sprinkling	Sprinkling	Microsprinkling	Microsprinkling	Microsprinkling	Drip method	Microsprinkling	Microsprinkling	Microsprinkling	Microsprinkling
Harvesting period	15/1	15/1	15/1	19-20/12	19-20/12	22/10	22/10	15/1	22/10	19-20/12

Tab. LV: List of management practices applied to Treviso red chicory cultivation in 2012.

B- Management practices on white cabbage

Management practices White cabbage crop - 2013							
Fields	**CoMa**	**CoZo**	**CoZa**	**BiCm**	**BiMt**	**BiBg**	**BdTm**
Agriculture type	monoculture	monoculture	monoculture	polyculture	polyculture	polyculture	polyculture
Variety	Naruto (110-120 days)	Naruto (110-120 days)	Naruto (110-120 days)	Naruto (110-120 days)	Naruto (110-120 days)	Naruto (110-120 days)	Naruto (110-120 days)
Transplanting period	19-29/7	9-10/7	24/7	15-21/7	18/7	18/7	17-18/7
Planting layout (plants/m^2)	3	3,5	4,5	3	3	2	3
Ploughing	√ (40cm x2)	√ (35cm x2)	√ (35cm)				
Chopping				√	√	√	√
Vibrating tine cultivator					√		√
Subsoiling					√		√
Digging						√	
Rotary tillage pre	√ (x2)	√ (x3)	√ (x2)	√	√	√	

Harrowing	√						
Weeding	√	√ (x3)		√	√ (x2)	√	√ (x4)
Rotary tillage post	√		√		√	√	
Hilling	√						
Inter row hoeing				√	√		√
Fertilization	Nitrophoska [12:12:17] (3q/ha)- Manure (200q/ha)	YaraMila Grower [12:6:18] (100kg/2000mq)	Manure (30q/ha) + Grower		Stillage [3:0:5]- (25q/ha)	Fomet stable manure [3:3:3] – (50q/ha)	Manure (500q/ha)- Prep.500 (x2)
Green manure				Crop residues	Barley-rye-vetch	Crop residues	Crop residues
Extra fertilization	Nitrophoska (3q/ha)						Prep. 501
Weed control	Stomp Aqua (2,5l/ha)	Stomp Aqua (2,5l/ha)	Stomp Aqua (1,5l/ha)		Stale seedbed		Stale seedbed (x2)
Irrigation	Sprinkling	Sprinkling	Sprinkling	Drip method	Microsprinkling	Microsprinkling	Microsprinkling
Harvesting period	18/11	18/11	16/12	18/11	18/11	18/11	18/11

Tab. LVI: List of management practices applied to white cabbage cultivation in 2013.

C- Pesticides treatments on Treviso red chicory and white cabbage

Management	Crop	Mean pesticide treatments	Active components	Main crop pest targets
Organic-biodynamic	*Chicorium intybus*	0,4	*Bacillus thuringiensis*	*M. brassicae, A. gamma, S. littoralis, H. armigera*
			Spinosyn A e D (from *Saccharopolyspora spinosa*)	Lepidoptera, Diptera, Hymenoptera, Siphonaptera, Tysanoptera and some Coleoptera
	Brassica oleracea	1	Pyrethrum	Aphids, Pentatomidae, Coleoptera (flea beetle), Miridae, Cicadellidae, Aleurodidae, Lepidoptera
			Spinosyn A e D (from *Saccharopolyspora spinosa*)	Lepidoptera, Diptera, Hymenoptera, Siphonaptera, Tysanoptera and some Coleoptera

Conventional	*Chicorium intybus*	2	Indoxacarb (30g)	*H. armigera, S. littoralis, C. chalcites, M. unipuncta*
			Deltamethrin (25g/l)	*N. ribis-nigri, S. littoralis, S. exigua, M. brassicae, A. rosae*
			Imidacloprid (200g/l)	*B. brassicae, M. persicae*
			Etofenprox (280g/l)	Miridae, Noctuidae
			Chlorantranilprole (100g/l) Lambda-cyhalothrin (50g/l)	*H. armigera, Spodoptera* spp.
	Brassica oleracea	2	Imidacloprid (200g/l)	*B. brassica, M. persicae*
			Bacillus thuringiensis	*M. brassicae, Pieris* spp.
			Emamectin benzoate (0,95g/100g) 3,6-dibutilnaftalene- 1-sulphonate sodium (0,05g/100g)	*H. armigera, Spodoptera spp., O. nubilalis, P. gamma, P. brassicae, P. xylostella, D . erinaceella, T. absoluta*
			Deltamethrin (25g/l)	*N. ribis-nigri, S. littoralis, S. exigua, M. brassicae, A. rosae*

Tab. LVII: List of pesticides applied to Treviso red chicory in 2012 and to white cabbage in 2013.

D- Soil physical- chemical analyses

Field code	pH in H_2O	Electric. Cond. (µS/cm)	Clay (%)	Silt (%)	Sand (%)	Soil texture	Tot N dm (%)	Tot C dm (%)	In C dm (%)	T.O.C. (%)	Org. Matter (%)	Tot. Calc. (%)	C.S.C. (meq/100g)	P (Olsen) (mg/l)	Exch. K (mg/l)	Exch. Na (mg/l)	Exch. Mg (mg/l)	Exch. Ca (mg/l)	Mineralization Coefficient (Remy e Marin-Lafleche)	C/N (Humification)
BdTmp	7,88	480	14	14	71	FS	0,14	8,98	7,74	1,24	2,14	64,47	26	213	186	274	724	1030	0,41	8,93
CoTmp	8,24	442	14	12	73	FS	0,09	8,47	7,55	0,92	1,59	62,93	19	199	114	127	353	6948	0,42	10,47
CoZa	7,94	707	19	17	64	FS	0,11	0,94	0,29	0,65	1,13	2,40	23	229	153	456	934	8650	1,37	5,73
BiBg	8,10	603	25	15	60	FSA	0,15	1,69	0,78	0,91	1,57	6,48	20	867	149	379	706	7156	1,01	6,24
CoZo	8,32	508	38	22	39	FA	0,14	2,45	1,61	0,84	1,44	13,42	19	408	207	297	398	5902	0,62	6,05
BdTm	8,42	452	10	18	71	FS	0,15	8,96	7,58	1,38	2,38	63,18	25	278	163	544	722	9164	0,48	9,07
CoTm	8,21	573	16	16	67	FS	0,11	8,85	7,58	1,27	2,18	63,20	20	187	78	112	440	5490	0,40	11,41
BiMt	8,10	840	22	16	61	FSA	0,16	2,14	0,74	1,40	2,42	6,12	21	453	282	596	635	7582	1,09	8,60
CoMa	7,84	935	28	20	51	FSA	0,13	1,26	0,40	0,86	1,48	3,35	21	315	143	288	644	1021	1,06	6,54
BiCm	7,89	892	19	23	58	FS	0,13	1,08	0,26	0,82	1,42	2,16	18	729	165	415	2008	1918	1,39	6,46

CoMi	8,20	577	44	18	37	A	0,18	2,25	1,00	1,25	2,16	8,32	22	118	113	342	1604	1287	0,67	7,02

Tab. LVIII: Detailed data of soil physical-chemical analyses.

E- Carabid species list

Species	BdTm	BdTmp	BiBg	BiCm	BiMt	CoMa	CoMi	CoTm	CoTmp	CoZa	CoZo
Acupalpus elegans	0	0	0	0	0	0	0	0	0	0,119048	0
Acupalpus meridianus	0,022422	0	0	0	0	0	0,144928	0	0	0	0,012531
Agonum muelleri	0	0	0	0	0	0	0	0,043956	0	0	0
Amara aenea	0,30705	0,034014	0,033482	0,214219	0,153846	0,028195	0	0,043956	0,661376	0,357143	0
Amara eurynota	0	0	0	0	0,010989	0	0	0	0	0	0
Amara similata	0	0	0	0	0	0	0	0,043956	0,026455	0	0
Anchomenus dorsalis	0,056054	0,012987	0,042217	0,208628	0,285714	0,018797	0,289855	0	0	0	0
Anisodactylus binotatus	0,011211	0	0	0	0	0	0	0	0	0	0
Anisodactylus signatus	0,011211	0,103896	0,033482	0	0	0,009398	0	0,021978	0	0	0
Asaphidion stierlini	0,095736	0	0	0	0	0,02551	0	0	0	0,164835	0
Bembidion quadrimaculatum	2,042761	0,090909	1,154018	0,540156	0,086735	0,879121	0,10352	1,164835	0,026455	0	0,132832
Brachinus crepitans	0	0	0	0,228052	0	0	0	0	0	0	0
Brachinus sclopeta	0	0	0	0,041717	0	0	0	0	0	0	0
Bradycellus sp.	0	0,012987	0	0	0	0	0	0	0	0	0
Broscus cephalotes	0	0	0	0	0	0	0	0	0,132275	0	0
Calathus cfr. cintus	0	0	0	0	0	0	0	0	0	0	0
Calathus fuscipes graecus	0	0,762214	0,310559	0,857803	0,062009	0	0	0,043956	0,15873	0,430885	0,143215
Carabus coriaceus	0	0	0	0	0	0	0	0	0,05291	0	0
Carabus violaceus	0	0	0,011161	0	0	0	0	0	0	0	0
Cicindela campestris	0	0,038961	0	0	0	0	0	0	0,079365	0	0
Clivina collaris	0,75993	0	0,05878	0	0	0	0,082816	0,351648	0	0	0,050125
Clivina fossor	0,398516	0,012987	0,011161	0	0,010989	0,028195	0,186335	0,21978	0	0	0
Cylindera germanica	0	0	0,285714	0,031983	0	0	0	0	0	0	0
Diachromus sp.	0	0	0	0	0	0	0	0	0	0,119048	0

Dinodes decipiens	0	0	0	0	0	0	0	0	0	0	0,012531
Dripta dentata	0	0	0	0	0	0	0	0	0	0,119048	0
Dyschiriodes chalybaeus	0	0	0	0	0	0	0	0	0,026455	0	0
Egadroma marginatum	3,27381	0,069444	0,47619	0,595238	0	0	0	0,021978	0	6,071429	0,012531
Harpalus affinis	0,141469	0,095418	0	0,119048	0,010989	0	0	0,10989	0	1,309524	0,06015
Harpalus dimidiatus	0	0	0	0,022321	0	0	0	0	0	0	0
Harpalus distinguendus	1,756175	1,242914	1,749224	2,307161	0,284537	0,58942	0,041408	0,087912	1,402116	1,477733	1,418932
Harpalus oblitus	0	0	0,011161	0,010661	0,021978	0,064344	0	0	0	0	0
Harpalus pumilus	0	0	0	0	0	0	0	0	0,026455	0	0
Harpalus pygmaeus	0,011211	0	0	0	0,010989	0,009398	0	0,021978	0	0,10989	0
Harpalus rubripes	0	0	0	0,031056	0	0	0	0	0	0	0
Harpalus smaragdinus	0	0	0	0	0	0	0	0	0	0	0
Lasiotrechus (Blemus) discus	0	0	0	0	0	0	0	0	0	0	0,032051
Microlestes corticalis	0,297619	0	0	0,47619	0,714286	0,10989	0	0	0	0,833333	0,238095
Microlestes minutulus	0	0	0	0	0	0	0	0	0,026455	0	0
Metallina lampros	0	0	0	0	0	0	0,020704	0	0	0	0
Metallina properans	0,044843	0,119048	0	0,010661	0,010989	0	0	0	0	0	0,032051
Nebria brevicollis	0	0	0	0	0	0,009398	0	0,021978	0	0	0
Notiophilus biguttatus	0	0	0	0	0,010989	0	0	0	0	0	0
Ocydromus andreae	0	0,350649	0	0	0	0	0	0	0	0	0
Ocydromus femoratus	0	0	0	0	0	0	0	0	0,026455	0	0
Ocydromus hypocrita	0	0	0	0,022321	0	0	0	0	0	0	0,032051
Ocys sp.	0	0,05102	0	0	0	0	0	0	0	0	0
Olistophus fuscatus	0	0,012987	0	0	0	0	0	0	0	0	0
Ophonus diffinis	0,059524	0	0	0,031056	0	0	0	0	0	0,119048	0
Parophonus hirsutulus	0	0	0	0	0	0	0	0	0	0,119048	0
Parophonus maculicornis	0	0	0	0	0	0	0	0	0,026455	0	0
Parophonus cfr. planicollis	0	0	0	0	0	0	0	0	0	0,119048	0
Philochtus lunulatus	0,022422	0	0,238095	0	0	0	0,10352	0	0	0	0
Poecilus cupreus	1,812407	0,077922	1,930221	1,684063	2,002747	0,581984	2,153209	0,879121	0	2,261905	18,04518

Poecilus lepidus	0	0,025974	0	0	0	0	0	0	0,079365	0	0
Pseudophonus griseus	0	0,303211	0,124224	0,16594	0	0	0	0,021978	0,05291	0	0,142857
Pseudophonus rifipes	0,78502	0,380205	3,066479	3,605536	0,189953	0,263092	0,186335	0,10989	0,185185	0,37594	0,538847
Pterostichus melanarius	0	0,012987	0,202349	0,124224	0,491758	0	0	0	0	0	0,025063
Pterostichus melas	0,059524	0	0,435753	4,107693	1,535714	0	0	0,021978	0,05291	0	1,126029
Pterostichus niger	0,119048	0	0,63519	0,507555	1,498823	0,067376	0,062112	0	0	0,054945	1,652345
Sinechostictus ruficornis	0	0	0	0	0	0	0,020704	0	0	0	0
Stenolophus skrimshiranus	0,119048	0	0,047619	0	0	0	0	0	0	0,357143	0,095238
Stenolophus teutonus	0,044843	0	0	0,233537	0,010989	0	0	0,043956	0	12,55495	0,428571
Tachyura quadrisignata	0,059524	0	0	0	0	0	0	0	0	0	0
Trechus quadristriatus	0,202683	0,572047	0,123318	0,041717	0,3281	0,345547	0,124224	0,043956	0,05291	0,480046	0,143773

Tab. LIX: Detailed results of mean activity density (DA_{10}) data of each carabid species sampled during the two years of fieldwork.

F- Crop properties: TV red chicory

		Leaf colour		
Sample	**Commercial plant weight (g)**	**L**	**a**	**b**
1- BiCm	354	28,94	25,48	3,08
	335	29,90	19,00	4,50
	347	29,06	15,20	1,65
	338	29,80	18,88	2,83
	282	24,67	24,91	1,89
2- BiMt	289	31,13	21,18	5,04
	336	31,45	18,57	3,73
	330	29,61	22,28	3,82
	315	29,50	19,59	2,26
	287	31,68	19,80	4,24
3- BdTm	331	32,78	18,77	2,47
	720	29,45	15,54	2,81
	476	31,51	17,27	3,99
	519	31,86	14,77	2,66
	462	30,77	16,50	3,33
4- CoTm	148	31,98	8,82	2,33
	142	28,53	7,42	0,68
	190	31,49	10,78	0,93
	203	31,14	6,08	1,15
	214	32,24	13,85	1,75
5- BdTmp	89	30,93	8,15	0,96
	89	30,96	12,77	0,32
	76	31,18	13,28	1,47
	73	32,81	11,75	0,98
	96	32,85	16,77	1,43
6- CoTmp	85	31,78	7,02	2,52
	64	28,99	3,11	0,95
	74	30,53	6,76	1,65

	46	29,84	4,90	-0,77
	54	30,99	7,20	1,94
7- CoMi	265	38,86	19,48	5,75
	272	34,53	24,59	4,54
	170	33,62	19,24	3,66
	296	33,93	24,61	4,38
	239	32,33	19,56	2,05
8- CoMa	214	32,83	15,48	1,62
	224	29,55	21,52	2,91
	159	32,97	14,62	3,63
	231	30,43	10,27	-0,37

	191	33,46	19,18	2,64
9- CoZo	209	39,64	32,76	6,80
	231	38,79	17,32	4,71
	201	33,74	22,58	6,08
	207	36,87	25,20	4,13
	196	30,86	17,51	2,85
10- BiBg	171	33,47	14,87	3,87
	266	33,09	26,14	5,24
	298	32,54	13,00	1,92
	186	36,22	23,57	6,08
	161	35,02	17,74	4,41

Tab. LX: Results of Treviso red chicory physical properties; varieties: early -period: July- October (BiCm, BiMt, BdTm, CoTm, BdTmp, CoTmp); late- period: July- January (CoMi, CoMa, CoZo, BiBg).

Sample	d.m	FRAP	Folin	Ascorbic acid	N Kjeldhal	Tot N	Cl^-	NO_3^-	PO_4^{---}	SO_4^{--}	Na^+	NH_4^+	K^+	Mg^{++}	Ca^{++}	Chlorogenic acid	Chicoric acid	Cyanidin-3-glu	Cyan-3-mal glu*	Glucose	Fructose
1- BiCm A	5,6	78549,8	2076,1	2243,5	3,3	3,5	10450,6	9243,5	10705,1	8466,5	6522,2	/	39762,6	1212,0	5289,8	94,7	165,0	178,3	3598,8	141413,6	140148,5
BiCm B	5,4	76012,4	6895,6	2807,3	3,3	3,4	6635,4	5920,9	5635,0	4408,9	5111,6	/	41436,2	1063,0	5355,2	522,3	2357,5	160,5	3474,3	140419,1	142764,1
BiCm C	6,2	81087,2	7476,3	3186,2	3,8	3,8	4943,3	3450,6	5873,1	4304,9	2175,2	/	34727,5	394,6	3131,8	1878,5	2566,2	196,0	3723,2	142412,4	137522,4
2- BiMt A	5,7	43769,9	4450,4	2764,4	3,6	3,7	11093,1	4584,0	11492,2	4470,6	5821,2	239,3	38071,3	1993,7	6940,4	523,8	1269,4	0,0	1232,7	186374,4	149694,0
BiMt B	5,9	18991,1	1715,0	2006,2	3,4	3,6	14529,9	10850,3	8867,8	6627,0	5802,5	200,0	39856,6	1638,1	5876,5	6,3	0,0	0,0	8,7	145435,2	157905,6
BiMt C	5,8	52634,5	4340,6	2924,6	3,9	4,1	8500,7	8161,1	5882,8	5015,3	7090,2	385,5	47651,9	2196,0	7590,2	447,4	1199,2	0,0	1382,0	161010,8	157270,7
3- BdTm A	5,3	62533,4	7556,4	10570,8	3,7	4,0	10633,6	11202,9	6747,3	4881,8	2093,3	289,6	65728,1	1766,1	7772,1	227,4	1548,8	0,0	409,4	96232,2	132729,2
BdTm B	6,1	66815,3	7008,6	7380,9	3,8	3,9	7745,1	6605,6	6505,5	4588,3	1837,1	327,4	55698,2	1648,7	6339,1	219,0	841,6	0,0	303,9	94822,2	115973,5
BdTm C	5,2	81146,8	8104,2	11155,9	3,4	3,7	12149,1	11191,4	7687,7	5604,4	2097,9	410,6	70584,4	1688,2	7617,1	210,6	1146,5	0,0	163,8	153123,4	152020,0
4- CoTm A	6,5	82891,6	8597,7	2333,8	2,3	2,3	13674,2	1147,6	3968,4	3263,8	1408,2	506,2	50843,9	1407,0	6420,9	2843,0	2598,8	198,3	1983,9	97420,7	132560,4
CoTm B	6,2	72856,2	7247,7	7212,1	3,1	3,1	9391,0	583,4	2642,5	1803,5	2081,8	381,9	46143,6	1455,0	7049,2	5387,9	4669,8	365,5	1368,4	173424,1	178762,1
CoTm C	8,5	78153,1	6428,3	3176,7	3,4	3,4	16834,3	1301,0	5508,2	4310,2	1372,2	428,8	54847,9	1730,5	8595,0	3332,6	2283,8	167,1	1898,9	111894,0	123290,4
5- BdTmp A	7,4	64707,4	6847,5	2366,1	3,8	3,8	6576,2	1477,6	4151,3	1782,5	2070,9	485,2	58894,5	1369,6	5933,8	1172,4	1807,3	249,8	1689,6	56020,7	89060,8

BdTmp B	7,8	38582,5	4562,4	2416,2	3,8	3,9	5702,1	1734,1	4330,6	1880,1	1999,8	518,3	60172,2	1481,1	6764,6	545,2	766,5	221,9	150,5	75726,7	113161,9
BdTmp C	8,6	62981,1	6024,3	3146,1	3,8	3,8	3732,5	573,1	3108,4	1249,5	2231,5	475,0	54970,7	1361,7	6203,5	1799,6	1665,3	194,0	1600,5	110127,8	104800,1
6- CoTmp A	8,6	89169,4	8041,6	2822,9	3,1	3,1	3391,8	74,3	1541,7	499,7	2293,3	388,1	43950,9	1465,0	4450,6	2876,2	2440,8	339,6	2345,0	71448,7	94681,6
CoTmp B	8,4	84711,0	8920,6	3157,0	3,1	3,1	4413,9	146,2	1908,2	615,6	2942,9	205,0	47240,2	1431,5	5197,9	3353,1	2251,4	269,5	2042,6	83463,4	102791,3
CoTmp C	8,5	98997,0	8731,5	3670,3	3,0	3,0	4738,0	198,8	2059,2	812,2	2873,6	383,4	48839,1	1661,8	6329,4	4164,8	2681,7	297,1	2812,8	76976,2	95539,0
7- CoMi A	6,9	36487,5	3826,7	2175,9	4,1	4,1	3635,8	41,6	6607,6	2551,4	3808,3	360,6	39145,1	1724,1	6207,1	2309,9	653,5	19,4	430,4	196797,6	171127,2
CoMi B	6,4	35134,5	3085,6	2698,5	4,2	4,2	4231,1	41,4	6827,6	2479,9	3423,6	297,4	40235,5	1739,3	6616,9	2252,4	700,5	27,9	460,4	189388,8	177543,6
CoMi C	6,8	35872,9	3544,1	3038,9	4,0	4,0	5908,1	79,8	6717,6	2515,7	2661,3	281,7	39580,3	1782,1	6825,2	2630,5	711,6	39,3	562,7	191323,2	183435,6
8- CoMa A	5,7	33345,3	4388,6	2381,9	4,0	4,0	6576,8	95,1	5732,2	2813,7	2144,4	242,8	51786,6	1450,7	6277,3	2158,6	588,3	37,6	551,6	160197,6	188029,2
CoMa B	5,9	32421,4	4571,5	1847,4	4,0	4,0	5926,3	99,6	5101,4	2497,9	2282,6	337,6	53577,0	1531,9	6422,0	1756,9	529,9	32,2	463,2	166888,8	173408,4
CoMa C	6,1	32883,3	5659,4	2922,9	4,2	4,2	4418,4	47,0	4392,1	2132,7	2428,3	374,9	49934,8	1493,0	6766,8	3414,5	831,4	67,3	796,0	179910,0	186330,0
9- CoZo A	5,6	29067,7	3574,3	1979,2	3,4	3,4	4009,3	47,8	5344,4	2757,0	3356,9	263,3	44173,9	1838,5	6824,1	1791,4	637,7	16,9	342,7	234794,4	174680,4
CoZo B	5,3	33234,7	4348,3	2559,2	3,2	3,2	5947,6	49,3	7034,2	3076,0	3430,8	190,9	44476,7	1611,0	5930,0	2010,5	574,8	18,9	346,6	227686,8	183428,4
CoZo C	5,4	30333,5	2779,5	2396,4	3,2	3,2	8963,8	79,3	6189,3	2916,5	2800,5	183,4	55234,8	1920,0	6921,8	2036,3	589,6	15,0	258,1	232759,2	173990,4
10- BiBg A	5,8	49318,6	4294,7	2363,3	3,7	3,7	5558,3	67,8	8019,2	2891,1	3019,7	117,2	47167,8	1583,7	6270,7	3094,7	1469,1	48,1	733,2	150528,0	188235,6
BiBg B	5,8	51541,9	5948,2	2629,4	3,8	3,8	5303,2	46,9	7056,2	2366,1	3243,0	136,2	51353,3	1892,8	7085,2	3566,3	1627,8	57,9	798,0	163537,2	179486,4
BiBg C	5,8	44875,4	4207,2	2600,1	3,8	3,8	4712,3	57,4	6355,5	1755,8	2977,5	126,7	47275,7	1565,8	5989,5	2343,9	1178,6	57,9	622,7	153774,0	175320,0

Tab. LXI: Results of Treviso red chicory nutritional properties; varieties: early -period: July- October-(BiCm, BiMt, BdTm, CoTm, BdTmp, CoTmp); late- period: July- January (CoMi, CoMa, CoZo, BiBg). Data are referred to dry weight. D.m. in %; FRAP in mg Fe $^{2+}$E/kg; Folin in mg GAE/kg; N in %; all the other data are expressed in mg/kg.

G- Crop properties: white cabbage

		Flower head colour		
Sample	**Commercial plant weight (g)**	**L**	**a**	**b**
1- CoZo	1119	82,53	-5,42	18,38
	1519	82,25	-5,79	18,08
	883	81,35	-5,35	18,98
	1306	85,00	-5,92	18,92
	1505	85,11	-6,27	18,80
2- BiMt	1695	83,01	-6,61	18,47
	862	82,77	-6,09	18,00
	976	81,93	-5,78	16,35

	780	84,20	-5,76	17,50
	713	80,70	-5,72	18,44
3- CoMa	1163	84,41	-5,84	17,62
	1425	81,43	-5,23	18,69
	1291	81,45	-6,26	17,83
	1362	78,35	-5,12	16,50
	801	80,49	-5,70	17,67
4- BdTm	1684	80,61	-5,65	19,98
	1399	84,07	-6,06	18,12
	1402	83,77	-5,85	16,76
	1163	83,20	-5,82	17,95
	1934	82,03	-6,09	17,73
5- BiBg	1026	81,32	-5,79	18,11
	1330	81,77	-5,98	15,88
	753	82,56	-6,21	19,85
	1270	82,78	-6,05	17,80
	929	80,81	-5,93	19,05
6- BiCm	302	83,53	-8,41	27,72
	285	82,55	-7,01	19,98
	275	84,59	-7,61	23,07
	204	83,25	-7,12	19,91
	304	78,13	-6,90	18,81
	354	82,93	-7,27	19,16
7- CoZa	1445	80,75	-5,84	21,88
	1003	81,53	-5,74	20,46
	1550	80,06	-5,70	19,72
	907	77,53	-5,28	20,21
	1416	77,44	-5,74	19,17

Tab. LXII: Results of white cabbage physical properties; variety: Naruto; class: 110-120 days; period: July- November.

Sample	d.m	FRAP	Folin	Ascorbic Acid	N	Cl^-	NO_2^-	NO_3^-	PO_4^{---}	SO_4^{--}	Na^+	NH_4^+	K^+	Mg^{++}	Ca^{++}	Chlorogenic acid	Caffeic acid	Coumaric acid	Ferulic acid	Sinapic acid	Sulforaphane	Glucose	Fructose
1- CoZo A	6,8	19768,7	2424,5	7692,9	3,3	1994,2	7,9	164,3	7449,7	5451,4	1383,4	27,1	30116,3	1219,7	4835,6	/	13,3	3,5	1,4	11,4	10,8	5764,9	6155,6
CoZo B	7,1	18967,2	2072,8	7299,5	3,4	1898,0	54,2	204,5	6876,2	5202,1	1469,9	22,8	31042,9	1139,0	4412,4	/	15,0	3,9	2,2	14,1	20,3	5604,1	7046,0
CoZo C	6,8	15450,8	1943,5	8086,3	3,8	1785,9	50,8	124,1	7785,3	5059,1	1425,3	31,5	30501,2	1158,6	4384,6	/	13,7	3,1	2,6	10,4	8,3	5684,5	5081,7
2- BiMt A	6,6	24420,8	2190,6	2809,2	3,0	3664,1	16,2	265,2	6736,7	6325,8	1104,9	26,6	32540,2	1062,8	4756,7	/	15,5	/	2,0	14,3	16,7	3952,3	5872,0
BiMt B	6,6	26236,1	2173,6	3587,6	3,1	3354,8	22,6	284,7	6636,0	6157,5	1197,5	25,4	32346,9	1100,4	5172,9	/	11,6	/	0,3	6,4	10,2	3248,1	10325,4
BiMt C	6,5	20978,9	1927,0	3198,4	3,1	3515,3	70,5	245,6	6402,4	6136,0	1235,4	27,8	31275,5	1203,9	5189,8	/	10,9	/	0,5	5,4	23,3	2543,9	5172,5
3- CoMa A	7,4	29494,0	2385,9	5901,4	3,5	2350,9	62,3	948,9	7273,9	4743,5	1694,6	62,2	31439,8	1107,9	4342,7	/	13,8	2,4	2,8	13,7	15,9	3851,4	5335,2
CoMa B	7,2	23506,2	2125,5	6617,1	3,8	2762,5	77,6	1026,2	7715,9	5217,8	1908,6	52,0	33235,8	1234,6	4813,5	/	18,9	2,0	3,1	16,9	42,2	3367,4	4982,9
CoMa C	7,2	24886,1	2214,2	6406,5	3,7	2520,9	70,0	987,6	7906,5	4828,5	1791,4	57,1	31576,2	1158,6	4574,7	/	14,6	1,0	2,2	16,5	11,3	2883,3	5537,9
4- BdTm A	7,4	28770,1	2178,2	7646,0	2,9	1945,9	55,1	370,7	6815,5	5822,6	898,9	27,7	32868,8	1160,0	4733,3	/	21,4	/	0,4	11,9	19,2	5195,7	5873,5

BdTm B	7,5	26275,3	2107,6	7877,2	3,0	1934,8	45,0	446,1	7037,5	5619,4	910,2	32,0	33548,0	1169,7	4588,6	/	15,7	/	0,8	12,3	11,4	5075,7	6159,7
BdTm C	7,6	25763,2	2086,9	7414,8	3,0	1847,0	91,3	295,3	7280,7	5845,1	754,3	23,5	35203,3	1073,9	4203,6	/	20,4	/	1,9	20,2	10,1	4955,6	6497,5
5- BiBg A	6,6	33884,2	2640,4	9248,1	3,3	1878,2	33,2	426,2	7687,1	6733,2	1072,7	21,6	33864,6	1192,7	5015,5	/	16,4	/	0,4	9,6	14,6	4899,6	6932,9
BiBg B	6,6	30570,2	2283,8	9329,6	3,1	1770,6	28,4	437,6	7819,5	6692,1	1055,6	24,4	33844,9	1312,2	5160,0	/	17,7	/	0,5	10,1	18,6	5035,8	5867,4
BiBg C	6,5	31647,7	2537,3	9998,3	3,1	1913,0	33,4	414,8	7673,0	7228,7	1043,3	18,8	34019,3	1335,0	5037,4	/	21,6	/	0,6	10,0	9,8	4763,4	7507,0
6- BiCm A	7,8	38173,8	2919,5	8227,4	2,86	1907,1	33,9	246,1	6125,7	4961,6	1214,6	24,2	32462,9	1431,8	5676,3	28,51	28,8	13,5	13,4	34,0	0,0	6985,4	8357,1
BiCm B	7,9	35352,9	2876,9	8406,8	2,85	1949,7	15,6	234,1	6380,0	5090,1	1083,3	20,9	33336,7	1321,4	5343,1	35,08	31,7	16,2	15,7	41,8	0,0	6404,4	6913,0
BiCm C	7,8	37596,9	2799,7	9452,6	2,86	2175,3	47,2	254,2	6542,4	5046,2	1228,1	27,4	33124,3	1490,5	5465,3	44,38	34,2	18,2	20,8	50,3	0,0	5823,4	7622,3
7- CoZa A	7,3	37421,9	2915,0	8467,0	4,10	2088,5	188,6	443,8	8193,4	5725,6	1255,8	35,5	41312,5	1381,6	4462,4	/	17,6	/	0,9	10,6	24,1	1872,7	4564,5
CoZa B	7,2	31860,2	2621,2	8926,4	4,04	1994,1	225,4	329,9	10129,8	5903,0	1280,7	20,2	41968,7	1435,1	4800,3	/	18,8	/	2,2	11,7	12,7	1436,6	4662,1
CoZa C	7,4	32456,6	2458,1	7997,7	4,07	2162,4	207,0	216,0	9597,5	5985,8	1371,9	50,8	42589,1	1470,0	4950,7	/	21,8	/	1,5	11,0	10,7	2863,4	4645,1

Tab. LXIII: Results about white cabbage nutritional properties; variety: Naruto; class: 110-120 days; period: July- November. Data are referred to dry weight. D.m. in %; FRAP in mg Fe2+E/kg; Folin in mg GAE/kg; N in %; all the other data are expressed in mg/kg.

H- Significant correlation coefficients between all measured indicators

Indicator	Variable A	Variable B	Correlation coefficient	Significance	Test	N° correlations
AMF	AMF	F	**0,79098**	0,034156	Pearson	*
AMF	AMF	Water resp.	**0,73097**	0,016316	Pearson	*
AMF	AMF	S.I.R.	**0,71129**	0,02108	Pearson	*
AMF	AMF	dsDNA	**0,9281**	0,007569	Pearson	**
AMF	AMF	AryS	**0,96401**	0,00192	Pearson	**
AMF	AMF	acP	**0,90355**	0,013506	Pearson	*
AMF	AMF	Piro	**0,8567**	0,029332	Pearson	*
AMF	AMF	alkP	**0,86017**	0,027961	Pearson	*
AMF	AMF	Leu	**0,83606**	0,038112	Pearson	*
AMF	AMF	Ester	**0,8539**	0,030459	Pearson	*
AMF	AMF	QBS-ar	**0,8834**	0,000701	Pearson	***
AMF	AMF	N	**-0,76064**	0,047095	Pearson	*
AMF	AMF	Fructose	**0,87842**	0,009262	Pearson	**
AMF	AMF	Dominance_D_Mesof	**-0,71199**	0,047567	Pearson	**
AMF	AMF	Simpson_1-D_Mesof	**0,71199**	0,047567	Pearson	*
AMF	AMF	Araneae	**0,85236**	0,014832	Pearson	*
AMF	AMF	Nabidae	**0,75463**	0,049934	Pearson	*
AMF	AMF	Staphylinidae	**0,78405**	0,036913	Pearson	*
AMF	AMF	Equitability_J_BARISA	**-0,63592**	0,048114	Pearson	*
AMF	AMF	Taxa_S_Phyt	**0,77521**	0,040597	Pearson	*
AMF	AMF	Dominance_D_Phyt	**-0,79393**	0,033019	Pearson	*

AMF	AMF	Simpson_1-D_Phyt	**0,79393**	0,033019	Pearson	*	
AMF	AMF	Shannon_H_Phyt	**0,83795**	0,01857	Pearson	*	
AMF	AMF	Evenness_e^H/S_Carab	**0,7326**	0,024772	Pearson	*	24
B16S	Dominance_D_B16S	Evenness_e^H/S_FARISA	**-0,86667**	0,003075	Spearman	**	
B16S	Dominance_D_B16S	Equitability_J_FARISA	**-0,8**	0,010769	Spearman	*	
B16S	Dominance_D_B16S	Aleyrodidae	**0,84391**	0,016966	Pearson	*	
B16S	Dominance_D_B16S	T.O.C.	**0,83548**	0,005044	Pearson	**	
B16S	Dominance_D_B16S	Org. matter	**0,83539**	0,005052	Pearson	**	
B16S	Dominance_D_B16S	Ascorbic acid	**-0,87728**	0,009476	Pearson	**	
B16S	Dominance_D_B16S	Mg++	**-0,81679**	0,024936	Pearson	*	
B16S	Dominance_D_B16S	Folin	**-0,78521**	0,036443	Pearson	*	8
B16S	Equitability_J_B16S	Chrysopidae	**0,87845**	0,009256	Pearson	**	
B16S	Equitability_J_B16S	Taxa_S_Mesof	**0,7301**	0,025522	Pearson	*	
B16S	Equitability_J_B16S	Silk N % degrad	**-0,76412**	0,016517	Pearson	*	
B16S	Equitability_J_B16S	NO3-	**-0,76927**	0,04318	Pearson	*	4
B16S	Evenness_e^H/S_B16S	Chrysopidae	**0,87588**	0,009739	Pearson	**	
B16S	Evenness_e^H/S_B16S	Taxa_S_Mesof	**0,71793**	0,029395	Pearson	*	
B16S	Evenness_e^H/S_B16S	Silk N % degrad	**-0,74991**	0,019966	Pearson	*	
B16S	Evenness_e^H/S_B16S	NO3-	**-0,78277**	0,037434	Pearson	*	4
B16S	Shannon_H_B16S	Chrysopidae	**0,86425**	0,012106	Pearson	*	
B16S	Shannon_H_B16S	Taxa_S_Mesof	**0,70382**	0,034344	Pearson	*	
B16S	Shannon_H_B16S	Silk N % degrad	**-0,72886**	0,025902	Pearson	*	
B16S	Shannon_H_B16S	NO3-	**-0,80464**	0,029075	Pearson	*	4
B16S	Simpson_1-D_B16S	Evenness_e^H/S_FARISA	**0,86667**	0,003075	Spearman	**	
B16S	Simpson_1-D_B16S	Equitability_J_FARISA	**0,8**	0,010769	Spearman	*	
B16S	Simpson_1-D_B16S	Aleyrodidae	**-0,84399**	0,016945	Pearson	*	
B16S	Simpson_1-D_B16S	T.O.C.	**-0,83543**	0,005049	Pearson	**	
B16S	Simpson_1-D_B16S	Org. matter	**-0,83535**	0,005057	Pearson	**	
B16S	Simpson_1-D_B16S	Ascorbic acid	**0,87734**	0,009465	Pearson	**	
B16S	Simpson_1-D_B16S	Mg++	**0,81651**	0,025026	Pearson	*	
B16S	Simpson_1-D_B16S	Folin	**0,78493**	0,036553	Pearson	*	8
B16S	Taxa_S_B16S	Urban150	**-0,84414**	0,004211	Pearson	**	
B16S	Taxa_S_B16S	Shannon_H_Carab	**0,82617**	0,011479	Pearson	*	
B16S	Taxa_S_B16S	Equitability_J_Carab	**0,81938**	0,012807	Pearson	*	
B16S	Taxa_S_B16S	Simpson_1-D_Wm	**0,76667**	0,02139	Spearman	*	
B16S	Taxa_S_B16S	Urban500	**-0,71629**	0,029945	Pearson	*	
B16S	Taxa_S_B16S	Shannon_H_Wf	**-0,74505**	0,033912	Pearson	*	
B16S	Taxa_S_B16S	Dominance_D_Phyt	**-0,791**	0,03415	Pearson	*	
B16S	Taxa_S_B16S	Simpson_1-D_Phyt	**0,791**	0,03415	Pearson	*	
B16S	Taxa_S_B16S	Equitability_J_Phyt	**0,78025**	0,038473	Pearson	*	
B16S	Taxa_S_B16S	Evenness_e^H/S_Carab	**0,73162**	0,039123	Pearson	*	
B16S	Taxa_S_B16S	Evenness_e^H/S_Phyt	**0,75536**	0,049584	Pearson	*	
B16S	Taxa_S_B16S	Sand	**0,87407**	0,002059	Pearson	**	
B16S	Taxa_S_B16S	Clay	**-0,83877**	0,004715	Pearson	**	
B16S	Taxa_S_B16S	F	**0,84187**	0,017507	Pearson	*	
B16S	Taxa_S_B16S	Basal resp.	**0,72143**	0,028244	Pearson	*	
B16S	Taxa_S_B16S	C.S.C.	**0,6785**	0,044519	Pearson	*	16
B_ARISA	Dominance_D_BARISA	Mineral. Coeff.	**0,61977**	0,041964	Pearson	*	1
B_ARISA	Equitability_J_BARISA	AMF	**-0,63592**	0,048114	Pearson	*	
B_ARISA	Equitability_J_BARISA	Cicadellidae	**0,92988**	0,002408	Pearson	**	
B_ARISA	Equitability_J_BARISA	Leu	**-0,94798**	0,003989	Pearson	**	
B_ARISA	Equitability_J_BARISA	QBS-ar	**-0,78614**	0,007006	Pearson	**	
B_ARISA	Equitability_J_BARISA	Gluc	**-0,91877**	0,009629	Pearson	**	
B_ARISA	Equitability_J_BARISA	SO4--	**-0,8575**	0,013614	Pearson	*	
B_ARISA	Equitability_J_BARISA	dsDNA	**-0,88972**	0,017572	Pearson	*	
B_ARISA	Equitability_J_BARISA	acP	**-0,88582**	0,01881	Pearson	*	
B_ARISA	Equitability_J_BARISA	QBS-e	**-0,68949**	0,02739	Pearson	*	
B_ARISA	Equitability_J_BARISA	Aphididae	**-0,80843**	0,027746	Pearson	*	
B_ARISA	Equitability_J_BARISA	Ester	**-0,85255**	0,03101	Pearson	*	
B_ARISA	Equitability_J_BARISA	Tot N dm	**-0,64125**	0,033472	Pearson	*	

B_ARISA	Equitability_J_BARISA	Exch. Na	**-0,63207**	0,036937	Pearson	*	
B_ARISA	Equitability_J_BARISA	alkP	**-0,8345**	0,03882	Pearson	*	
B_ARISA	Equitability_J_BARISA	AryS	**-0,83295**	0,039527	Pearson	*	
B_ARISA	Equitability_J_BARISA	Syrphidae	**-0,76035**	0,047231	Pearson	*	16
B_ARISA	Evenness_e^H/S_BARISA	Cicadellidae	**0,95114**	0,000987	Pearson	***	
B_ARISA	Evenness_e^H/S_BARISA	QBS-ar	**-0,79005**	0,00654	Pearson	**	
B_ARISA	Evenness_e^H/S_BARISA	Leu	**-0,93079**	0,007018	Pearson	**	
B_ARISA	Evenness_e^H/S_BARISA	Gluc	**-0,89432**	0,016163	Pearson	*	
B_ARISA	Evenness_e^H/S_BARISA	Tot N dm	**-0,69298**	0,018072	Pearson	*	
B_ARISA	Evenness_e^H/S_BARISA	Exch. Na	**-0,67988**	0,021352	Pearson	*	
B_ARISA	Evenness_e^H/S_BARISA	Syrphidae	**-0,82289**	0,022993	Pearson	*	
B_ARISA	Evenness_e^H/S_BARISA	SO4--	**-0,81545**	0,025373	Pearson	*	
B_ARISA	Evenness_e^H/S_BARISA	dsDNA	**-0,86688**	0,025401	Pearson	*	
B_ARISA	Evenness_e^H/S_BARISA	Ester	**-0,84515**	0,034112	Pearson	*	
B_ARISA	Evenness_e^H/S_BARISA	acP	**-0,83948**	0,036582	Pearson	*	
B_ARISA	Evenness_e^H/S_BARISA	C/N (Humific.)	**0,62226**	0,040908	Pearson	*	
B_ARISA	Evenness_e^H/S_BARISA	Aphididae	**-0,76138**	0,046755	Pearson	*	
B_ARISA	Evenness_e^H/S_BARISA	Taxa_S_Mesof	**-0,63537**	0,048369	Pearson	*	14
B_ARISA	Shannon_H_BARISA	Cicadellidae	**0,93191**	0,002239	Pearson	**	
B_ARISA	Shannon_H_BARISA	Leu	**-0,95909**	0,002476	Pearson	**	
B_ARISA	Shannon_H_BARISA	QBS-ar	**-0,79334**	0,006166	Pearson	**	
B_ARISA	Shannon_H_BARISA	Gluc	**-0,93051**	0,007077	Pearson	**	
B_ARISA	Shannon_H_BARISA	dsDNA	**-0,9017**	0,01402	Pearson	*	
B_ARISA	Shannon_H_BARISA	Tot N dm	**-0,68279**	0,020589	Pearson	*	
B_ARISA	Shannon_H_BARISA	acP	**-0,88015**	0,020685	Pearson	*	
B_ARISA	Shannon_H_BARISA	SO4--	**-0,81027**	0,027113	Pearson	*	
B_ARISA	Shannon_H_BARISA	Syrphidae	**-0,8039**	0,029337	Pearson	*	
B_ARISA	Shannon_H_BARISA	Ester	**-0,85305**	0,030805	Pearson	*	
B_ARISA	Shannon_H_BARISA	AryS	**-0,84836**	0,032747	Pearson	*	
B_ARISA	Shannon_H_BARISA	Exch. Na	**-0,63388**	0,036236	Pearson	*	
B_ARISA	Shannon_H_BARISA	QBS-e	**-0,66093**	0,037463	Pearson	*	
B_ARISA	Shannon_H_BARISA	alkP	**-0,83573**	0,03826	Pearson	*	
B_ARISA	Shannon_H_BARISA	Aphididae	**-0,76622**	0,044547	Pearson	*	15
B_ARISA	Simpson_1-D_BARISA	Mineral. Coeff.	**-0,6194**	0,042121	Pearson	*	1
B_ARISA	Taxa_S_BARISA	Mineral. Coeff.	**-0,7374**	0,009604	Spearman	**	
B_ARISA	Taxa_S_BARISA	Tot. Calc.	**0,72818**	0,011054	Spearman	*	
B_ARISA	Taxa_S_BARISA	In C dm	**0,7206**	0,01236	Spearman	*	
B_ARISA	Taxa_S_BARISA	Equitability_J_Earthw	**-0,66678**	0,035222	Spearman	*	
B_ARISA	Taxa_S_BARISA	Evenness_e^H/S_Mesof	**-0,76109**	0,036905	Spearman	*	
B_ARISA	Taxa_S_BARISA	Tot C dm	**0,6314**	0,037202	Spearman	*	6
Carab	Dominance_D_Carab	FRAP	**-0,9269**	0,00782	Pearson	**	
Carab	Dominance_D_Carab	Exch. Na	**-0,80484**	0,008882	Pearson	**	
Carab	Dominance_D_Carab	Mineral. Coeff.	**-0,74448**	0,0214	Pearson	*	
Carab	Dominance_D_Carab	C/N (Humific.)	**0,74297**	0,021811	Pearson	*	
Carab	Dominance_D_Carab	Taxa_S_Wm	**-0,72848**	0,026018	Pearson	*	
Carab	Dominance_D_Carab	Evenness_e^H/S_Pred	**-0,95512**	0,044885	Pearson	*	
Carab	Dominance_D_Carab	P (Olsen)	**-0,67257**	0,047151	Pearson	*	7
Carab	Equitability_J_Carab	Arable500	**0,67874**	0,04441	Pearson	*	
Carab	Equitability_J_Carab	Urban150	**-0,67531**	0,045921	Pearson	*	
Carab	Equitability_J_Carab	Equitability_J_Phyt	**0,98797**	0,000216	Pearson	***	
Carab	Equitability_J_Carab	Phyllotreta sp.	**-0,97386**	0,001016	Pearson	**	
Carab	Equitability_J_Carab	Evenness_e^H/S_Phyt	**0,97233**	0,001138	Pearson	**	
Carab	Equitability_J_Carab	Shannon_H_Phyt	**0,95312**	0,003245	Pearson	**	
Carab	Equitability_J_Carab	Dominance_D_Phyt	**-0,93646**	0,005929	Pearson	**	
Carab	Equitability_J_Carab	Simpson_1-D_Phyt	**0,93646**	0,005929	Pearson	**	
Carab	Equitability_J_Carab	Gluc	**0,95177**	0,012621	Pearson	*	
Carab	Equitability_J_Carab	Taxa_S_B16S	**0,81938**	0,012807	Pearson	*	
Carab	Equitability_J_Carab	Nabidae	**0,8833**	0,019635	Pearson	*	
Carab	Equitability_J_Carab	Sand	**0,75044**	0,01983	Pearson	*	
Carab	Equitability_J_Carab	Leu	**0,93464**	0,019863	Pearson	*	

Carab	Equitability_J_Carab	Clay	**-0,72568**	0,026887	Pearson	*	
Carab	Equitability_J_Carab	F	**0,85105**	0,031629	Pearson	*	
Carab	Equitability_J_Carab	Araneae	**0,83282**	0,039588	Pearson	*	
Carab	Equitability_J_Carab	AryS	**0,89266**	0,041528	Pearson	*	
Carab	Equitability_J_Carab	Na+	**-0,81142**	0,04999	Pearson	*	18
Carab	Evenness_e^H/S_Carab	AMF	**0,7326**	0,024772	Pearson	*	
Carab	Evenness_e^H/S_Carab	Equitability_J_Phyt	**0,97673**	0,000806	Pearson	***	
Carab	Evenness_e^H/S_Carab	Phyllotreta sp.	**-0,97186**	0,001177	Pearson	**	
Carab	Evenness_e^H/S_Carab	Evenness_e^H/S_Phyt	**0,96808**	0,001512	Pearson	**	
Carab	Evenness_e^H/S_Carab	Shannon_H_Phyt	**0,9627**	0,002061	Pearson	**	
Carab	Evenness_e^H/S_Carab	Nabidae	**0,9382**	0,005611	Pearson	**	
Carab	Evenness_e^H/S_Carab	Gluc	**0,9683**	0,006742	Pearson	**	
Carab	Evenness_e^H/S_Carab	Leu	**0,96829**	0,006745	Pearson	**	
Carab	Evenness_e^H/S_Carab	AryS	**0,966**	0,007488	Pearson	**	
Carab	Evenness_e^H/S_Carab	Dominance_D_Phyt	**-0,92197**	0,008895	Pearson	**	
Carab	Evenness_e^H/S_Carab	Simpson_1-D_Phyt	**0,92197**	0,008895	Pearson	**	
Carab	Evenness_e^H/S_Carab	dsDNA	**0,94364**	0,015923	Pearson	*	
Carab	Evenness_e^H/S_Carab	F	**0,88542**	0,018942	Pearson	*	
Carab	Evenness_e^H/S_Carab	Araneae	**0,86918**	0,024553	Pearson	*	
Carab	Evenness_e^H/S_Carab	Taxa_S_B16S	**0,73162**	0,039123	Pearson	*	
Carab	Evenness_e^H/S_Carab	Na+	**-0,82632**	0,042629	Pearson	*	
Carab	Evenness_e^H/S_Carab	acP	**0,8443**	0,072006	Pearson	*	17
Carab	Shannon_H_Carab	Equitability_J_Phyt	**0,97675**	0,000805	Pearson	***	
Carab	Shannon_H_Carab	Phyllotreta sp.	**-0,95532**	0,00295	Pearson	**	
Carab	Shannon_H_Carab	Evenness_e^H/S_Phyt	**0,95235**	0,003352	Pearson	**	
Carab	Shannon_H_Carab	Shannon_H_Phyt	**0,94819**	0,003957	Pearson	**	
Carab	Shannon_H_Carab	Taxa_S_B16S	**0,82617**	0,011479	Pearson	*	
Carab	Shannon_H_Carab	Dominance_D_Phyt	**-0,89552**	0,015802	Pearson	*	
Carab	Shannon_H_Carab	Simpson_1-D_Phyt	**0,89552**	0,015802	Pearson	*	
Carab	Shannon_H_Carab	Gluc	**0,92782**	0,023025	Pearson	*	
Carab	Shannon_H_Carab	F	**0,8637**	0,0266	Pearson	*	
Carab	Shannon_H_Carab	Clay	**-0,72108**	0,028358	Pearson	*	
Carab	Shannon_H_Carab	Nabidae	**0,85615**	0,029552	Pearson	*	
Carab	Shannon_H_Carab	Leu	**0,91246**	0,030682	Pearson	*	
Carab	Shannon_H_Carab	Sand	**0,71065**	0,031884	Pearson	*	
Carab	Shannon_H_Carab	Na+	**-0,84603**	0,033734	Pearson	*	
Carab	Shannon_H_Carab	Basal resp.	**0,69035**	0,039544	Pearson	*	
Carab	Shannon_H_Carab	Araneae	**0,82926**	0,041238	Pearson	*	
Carab	Shannon_H_Carab	AryS	**0,88522**	0,045865	Pearson	*	17
Carab	Simpson_1-D_Carab	Urban500	**-0,83055**	0,040636	Pearson	*	
Carab	Simpson_1-D_Carab	FRAP	**0,92077**	0,009167	Pearson	**	
Carab	Simpson_1-D_Carab	Exch. Mg	**0,83758**	0,037429	Pearson	*	
Carab	Simpson_1-D_Carab	Clay	**-0,82682**	0,042392	Pearson	*	4
Carab	Taxa_S_Carab	Exch. Mg	**0,70785**	0,032878	Pearson	*	
Carab	Taxa_S_Carab	Shannon_H_FITS	**-0,73206**	0,038943	Pearson	*	2
Crop NP	Ascorbic acid	Aleyrodidae	**-0,94131**	0,001553	Pearson	**	
Crop NP	Ascorbic acid	Simpson_1-D_B16S	**0,87734**	0,009465	Pearson	**	
Crop NP	Ascorbic acid	Dominance_D_B16S	**-0,87728**	0,009476	Pearson	**	
Crop NP	Ascorbic acid	Evenness_e^H/S_Mesof	**-0,8516**	0,031402	Pearson	*	
Crop NP	Ascorbic acid	Evenness_e^H/S_FARISA	**0,82143**	0,034127	Spearman	*	
Crop NP	Ascorbic acid	Equitability_J_FARISA	**0,78571**	0,048016	Spearman	*	
Crop NP	Ascorbic acid	Exch. K	**-0,80131**	0,030273	Pearson	*	7
Crop NP	Ca++	Syrphidae	**0,89273**	0,006826	Pearson	**	
Crop NP	Ca++	Formicidae	**0,85262**	0,01477	Pearson	*	
Crop NP	Ca++	Staphylinidae	**0,81063**	0,02699	Pearson	*	
Crop NP	Ca++	Equitability_J_Pred	**0,96218**	0,03782	Pearson	*	
Crop NP	Ca++	Taxa_S_Mesof	**0,77798**	0,03942	Pearson	*	
Crop NP	Ca++	Evenness_e^H/S_FITS	**-0,81481**	0,048265	Pearson	*	
Crop NP	Ca++	Taxa_S_paras	**-0,82944**	0,021003	Pearson	*	
Crop NP	Ca++	Evenness_e^H/S_paras	**0,7821**	0,037708	Pearson	*	

Crop NP	Ca++	P (Olsen)	**0,76636**	0,044483	Pearson	*	9
Crop NP	Caffeic acid	Evenness_e^H/S_Pred	**0,9986**	0,001405	Pearson	**	
Crop NP	Caffeic acid	Sinapic acid	**0,90179**	0,005503	Pearson	**	
Crop NP	Caffeic acid	Shannon_H_FITS	**-0,85135**	0,031505	Pearson	*	
Crop NP	Caffeic acid	Formicidae	**0,77011**	0,042813	Pearson	*	
Crop NP	Caffeic acid	Equitability_J_FITS	**-0,82539**	0,043069	Pearson	*	
Crop NP	Caffeic acid	Exch. Mg	**0,93058**	0,002349	Pearson	**	
Crop NP	Caffeic acid	Folin	**0,84225**	0,017405	Pearson	*	
Crop NP	Caffeic acid	FRAP	**0,80978**	0,02728	Pearson	*	8
Crop NP	Cl-	Pentatomidae	**-0,81537**	0,038095	Spearman	*	
Crop NP	Cl-	Cotton ctrl % degrad	**-0,82143**	0,034127	Spearman	*	2
Crop NP	dry matter	Pulmonata	**-0,90633**	0,028571	Spearman	*	
Crop NP	dry matter	Aphididae	**-0,80358**	0,029451	Pearson	*	
Crop NP	dry matter	Sinapic acid	**0,79264**	0,033514	Pearson	*	3
Crop NP	Ferulic acid	SO4--	**-0,92857**	0,006746	Spearman	**	
Crop NP	Ferulic acid	Silt	**0,92857**	0,006746	Spearman	**	2
Crop NP	Folin	Mg++	**0,96811**	0,000343	Pearson	***	
Crop NP	Folin	Simpson_1-D_Pred	**0,98482**	0,015184	Pearson	*	
Crop NP	Folin	Dominance_D_Pred	**-0,9847**	0,015298	Pearson	*	
Crop NP	Folin	Caffeic acid	**0,84225**	0,017405	Pearson	*	
Crop NP	Folin	Dominance_D_B16S	**-0,78521**	0,036443	Pearson	*	
Crop NP	Folin	Simpson_1-D_B16S	**0,78493**	0,036553	Pearson	*	
Crop NP	Folin	FRAP	**0,89586**	0,006351	Pearson	**	
Crop NP	Folin	Exch. Mg	**0,84751**	0,016036	Pearson	*	
Crop NP	Folin	Mineral. Coeff.	**0,77205**	0,04196	Pearson	*	9
Crop NP	FRAP	Folin	**0,89586**	0,006351	Pearson	**	
Crop NP	FRAP	Dominance_D_Carab	**-0,9269**	0,00782	Pearson	**	
Crop NP	FRAP	Simpson_1-D_Carab	**0,92077**	0,009167	Pearson	**	
Crop NP	FRAP	Mg++	**0,83676**	0,018899	Pearson	*	
Crop NP	FRAP	Caffeic acid	**0,80978**	0,02728	Pearson	*	
Crop NP	FRAP	K+	**0,78571**	0,048016	Spearman	*	
Crop NP	FRAP	Exch. Mg	**0,89278**	0,006819	Pearson	**	7
Crop NP	Fructose	AMF	**0,87842**	0,009262	Pearson	**	
Crop NP	Fructose	Taxa_S_Phyt	**0,95158**	0,000965	Pearson	***	
Crop NP	Fructose	Dominance_D_Mesof	**-0,93433**	0,006327	Pearson	**	
Crop NP	Fructose	Simpson_1-D_Mesof	**0,93433**	0,006327	Pearson	**	
Crop NP	Fructose	Formicidae	**0,8528**	0,014725	Pearson	*	
Crop NP	Fructose	Shannon_H_Earthw	**0,84276**	0,017268	Pearson	*	
Crop NP	Fructose	Araneae	**0,84201**	0,017468	Pearson	*	
Crop NP	Fructose	Staphylinidae	**0,80839**	0,027758	Pearson	*	
Crop NP	Fructose	Evenness_e^H/S_paras	**0,82563**	0,022148	Pearson	*	
Crop NP	Fructose	N	**-0,90855**	0,004622	Pearson	**	
Crop NP	Fructose	S.I.R.	**0,87**	0,010899	Pearson	*	
Crop NP	Fructose	PO4---	**-0,86653**	0,011618	Pearson	*	
Crop NP	Fructose	NO2-	**-0,84654**	0,016285	Pearson	*	
Crop NP	Fructose	QBS-ar	**0,82127**	0,0235	Pearson	*	
Crop NP	Fructose	P (Olsen)	**0,81044**	0,027053	Pearson	*	15
Crop NP	Glucose	Taxa_S_Wf	**0,84347**	0,017081	Pearson	*	
Crop NP	Glucose	Taxa_S_Phyt	**0,81301**	0,026185	Pearson	*	
Crop NP	Glucose	Evenness_e^H/S_Pred	**0,96044**	0,039561	Pearson	*	
Crop NP	Glucose	Cotton ctrl % degrad	**0,93321**	0,002136	Pearson	**	4
Crop NP	K+	FRAP	**0,78571**	0,048016	Spearman	*	1
Crop NP	Mg++	Evenness_e^H/S_FARISA	**0,85714**	0,012302	Spearman	*	
Crop NP	Mg++	Simpson_1-D_Pred	**0,9816**	0,018396	Pearson	*	
Crop NP	Mg++	Dominance_D_Pred	**-0,98142**	0,018576	Pearson	*	
Crop NP	Mg++	Dominance_D_B16S	**-0,81679**	0,024936	Pearson	*	
Crop NP	Mg++	Simpson_1-D_B16S	**0,81651**	0,025026	Pearson	*	
Crop NP	Mg++	Equitability_J_FARISA	**0,78571**	0,048016	Spearman	*	
Crop NP	Mg++	Folin	**0,96811**	0,000343	Pearson	***	
Crop NP	Mg++	FRAP	**0,83676**	0,018899	Pearson	*	8

Crop NP	N	AMF	**-0,76064**	0,047095	Pearson	*	
Crop NP	N	Fructose	**-0,90855**	0,004622	Pearson	**	
Crop NP	N	PO4---	**0,88201**	0,00861	Pearson	**	
Crop NP	N	Araneae	**-0,87563**	0,009788	Pearson	**	
Crop NP	N	Shannon_H_Earthw	**-0,86183**	0,012634	Pearson	*	
Crop NP	N	Taxa_S_Phyt	**-0,82534**	0,022234	Pearson	*	
Crop NP	N	Formicidae	**-0,82474**	0,022418	Pearson	*	
Crop NP	N	Taxa_S_Wm	**-0,81758**	0,024677	Pearson	*	
Crop NP	N	NO2-	**0,78872**	0,035043	Pearson	*	
Crop NP	N	Dominance_D_Mesof	**0,84282**	0,035115	Pearson	*	
Crop NP	N	Simpson_1-D_Mesof	**-0,84282**	0,035115	Pearson	*	
Crop NP	N	Shannon_H_Phyt	**-0,78445**	0,036747	Pearson	*	
Crop NP	N	Evenness_e^H/S_Wf	**0,77206**	0,041959	Pearson	*	
Crop NP	N	S.I.R.	**-0,97527**	0,000182	Pearson	***	
Crop NP	N	Basal resp.	**-0,78927**	0,034825	Pearson	*	15
Crop NP	Na+	Dominance_D_Earthw	**0,87262**	0,010372	Pearson	*	
Crop NP	Na+	Simpson_1-D_Earthw	**-0,87262**	0,010372	Pearson	*	
Crop NP	Na+	Arable500	**-0,84925**	0,0156	Pearson	*	
Crop NP	Na+	Shannon_H_Wm	**-0,8299**	0,020865	Pearson	*	
Crop NP	Na+	Dominance_D_Wm	**0,80587**	0,028637	Pearson	*	
Crop NP	Na+	NH4+	**0,79776**	0,031578	Pearson	*	
Crop NP	Na+	Shannon_H_Carab	**-0,84603**	0,033734	Pearson	*	
Crop NP	Na+	Urban500	**0,77789**	0,039457	Pearson	*	
Crop NP	Na+	Evenness_e^H/S_Carab	**-0,82632**	0,042629	Pearson	*	
Crop NP	Na+	Taxa_S_Wm	**-0,76228**	0,04634	Pearson	*	
Crop NP	Na+	Equitability_J_Carab	**-0,81142**	0,04999	Pearson	*	
Crop NP	Na+	Silk P % degrad	**-0,84993**	0,015428	Pearson	*	
Crop NP	Na+	QBS-e	**-0,80473**	0,029043	Pearson	*	
Crop NP	Na+	Leu	**-0,85209**	0,031199	Pearson	*	
Crop NP	Na+	Ester	**-0,84617**	0,033676	Pearson	*	15

Crop NP	NH4+	Dominance_D_Earthw	**0,97048**	0,000283	Pearson	***	
Crop NP	NH4+	Simpson_1-D_Earthw	**-0,97048**	0,000283	Pearson	***	
Crop NP	NH4+	Lepidoptera	**0,86498**	0,011949	Pearson	*	
Crop NP	NH4+	Shannon_H_Earthw	**-0,83953**	0,018137	Pearson	*	
Crop NP	NH4+	Dominance_D_Mesof	**0,86002**	0,028019	Pearson	*	
Crop NP	NH4+	Simpson_1-D_Mesof	**-0,86002**	0,028019	Pearson	*	
Crop NP	NH4+	Thripidae	**-0,86692**	0,028571	Spearman	*	
Crop NP	NH4+	Dominance_D_Wm	**0,79284**	0,033437	Pearson	*	
Crop NP	NH4+	Cicadellidae	**0,76573**	0,044765	Pearson	*	
Crop NP	NH4+	Shannon_H_Wm	**-0,76201**	0,046464	Pearson	*	
Crop NP	NH4+	Ester	**-0,90079**	0,014275	Pearson	*	
Crop NP	NH4+	Na+	**0,79776**	0,031578	Pearson	*	12
Crop NP	NO2-	Dominance_D_Mesof	**0,98608**	0,000289	Pearson	***	
Crop NP	NO2-	Simpson_1-D_Mesof	**-0,98608**	0,000289	Pearson	***	
Crop NP	NO2-	Taxa_S_Phyt	**-0,90527**	0,005039	Pearson	**	
Crop NP	NO2-	PO4---	**0,85552**	0,014077	Pearson	*	
Crop NP	NO2-	Fructose	**-0,84654**	0,016285	Pearson	*	
Crop NP	NO2-	Taxa_S_Pred	**-0,97601**	0,023992	Pearson	*	
Crop NP	NO2-	Thripidae	**-0,86692**	0,028571	Spearman	*	
Crop NP	NO2-	Shannon_H_Earthw	**-0,78069**	0,038287	Pearson	*	
Crop NP	NO2-	S.I.R.	**-0,81506**	0,025503	Pearson	*	
Crop NP	NO2-	N	**0,78872**	0,035043	Pearson	*	
Crop NP	NO2-	Cotton ctrl % degrad	**-0,78524**	0,036429	Pearson	*	
Crop NP	NO2-	P (Olsen)	**-0,76293**	0,046042	Pearson	*	
Crop NP	NO2-	Tot N dm	**-0,75505**	0,049734	Pearson	*	13
Crop NP	NO3-	Lepidoptera	**0,93809**	0,001771	Pearson	**	
Crop NP	NO3-	Dominance_D_Wm	**0,80466**	0,029066	Pearson	*	
Crop NP	NO3-	Shannon_H_B16S	**-0,80464**	0,029075	Pearson	*	
Crop NP	NO3-	Chrysopidae	**-0,8027**	0,029768	Pearson	*	
Crop NP	NO3-	Evenness_e^H/S_B16S	**-0,78277**	0,037434	Pearson	*	

Crop NP	NO3-	Equitability_J_B16S	**-0,76927**	0,04318	Pearson	*	
Crop NP	NO3-	Shannon_H_Wm	**-0,76657**	0,044389	Pearson	*	
Crop NP	NO3-	Equitability_J_paras	**-0,8093**	0,027445	Pearson	*	8
Crop NP	PO4---	Dominance_D_Mesof	**0,91151**	0,011398	Pearson	*	
Crop NP	PO4---	Simpson_1-D_Mesof	**-0,91151**	0,011398	Pearson	*	
Crop NP	PO4---	Fructose	**-0,86653**	0,011618	Pearson	*	
Crop NP	PO4---	Taxa_S_Phyt	**-0,83472**	0,019472	Pearson	*	
Crop NP	PO4---	S.I.R.	**-0,93053**	0,002353	Pearson	**	
Crop NP	PO4---	N	**0,88201**	0,00861	Pearson	**	
Crop NP	PO4---	NO2-	**0,85552**	0,014077	Pearson	*	7
Crop NP	Sinapic acid	Evenness_e^H/S_Pred	**0,96588**	0,034125	Pearson	*	
Crop NP	Sinapic acid	Caffeic acid	**0,90179**	0,005503	Pearson	**	
Crop NP	Sinapic acid	Exch. Mg	**0,81167**	0,026637	Pearson	*	
Crop NP	Sinapic acid	Cotton P % degrad	**0,80881**	0,027612	Pearson	*	
Crop NP	Sinapic acid	dry matter	**0,79264**	0,033514	Pearson	*	5
Crop NP	SO4--	Urban1000	**-0,92383**	0,002951	Pearson	**	
Crop NP	SO4--	Ferulic acid	**-0,92857**	0,006746	Spearman	**	
Crop NP	SO4--	Aphididae	**0,87318**	0,010263	Pearson	*	
Crop NP	SO4--	Equitability_J_BARISA	**-0,8575**	0,013614	Pearson	*	
Crop NP	SO4--	Evenness_e^H/S_BARISA	**-0,81545**	0,025373	Pearson	*	
Crop NP	SO4--	Taxa_S_Earthw	**0,81535**	0,025408	Pearson	*	
Crop NP	SO4--	Shannon_H_BARISA	**-0,81027**	0,027113	Pearson	*	
Crop NP	SO4--	Taxa_S_FARISA	**0,80578**	0,02867	Pearson	*	
Crop NP	SO4--	Evenness_e^H/S_Earthw	**-0,77872**	0,039109	Pearson	*	
Crop NP	SO4--	Cicadellidae	**-0,76431**	0,045409	Pearson	*	
Crop NP	SO4--	Silt	**-0,89872**	0,005934	Pearson	**	
Crop NP	SO4--	QBS-e	**0,81237**	0,026401	Pearson	*	
Crop NP	SO4--	acP	**0,82417**	0,043658	Pearson	*	
Crop NP	SO4--	Leu	**0,81911**	0,046122	Pearson	*	14
dsDNA	dsDNA	AMF	**0,9281**	0,007569	Pearson	**	
dsDNA	dsDNA	Nabidae	**0,98876**	0,000189	Pearson	***	
dsDNA	dsDNA	AryS	**0,96558**	0,001756	Pearson	**	
dsDNA	dsDNA	acP	**0,965**	0,001816	Pearson	**	
dsDNA	dsDNA	Arable500	**0,9469**	0,004155	Pearson	**	
dsDNA	dsDNA	alkP	**0,94675**	0,004178	Pearson	**	
dsDNA	dsDNA	Leu	**0,94347**	0,004703	Pearson	**	
dsDNA	dsDNA	Cotton N % degrad	**0,98561**	0,005556	Spearman	**	
dsDNA	dsDNA	Gluc	**0,93294**	0,006595	Pearson	**	
dsDNA	dsDNA	Dominance_D_Phyt	**-0,90326**	0,013584	Pearson	*	
dsDNA	dsDNA	Simpson_1-D_Phyt	**0,90326**	0,013584	Pearson	*	
dsDNA	dsDNA	Shannon_H_BARISA	**-0,9017**	0,01402	Pearson	*	
dsDNA	dsDNA	Taxa_S_Earthw	**0,89696**	0,015379	Pearson	*	
dsDNA	dsDNA	Evenness_e^H/S_Carab	**0,94364**	0,015923	Pearson	*	
dsDNA	dsDNA	Araneae	**0,89066**	0,017278	Pearson	*	
dsDNA	dsDNA	Equitability_J_BARISA	**-0,88972**	0,017572	Pearson	*	
dsDNA	dsDNA	Evenness_e^H/S_Phyt	**0,88651**	0,018588	Pearson	*	
dsDNA	dsDNA	Shannon_H_Phyt	**0,88646**	0,018606	Pearson	*	
dsDNA	dsDNA	Equitability_J_Phyt	**0,87238**	0,023392	Pearson	*	
dsDNA	dsDNA	Evenness_e^H/S_BARISA	**-0,86688**	0,025401	Pearson	*	
dsDNA	dsDNA	Ester	**0,86215**	0,027195	Pearson	*	
dsDNA	dsDNA	QBS-ar	**0,86008**	0,027995	Pearson	*	
dsDNA	dsDNA	Evenness_e^H/S_Earthw	**-0,84544**	0,033988	Pearson	*	
dsDNA	dsDNA	Piro	**0,84456**	0,034363	Pearson	*	
dsDNA	dsDNA	Shannon_H_Earthw	**0,8321**	0,039921	Pearson	*	
dsDNA	dsDNA	QBS-e	**0,81156**	0,049918	Pearson	*	
dsDNA	dsDNA	F	**0,94268**	0,016332	Pearson	*	
dsDNA	dsDNA	Basal resp.	**0,89223**	0,016796	Pearson	*	28
Earthw	Dominance_D_Earthw	Pentatomidae	**-0,96362**	0,002381	Spearman	**	
Earthw	Dominance_D_Earthw	Taxa_S_Wm	**-0,68961**	0,027353	Pearson	*	
Earthw	Dominance_D_Earthw	Lepidoptera	**0,77029**	0,042732	Pearson	*	

Earthw	Dominance_D_Earthw	NH4+	**0,97048**	0,000283	Pearson	***	
Earthw	Dominance_D_Earthw	Na+	**0,87262**	0,010372	Pearson	*	
Earthw	Dominance_D_Earthw	Ester	**-0,87493**	0,022486	Pearson	*	6
Earthw	Equitability_J_Earthw	Taxa_S_BARISA	**-0,66678**	0,035222	Spearman	*	
Earthw	Equitability_J_Earthw	Chrysopidae	**0,78437**	0,036781	Pearson	*	2
Earthw	Evenness_e^H/S_Earthw	Nabidae	**-0,88413**	0,008239	Pearson	**	
Earthw	Evenness_e^H/S_Earthw	SemiNatural500	**0,7744**	0,008543	Spearman	**	
Earthw	Evenness_e^H/S_Earthw	Evenness_e^H/S_Phyt	**-0,83349**	0,019824	Pearson	*	
Earthw	Evenness_e^H/S_Earthw	Equitability_J_Phyt	**-0,80288**	0,029704	Pearson	*	
Earthw	Evenness_e^H/S_Earthw	Dominance_D_Phyt	**0,76663**	0,044358	Pearson	*	
Earthw	Evenness_e^H/S_Earthw	Simpson_1-D_Phyt	**-0,76663**	0,044358	Pearson	*	
Earthw	Evenness_e^H/S_Earthw	Gluc	**-0,90577**	0,012901	Pearson	*	
Earthw	Evenness_e^H/S_Earthw	Leu	**-0,86229**	0,027141	Pearson	*	
Earthw	Evenness_e^H/S_Earthw	Silk ctrl % degrad	**-0,68533**	0,028725	Pearson	*	
Earthw	Evenness_e^H/S_Earthw	dsDNA	**-0,84544**	0,033988	Pearson	*	
Earthw	Evenness_e^H/S_Earthw	QBS-e	**-0,66683**	0,035203	Pearson	*	
Earthw	Evenness_e^H/S_Earthw	SO4--	**-0,77872**	0,039109	Pearson	*	
Earthw	Evenness_e^H/S_Earthw	acP	**-0,827**	0,042305	Pearson	*	13
Earthw	Shannon_H_Earthw	Taxa_S_Wm	**0,74767**	0,012909	Pearson	*	
Earthw	Shannon_H_Earthw	Taxa_S_Phyt	**0,81091**	0,026894	Pearson	*	
Earthw	Shannon_H_Earthw	Araneae	**0,80322**	0,029582	Pearson	*	
Earthw	Shannon_H_Earthw	Shannon_H_Phyt	**0,77916**	0,038927	Pearson	*	
Earthw	Shannon_H_Earthw	Aphididae	**0,77218**	0,041903	Pearson	*	
Earthw	Shannon_H_Earthw	Nabidae	**0,76817**	0,04367	Pearson	*	
Earthw	Shannon_H_Earthw	Ester	**0,94023**	0,005251	Pearson	**	
Earthw	Shannon_H_Earthw	N	**-0,86183**	0,012634	Pearson	*	
Earthw	Shannon_H_Earthw	P (Olsen)	**0,74213**	0,013979	Pearson	*	
Earthw	Shannon_H_Earthw	AryS	**0,89833**	0,01498	Pearson	*	
Earthw	Shannon_H_Earthw	Piro	**0,89502**	0,015952	Pearson	*	
Earthw	Shannon_H_Earthw	Fructose	**0,84276**	0,017268	Pearson	*	
Earthw	Shannon_H_Earthw	NH4+	**-0,83953**	0,018137	Pearson	*	
Earthw	Shannon_H_Earthw	acP	**0,87581**	0,022178	Pearson	*	
Earthw	Shannon_H_Earthw	QBS-e	**0,66608**	0,035486	Pearson	*	
Earthw	Shannon_H_Earthw	F	**0,7842**	0,036848	Pearson	*	
Earthw	Shannon_H_Earthw	NO2-	**-0,78069**	0,038287	Pearson	*	
Earthw	Shannon_H_Earthw	dsDNA	**0,8321**	0,039921	Pearson	*	18
Earthw	Simpson_1-D_Earthw	Pentatomidae	**0,96362**	0,002381	Spearman	**	
Earthw	Simpson_1-D_Earthw	Taxa_S_Wm	**0,68961**	0,027353	Pearson	*	
Earthw	Simpson_1-D_Earthw	Lepidoptera	**-0,77029**	0,042732	Pearson	*	
Earthw	Simpson_1-D_Earthw	NH4+	**-0,97048**	0,000283	Pearson	***	
Earthw	Simpson_1-D_Earthw	Na+	**-0,87262**	0,010372	Pearson	*	
Earthw	Simpson_1-D_Earthw	Ester	**0,87493**	0,022486	Pearson	*	6
Earthw	Taxa_S_Earthw	Nabidae	**0,87563**	0,009787	Pearson	**	
Earthw	Taxa_S_Earthw	SemiNatural500	**-0,70901**	0,021688	Spearman	*	
Earthw	Taxa_S_Earthw	Evenness_e^H/S_Phyt	**0,82431**	0,022551	Pearson	*	
Earthw	Taxa_S_Earthw	Aphididae	**0,81157**	0,026671	Pearson	*	
Earthw	Taxa_S_Earthw	Equitability_J_Phyt	**0,77934**	0,038852	Pearson	*	
Earthw	Taxa_S_Earthw	Arable500	**0,65348**	0,040448	Pearson	*	
Earthw	Taxa_S_Earthw	Shannon_H_Phyt	**0,77105**	0,042396	Pearson	*	
Earthw	Taxa_S_Earthw	QBS-e	**0,92916**	0,000101	Pearson	***	
Earthw	Taxa_S_Earthw	acP	**0,95628**	0,002826	Pearson	**	
Earthw	Taxa_S_Earthw	F	**0,87548**	0,009816	Pearson	**	
Earthw	Taxa_S_Earthw	Leu	**0,9121**	0,01125	Pearson	*	
Earthw	Taxa_S_Earthw	AryS	**0,90238**	0,013828	Pearson	*	
Earthw	Taxa_S_Earthw	dsDNA	**0,89696**	0,015379	Pearson	*	
Earthw	Taxa_S_Earthw	Gluc	**0,89506**	0,01594	Pearson	*	
Earthw	Taxa_S_Earthw	Piro	**0,89498**	0,015966	Pearson	*	
Earthw	Taxa_S_Earthw	SO4--	**0,81535**	0,025408	Pearson	*	
Earthw	Taxa_S_Earthw	Ester	**0,84909**	0,032442	Pearson	*	
Earthw	Taxa_S_Earthw	alkP	**0,83521**	0,038498	Pearson	*	

Earthw	Taxa_S_Earthw	Tot N dm	**0,6359**	0,048127	Pearson	*	19
Enzym Act	acP	AMF	**0,90355**	0,013506	Pearson	*	
Enzym Act	acP	Taxa_S_Earthw	**0,95628**	0,002826	Pearson	**	
Enzym Act	acP	alkP	**0,95395**	0,003132	Pearson	**	
Enzym Act	acP	Piro	**0,94719**	0,00411	Pearson	**	
Enzym Act	acP	Nabidae	**0,93837**	0,005581	Pearson	**	
Enzym Act	acP	Aphididae	**0,91375**	0,010837	Pearson	*	
Enzym Act	acP	Ester	**0,91165**	0,011363	Pearson	*	
Enzym Act	acP	Leu	**0,89941**	0,01467	Pearson	*	
Enzym Act	acP	Thripidae	**0,94112**	0,016667	Spearman	*	
Enzym Act	acP	Equitability_J_BARISA	**-0,88582**	0,01881	Pearson	*	
Enzym Act	acP	Shannon_H_BARISA	**-0,88015**	0,020685	Pearson	*	
Enzym Act	acP	Shannon_H_Earthw	**0,87581**	0,022178	Pearson	*	
Enzym Act	acP	Arable500	**0,86263**	0,02701	Pearson	*	
Enzym Act	acP	Evenness_e^H/S_BARISA	**-0,83948**	0,036582	Pearson	*	
Enzym Act	acP	Evenness_e^H/S_Earthw	**-0,827**	0,042305	Pearson	*	
Enzym Act	acP	QBS-e	**0,82606**	0,042751	Pearson	*	
Enzym Act	acP	SO4--	**0,82417**	0,043658	Pearson	*	
Enzym Act	acP	QBS-ar	**0,81705**	0,047142	Pearson	*	
Enzym Act	acP	Evenness_e^H/S_Carab	**0,8443**	0,072006	Pearson	*	
Enzym Act	acP	dsDNA	**0,965**	0,001816	Pearson	**	
Enzym Act	acP	AryS	**0,93396**	0,006398	Pearson	**	
Enzym Act	acP	Gluc	**0,87331**	0,023059	Pearson	*	
Enzym Act	acP	Tot N dm	**0,82316**	0,044145	Pearson	*	
Enzym Act	acP	F	**0,88405**	0,046561	Pearson	*	24
Enzym Act	alkP	AMF	**0,86017**	0,027961	Pearson	*	
Enzym Act	alkP	Cotton N % degrad	**0,94286**	0,002778	Spearman	**	
Enzym Act	alkP	Nabidae	**0,94316**	0,004755	Pearson	**	
Enzym Act	alkP	Arable500	**0,91314**	0,010988	Pearson	*	
Enzym Act	alkP	Aphididae	**0,87304**	0,023153	Pearson	*	
Enzym Act	alkP	QBS-ar	**0,87163**	0,023662	Pearson	*	
Enzym Act	alkP	Ester	**0,86925**	0,024525	Pearson	*	
Enzym Act	alkP	Evenness_e^H/S_Pred	**-0,99861**	0,033627	Pearson	*	
Enzym Act	alkP	Shannon_H_BARISA	**-0,83573**	0,03826	Pearson	*	
Enzym Act	alkP	Taxa_S_Earthw	**0,83521**	0,038498	Pearson	*	
Enzym Act	alkP	Equitability_J_BARISA	**-0,8345**	0,03882	Pearson	*	
Enzym Act	alkP	Leu	**0,81522**	0,048061	Pearson	*	
Enzym Act	alkP	Araneae	**0,81447**	0,04844	Pearson	*	
Enzym Act	alkP	acP	**0,95395**	0,003132	Pearson	**	
Enzym Act	alkP	dsDNA	**0,94675**	0,004178	Pearson	**	
Enzym Act	alkP	Piro	**0,89289**	0,016595	Pearson	*	
Enzym Act	alkP	Tot N dm	**0,858**	0,028812	Pearson	*	
Enzym Act	alkP	Basal resp.	**0,85547**	0,029825	Pearson	*	
Enzym Act	alkP	AryS	**0,85295**	0,030845	Pearson	*	
Enzym Act	alkP	Org. matter	**0,82012**	0,045624	Pearson	*	
Enzym Act	alkP	T.O.C.	**0,81795**	0,046695	Pearson	*	21
Enzym Act	AryS	AMF	**0,96401**	0,00192	Pearson	**	
Enzym Act	AryS	Shannon_H_Phyt	**0,95145**	0,003478	Pearson	**	
Enzym Act	AryS	Leu	**0,94531**	0,004404	Pearson	**	
Enzym Act	AryS	Nabidae	**0,94016**	0,005264	Pearson	**	
Enzym Act	AryS	acP	**0,93396**	0,006398	Pearson	**	
Enzym Act	AryS	Gluc	**0,93269**	0,006644	Pearson	**	
Enzym Act	AryS	Evenness_e^H/S_Carab	**0,966**	0,007488	Pearson	**	
Enzym Act	AryS	Evenness_e^H/S_Phyt	**0,92319**	0,008623	Pearson	**	
Enzym Act	AryS	Equitability_J_Phyt	**0,91667**	0,010127	Pearson	*	
Enzym Act	AryS	Taxa_S_Earthw	**0,90238**	0,013828	Pearson	*	
Enzym Act	AryS	Shannon_H_Earthw	**0,89833**	0,01498	Pearson	*	
Enzym Act	AryS	Thripidae	**0,94112**	0,016667	Spearman	*	
Enzym Act	AryS	Araneae	**0,89243**	0,016734	Pearson	*	
Enzym Act	AryS	Dominance_D_Phyt	**-0,88857**	0,017934	Pearson	*	

Enzym Act	AryS	Simpson_1-D_Phyt	**0,88857**	0,017934	Pearson	*	
Enzym Act	AryS	alkP	**0,85295**	0,030845	Pearson	*	
Enzym Act	AryS	Ester	**0,85078**	0,031737	Pearson	*	
Enzym Act	AryS	Arable500	**0,85049**	0,031859	Pearson	*	
Enzym Act	AryS	Shannon_H_BARISA	**-0,84836**	0,032747	Pearson	*	
Enzym Act	AryS	QBS-e	**0,843**	0,03504	Pearson	*	
Enzym Act	AryS	QBS-ar	**0,83711**	0,037638	Pearson	*	
Enzym Act	AryS	Equitability_J_BARISA	**-0,83295**	0,039527	Pearson	*	
Enzym Act	AryS	Piro	**0,83082**	0,040513	Pearson	*	
Enzym Act	AryS	Equitability_J_Carab	**0,89266**	0,041528	Pearson	*	
Enzym Act	AryS	Shannon_H_Carab	**0,88522**	0,045865	Pearson	*	
Enzym Act	AryS	dsDNA	**0,96558**	0,001756	Pearson	**	
Enzym Act	AryS	F	**0,98527**	0,00214	Pearson	**	
Enzym Act	AryS	Basal resp.	**0,8534**	0,030662	Pearson	*	
Enzym Act	AryS	P (Olsen)	**0,82634**	0,042619	Pearson	*	29
Enzym Act	Ester	AMF	**0,8539**	0,030459	Pearson	*	
Enzym Act	Ester	Shannon_H_Earthw	**0,94023**	0,005251	Pearson	**	
Enzym Act	Ester	Aphididae	**0,91824**	0,009755	Pearson	**	
Enzym Act	Ester	NH4+	**-0,90079**	0,014275	Pearson	*	
Enzym Act	Ester	Cotton N % degrad	**0,88571**	0,016667	Spearman	*	
Enzym Act	Ester	Thripidae	**0,94112**	0,016667	Spearman	*	
Enzym Act	Ester	Dominance_D_Earthw	**-0,87493**	0,022486	Pearson	*	
Enzym Act	Ester	Simpson_1-D_Earthw	**0,87493**	0,022486	Pearson	*	
Enzym Act	Ester	QBS-ar	**0,85768**	0,028943	Pearson	*	
Enzym Act	Ester	Shannon_H_BARISA	**-0,85305**	0,030805	Pearson	*	
Enzym Act	Ester	Equitability_J_BARISA	**-0,85255**	0,03101	Pearson	*	
Enzym Act	Ester	Taxa_S_Earthw	**0,84909**	0,032442	Pearson	*	
Enzym Act	Ester	Na+	**-0,84617**	0,033676	Pearson	*	
Enzym Act	Ester	Evenness_e^H/S_BARISA	**-0,84515**	0,034112	Pearson	*	
Enzym Act	Ester	acP	**0,91165**	0,011363	Pearson	*	

Enzym Act	Ester	Piro	**0,90297**	0,013665	Pearson	*	
Enzym Act	Ester	alkP	**0,86925**	0,024525	Pearson	*	
Enzym Act	Ester	dsDNA	**0,86215**	0,027195	Pearson	*	
Enzym Act	Ester	AryS	**0,85078**	0,031737	Pearson	*	
Enzym Act	Ester	Leu	**0,825**	0,043256	Pearson	*	20
Enzym Act	Gluc	Leu	**0,98996**	0,000151	Pearson	***	
Enzym Act	Gluc	Evenness_e^H/S_Phyt	**0,97747**	0,000756	Pearson	***	
Enzym Act	Gluc	Equitability_J_Phyt	**0,95057**	0,003604	Pearson	**	
Enzym Act	Gluc	Evenness_e^H/S_Carab	**0,9683**	0,006742	Pearson	**	
Enzym Act	Gluc	Shannon_H_BARISA	**-0,93051**	0,007077	Pearson	**	
Enzym Act	Gluc	Dominance_D_Phyt	**-0,92841**	0,007504	Pearson	**	
Enzym Act	Gluc	Simpson_1-D_Phyt	**0,92841**	0,007504	Pearson	**	
Enzym Act	Gluc	QBS-e	**0,92617**	0,007974	Pearson	**	
Enzym Act	Gluc	Shannon_H_Phyt	**0,92458**	0,008317	Pearson	**	
Enzym Act	Gluc	Equitability_J_BARISA	**-0,91877**	0,009629	Pearson	**	
Enzym Act	Gluc	Nabidae	**0,91136**	0,011437	Pearson	*	
Enzym Act	Gluc	Equitability_J_Carab	**0,95177**	0,012621	Pearson	*	
Enzym Act	Gluc	Evenness_e^H/S_Earthw	**-0,90577**	0,012901	Pearson	*	
Enzym Act	Gluc	Arable500	**0,89811**	0,015042	Pearson	*	
Enzym Act	Gluc	Taxa_S_Earthw	**0,89506**	0,01594	Pearson	*	
Enzym Act	Gluc	Evenness_e^H/S_BARISA	**-0,89432**	0,016163	Pearson	*	
Enzym Act	Gluc	Cotton N % degrad	**0,88571**	0,016667	Spearman	*	
Enzym Act	Gluc	Thripidae	**0,94112**	0,016667	Spearman	*	
Enzym Act	Gluc	Shannon_H_Carab	**0,92782**	0,023025	Pearson	*	
Enzym Act	Gluc	acP	**0,87331**	0,023059	Pearson	*	
Enzym Act	Gluc	Silk ctrl % degrad	**0,8509**	0,031688	Pearson	*	
Enzym Act	Gluc	Cicadellidae	**-0,84508**	0,034139	Pearson	*	
Enzym Act	Gluc	Silk P % degrad	**0,83881**	0,036881	Pearson	*	
Enzym Act	Gluc	F	**0,99664**	0,000234	Pearson	***	
Enzym Act	Gluc	dsDNA	**0,93294**	0,006595	Pearson	**	

Enzym Act	Gluc	AryS	**0,93269**	0,006644	Pearson	**	26
Enzym Act	Leu	AMF	**0,83606**	0,038112	Pearson	*	
Enzym Act	Leu	Shannon_H_BARISA	**-0,95909**	0,002476	Pearson	**	
Enzym Act	Leu	Evenness_e^H/S_Phyt	**0,9507**	0,003585	Pearson	**	
Enzym Act	Leu	Equitability_J_BARISA	**-0,94798**	0,003989	Pearson	**	
Enzym Act	Leu	QBS-e	**0,94235**	0,00489	Pearson	**	
Enzym Act	Leu	Evenness_e^H/S_Carab	**0,96829**	0,006745	Pearson	**	
Enzym Act	Leu	Evenness_e^H/S_BARISA	**-0,93079**	0,007018	Pearson	**	
Enzym Act	Leu	Equitability_J_Phyt	**0,91945**	0,00947	Pearson	**	
Enzym Act	Leu	Taxa_S_Earthw	**0,9121**	0,01125	Pearson	*	
Enzym Act	Leu	Shannon_H_Phyt	**0,91166**	0,011361	Pearson	*	
Enzym Act	Leu	Nabidae	**0,90473**	0,013182	Pearson	*	
Enzym Act	Leu	Arable500	**0,89648**	0,015521	Pearson	*	
Enzym Act	Leu	Cotton N % degrad	**0,88571**	0,016667	Spearman	*	
Enzym Act	Leu	Thripidae	**0,94112**	0,016667	Spearman	*	
Enzym Act	Leu	Cicadellidae	**-0,89233**	0,016764	Pearson	*	
Enzym Act	Leu	Dominance_D_Phyt	**-0,88807**	0,01809	Pearson	*	
Enzym Act	Leu	Simpson_1-D_Phyt	**0,88807**	0,01809	Pearson	*	
Enzym Act	Leu	Equitability_J_Carab	**0,93464**	0,019863	Pearson	*	
Enzym Act	Leu	Evenness_e^H/S_Earthw	**-0,86229**	0,027141	Pearson	*	
Enzym Act	Leu	Silk P % degrad	**0,85495**	0,030033	Pearson	*	
Enzym Act	Leu	Shannon_H_Carab	**0,91246**	0,030682	Pearson	*	
Enzym Act	Leu	Na+	**-0,85209**	0,031199	Pearson	*	
Enzym Act	Leu	Ester	**0,825**	0,043256	Pearson	*	
Enzym Act	Leu	SO4--	**0,81911**	0,046122	Pearson	*	
Enzym Act	Leu	Gluc	**0,98996**	0,000151	Pearson	***	
Enzym Act	Leu	F	**0,97781**	0,003956	Pearson	**	
Enzym Act	Leu	AryS	**0,94531**	0,004404	Pearson	**	
Enzym Act	Leu	dsDNA	**0,94347**	0,004703	Pearson	**	
Enzym Act	Leu	acP	**0,89941**	0,01467	Pearson	*	
Enzym Act	Leu	alkP	**0,81522**	0,048061	Pearson	*	30
Enzym Act	Piro	AMF	**0,8567**	0,029332	Pearson	*	
Enzym Act	Piro	Aphididae	**0,93043**	0,007092	Pearson	**	
Enzym Act	Piro	Ester	**0,90297**	0,013665	Pearson	*	
Enzym Act	Piro	Shannon_H_Earthw	**0,89502**	0,015952	Pearson	*	
Enzym Act	Piro	Taxa_S_Earthw	**0,89498**	0,015966	Pearson	*	
Enzym Act	Piro	alkP	**0,89289**	0,016595	Pearson	*	
Enzym Act	Piro	acP	**0,94719**	0,00411	Pearson	**	
Enzym Act	Piro	Tot N dm	**0,91705**	0,010037	Pearson	*	
Enzym Act	Piro	dsDNA	**0,84456**	0,034363	Pearson	*	
Enzym Act	Piro	AryS	**0,83082**	0,040513	Pearson	*	10
F_ARISA	Dominance_D_FARISA	Evenness_e^H/S_Wm	**-0,8102**	0,002497	Pearson	**	
F_ARISA	Dominance_D_FARISA	Equitability_J_Wm	**-0,73932**	0,009321	Pearson	**	
F_ARISA	Dominance_D_FARISA	Simpson_1-D_Wm	**-0,64545**	0,031963	Spearman	*	
F_ARISA	Dominance_D_FARISA	Dominance_D_Wm	**0,62287**	0,040653	Pearson	*	4
F_ARISA	Equitability_J_FARISA	Dominance_D_B16S	**-0,8**	0,010769	Spearman	*	
F_ARISA	Equitability_J_FARISA	Simpson_1-D_B16S	**0,8**	0,010769	Spearman	*	
F_ARISA	Equitability_J_FARISA	Ascorbic acid	**0,78571**	0,048016	Spearman	*	
F_ARISA	Equitability_J_FARISA	Mg++	**0,78571**	0,048016	Spearman	*	4
F_ARISA	Evenness_e^H/S_FARISA	Dominance_D_B16S	**-0,86667**	0,003075	Spearman	**	
F_ARISA	Evenness_e^H/S_FARISA	Simpson_1-D_B16S	**0,86667**	0,003075	Spearman	**	
F_ARISA	Evenness_e^H/S_FARISA	Mg++	**0,85714**	0,012302	Spearman	*	
F_ARISA	Evenness_e^H/S_FARISA	Ascorbic acid	**0,82143**	0,034127	Spearman	*	
F_ARISA	Evenness_e^H/S_FARISA	Org. matter	**-0,61818**	0,042646	Spearman	*	
F_ARISA	Evenness_e^H/S_FARISA	T.O.C.	**-0,61818**	0,042646	Spearman	*	
F_ARISA	Evenness_e^H/S_FARISA	Basal resp.	**-0,6383**	0,047024	Spearman	*	7
F_ARISA	Shannon_H_FARISA	Exch. Ca	**0,73636**	0,00976	Spearman	**	1
F_ARISA	Simpson_1-D_FARISA	Evenness_e^H/S_Wm	**0,8102**	0,002497	Pearson	**	
F_ARISA	Simpson_1-D_FARISA	Equitability_J_Wm	**0,73932**	0,009321	Pearson	**	
F_ARISA	Simpson_1-D_FARISA	Simpson_1-D_Wm	**0,64545**	0,031963	Spearman	*	

F_ARISA	Simpson_1-D_FARISA	Dominance_D_Wm	**-0,62287**	0,040653	Pearson	*	4
F_ARISA	Taxa_S_FARISA	Urban1000	**-0,68591**	0,019796	Pearson	*	
F_ARISA	Taxa_S_FARISA	Silk N % degrad	**0,76875**	0,009363	Pearson	**	
F_ARISA	Taxa_S_FARISA	Exch. Ca	**0,70788**	0,014798	Pearson	*	
F_ARISA	Taxa_S_FARISA	SO4--	**0,80578**	0,02867	Pearson	*	
F_ARISA	Taxa_S_FARISA	F	**0,71399**	0,046663	Pearson	*	
F_ARISA	Taxa_S_FARISA	Nabidae	**0,75743**	0,048603	Pearson	*	6
FDA	F	AMF	**0,79098**	0,034156	Pearson	*	
FDA	F	Gluc	**0,99664**	0,000234	Pearson	***	
FDA	F	Evenness_e^H/S_Phyt	**0,98733**	0,00024	Pearson	***	
FDA	F	Equitability_J_Phyt	**0,97332**	0,001058	Pearson	**	
FDA	F	AryS	**0,98527**	0,00214	Pearson	**	
FDA	F	Shannon_H_Phyt	**0,95765**	0,002653	Pearson	**	
FDA	F	Leu	**0,97781**	0,003956	Pearson	**	
FDA	F	QBS-e	**0,91101**	0,004323	Pearson	**	
FDA	F	Nabidae	**0,92839**	0,007507	Pearson	**	
FDA	F	Dominance_D_Phyt	**-0,92375**	0,0085	Pearson	**	
FDA	F	Simpson_1-D_Phyt	**0,92375**	0,0085	Pearson	**	
FDA	F	Taxa_S_Earthw	**0,87548**	0,009816	Pearson	**	
FDA	F	Cotton N % degrad	**0,89286**	0,012302	Spearman	*	
FDA	F	dsDNA	**0,94268**	0,016332	Pearson	*	
FDA	F	Taxa_S_B16S	**0,84187**	0,017507	Pearson	*	
FDA	F	Evenness_e^H/S_Carab	**0,88542**	0,018942	Pearson	*	
FDA	F	Shannon_H_Carab	**0,8637**	0,0266	Pearson	*	
FDA	F	Evenness_e^H/S_Wf	**-0,8045**	0,029123	Pearson	*	
FDA	F	Equitability_J_Carab	**0,85105**	0,031629	Pearson	*	
FDA	F	Shannon_H_Earthw	**0,7842**	0,036848	Pearson	*	
FDA	F	Phyllotreta sp.	**-0,83845**	0,037041	Pearson	*	
FDA	F	Araneae	**0,83062**	0,040603	Pearson	*	
FDA	F	Basal resp.	**0,76587**	0,044703	Pearson	*	
FDA	F	acP	**0,88405**	0,046561	Pearson	*	
FDA	F	Taxa_S_FARISA	**0,71399**	0,046663	Pearson	*	
FDA	F	S.I.R.	**0,75918**	0,047777	Pearson	*	
FDA	F	Sand	**0,7728**	0,024551	Pearson	*	27
Fertim	Cotton ctrl % degrad	Glucose	**0,93321**	0,002136	Pearson	**	
Fertim	Cotton ctrl % degrad	Dominance_D_Mesof	**-0,7581**	0,029278	Pearson	*	
Fertim	Cotton ctrl % degrad	Simpson_1-D_Mesof	**0,7581**	0,029278	Pearson	*	
Fertim	Cotton ctrl % degrad	Taxa_S_Wf	**0,75689**	0,02969	Pearson	*	
Fertim	Cotton ctrl % degrad	Cl-	**-0,82143**	0,034127	Spearman	*	
Fertim	Cotton ctrl % degrad	NO2-	**-0,78524**	0,036429	Pearson	*	
Fertim	Cotton ctrl % degrad	Taxa_S_Phyt	**0,77711**	0,03979	Pearson	*	7
Fertim	Cotton N % degrad	SemiNatural500	**-0,75001**	0,012475	Spearman	*	
Fertim	Cotton N % degrad	alkP	**0,94286**	0,002778	Spearman	**	
Fertim	Cotton N % degrad	dsDNA	**0,98561**	0,005556	Spearman	**	
Fertim	Cotton N % degrad	F	**0,89286**	0,012302	Spearman	*	
Fertim	Cotton N % degrad	Ester	**0,88571**	0,016667	Spearman	*	
Fertim	Cotton N % degrad	Gluc	**0,88571**	0,016667	Spearman	*	
Fertim	Cotton N % degrad	Leu	**0,88571**	0,016667	Spearman	*	
Fertim	Cotton N % degrad	Exch. Ca	**0,66061**	0,037588	Spearman	*	8
Fertim	Cotton P % degrad	Sinapic acid	**0,80881**	0,027612	Pearson	*	1
Fertim	Silk ctrl % degrad	Arable500	**0,75653**	0,011322	Pearson	*	
Fertim	Silk ctrl % degrad	Equitability_J_Phyt	**0,83178**	0,020316	Pearson	*	
Fertim	Silk ctrl % degrad	Evenness_e^H/S_Phyt	**0,80953**	0,027364	Pearson	*	
Fertim	Silk ctrl % degrad	SemiNatural500	**-0,68904**	0,027533	Spearman	*	
Fertim	Silk ctrl % degrad	Evenness_e^H/S_Earthw	**-0,68533**	0,028725	Pearson	*	
Fertim	Silk ctrl % degrad	Nabidae	**0,79843**	0,031329	Pearson	*	
Fertim	Silk ctrl % degrad	Phyllotreta sp.	**-0,79704**	0,031844	Pearson	*	
Fertim	Silk ctrl % degrad	Shannon_H_Phyt	**0,76657**	0,044388	Pearson	*	
Fertim	Silk ctrl % degrad	Arable1000	**0,64285**	0,044983	Pearson	*	
Fertim	Silk ctrl % degrad	Evenness_e^H/S_Wf	**-0,71203**	0,047548	Pearson	*	

Fertim	Silk ctrl % degrad	Gluc	**0,8509**	0,031688	Pearson	*	11
Fertim	Silk N % degrad	Taxa_S_FARISA	**0,76875**	0,009363	Pearson	**	
Fertim	Silk N % degrad	Equitability_J_B16S	**-0,76412**	0,016517	Pearson	*	
Fertim	Silk N % degrad	Evenness_e^H/S_B16S	**-0,74991**	0,019966	Pearson	*	
Fertim	Silk N % degrad	Shannon_H_B16S	**-0,72886**	0,025902	Pearson	*	
Fertim	Silk N % degrad	Taxa_S_Mesof	**-0,67198**	0,03331	Pearson	*	
Fertim	Silk N % degrad	Arable500	**0,6432**	0,044828	Pearson	*	6
Fertim	Silk P % degrad	Arable500	**0,7508**	0,012331	Pearson	*	
Fertim	Silk P % degrad	Na+	**-0,84993**	0,015428	Pearson	*	
Fertim	Silk P % degrad	Evenness_e^H/S_Phyt	**0,78795**	0,035345	Pearson	*	
Fertim	Silk P % degrad	Equitability_J_Phyt	**0,76576**	0,044754	Pearson	*	
Fertim	Silk P % degrad	Sand	**0,7131**	0,020607	Pearson	*	
Fertim	Silk P % degrad	Clay	**-0,7011**	0,023889	Pearson	*	
Fertim	Silk P % degrad	Leu	**0,85495**	0,030033	Pearson	*	
Fertim	Silk P % degrad	Gluc	**0,83881**	0,036881	Pearson	*	8
FITS	Dominance_D_FITS	Pentatomidae	**0,98561**	0,005556	Spearman	**	
FITS	Dominance_D_FITS	Agromyzidae	**0,9277**	0,007652	Pearson	**	
FITS	Dominance_D_FITS	QBS-e	**0,72937**	0,040039	Pearson	*	3
FITS	Equitability_J_FITS	Formicidae	**-0,90531**	0,013025	Pearson	*	
FITS	Equitability_J_FITS	Agromyzidae	**-0,87518**	0,022396	Pearson	*	
FITS	Equitability_J_FITS	Pentatomidae	**-0,84067**	0,044444	Spearman	*	
FITS	Equitability_J_FITS	Exch. Mg	**-0,74256**	0,034842	Pearson	*	
FITS	Equitability_J_FITS	Caffeic acid	**-0,82539**	0,043069	Pearson	*	5
FITS	Evenness_e^H/S_FITS	Formicidae	**-0,91667**	0,010127	Pearson	*	
FITS	Evenness_e^H/S_FITS	Agromyzidae	**-0,85085**	0,031708	Pearson	*	
FITS	Evenness_e^H/S_FITS	Pentatomidae	**-0,84067**	0,044444	Spearman	*	
FITS	Evenness_e^H/S_FITS	Exch. Mg	**-0,71977**	0,044102	Pearson	*	
FITS	Evenness_e^H/S_FITS	Ca++	**-0,81481**	0,048265	Pearson	*	5
FITS	Shannon_H_FITS	Agromyzidae	**-0,88174**	0,020152	Pearson	*	
FITS	Shannon_H_FITS	Taxa_S_Carab	**-0,73206**	0,038943	Pearson	*	
FITS	Shannon_H_FITS	Pentatomidae	**-0,84067**	0,044444	Spearman	*	
FITS	Shannon_H_FITS	Caffeic acid	**-0,85135**	0,031505	Pearson	*	4
FITS	Simpson_1-D_FITS	Pentatomidae	**-0,98561**	0,005556	Spearman	**	
FITS	Simpson_1-D_FITS	Agromyzidae	**-0,9277**	0,007652	Pearson	**	
FITS	Simpson_1-D_FITS	QBS-e	**-0,72937**	0,040039	Pearson	*	3
FITS	Taxa_S_FITS	Evenness_e^H/S_Mesof	**0,89533**	0,00643	Pearson	**	
FITS	Taxa_S_FITS	Equitability_J_Mesof	**0,88727**	0,007706	Pearson	**	
FITS	Taxa_S_FITS	Pulmonata	**0,94112**	0,016667	Spearman	*	
FITS	Taxa_S_FITS	Shannon_H_Mesof	**0,82448**	0,022499	Pearson	*	
FITS	Taxa_S_FITS	Lygus sp.	**-0,87095**	0,023905	Pearson	*	5
Landscape	Arable1000	Org. matter	**0,72724**	0,011211	Pearson	*	
Landscape	Arable1000	T.O.C.	**0,72644**	0,011344	Pearson	*	
Landscape	Arable1000	C/N (Humific.)	**0,67696**	0,022139	Pearson	*	
Landscape	Arable1000	Equitability_J_Wf	**-0,73899**	0,022917	Pearson	*	
Landscape	Arable1000	Nabidae	**0,78023**	0,038481	Pearson	*	
Landscape	Arable1000	Silk ctrl % degrad	**0,64285**	0,044983	Pearson	*	
Landscape	Arable1000	Shannon_H_Wf	**-0,67566**	0,045765	Pearson	*	
Landscape	Arable1000	Simpson_1-D_Pred	**-0,95274**	0,047257	Pearson	*	
Landscape	Arable1000	Dominance_D_Pred	**0,95236**	0,047638	Pearson	*	9
Landscape	Arable150	Evenness_e^H/S_paras	**0,84862**	0,015757	Pearson	*	
Landscape	Arable150	Equitability_J_paras	**0,76036**	0,047226	Pearson	*	
Landscape	Arable150	Water resp.	**0,74531**	0,013359	Pearson	*	
Landscape	Arable150	Equitability_J_Wf	**-0,73746**	0,023354	Pearson	*	
Landscape	Arable150	Shannon_H_Wm	**0,6609**	0,026829	Pearson	*	
Landscape	Arable150	Dominance_D_Wm	**-0,66066**	0,026905	Pearson	*	6
Landscape	Arable500	Simpson_1-D_Pred	**-0,99949**	0,000509	Pearson	***	
Landscape	Arable500	Dominance_D_Pred	**0,99945**	0,000553	Pearson	***	
Landscape	Arable500	Nabidae	**0,93956**	0,00167	Pearson	**	
Landscape	Arable500	dsDNA	**0,9469**	0,004155	Pearson	**	
Landscape	Arable500	Org. matter	**0,74465**	0,008565	Pearson	**	

Landscape	Arable500	T.O.C.	**0,74311**	0,008778	Pearson	**	
Landscape	Arable500	alkP	**0,91314**	0,010988	Pearson	*	
Landscape	Arable500	Silk ctrl % degrad	**0,75653**	0,011322	Pearson	*	
Landscape	Arable500	Silk P % degrad	**0,7508**	0,012331	Pearson	*	
Landscape	Arable500	Gluc	**0,89811**	0,015042	Pearson	*	
Landscape	Arable500	Leu	**0,89648**	0,015521	Pearson	*	
Landscape	Arable500	Na+	**-0,84925**	0,0156	Pearson	*	
Landscape	Arable500	C/N (Humific.)	**0,69038**	0,018692	Pearson	*	
Landscape	Arable500	Evenness_e^H/S_Wf	**-0,73608**	0,023751	Pearson	*	
Landscape	Arable500	acP	**0,86263**	0,02701	Pearson	*	
Landscape	Arable500	Araneae	**0,80586**	0,028641	Pearson	*	
Landscape	Arable500	AryS	**0,85049**	0,031859	Pearson	*	
Landscape	Arable500	Equitability_J_Wf	**-0,70671**	0,033287	Pearson	*	
Landscape	Arable500	Equitability_J_Phyt	**0,77839**	0,039247	Pearson	*	
Landscape	Arable500	Taxa_S_Earthw	**0,65348**	0,040448	Pearson	*	
Landscape	Arable500	Evenness_e^H/S_Phyt	**0,77393**	0,041146	Pearson	*	
Landscape	Arable500	Basal resp.	**0,65001**	0,041894	Pearson	*	
Landscape	Arable500	Equitability_J_Carab	**0,67874**	0,04441	Pearson	*	
Landscape	Arable500	Silk N % degrad	**0,6432**	0,044828	Pearson	*	
Landscape	Arable500	Equitability_J_Pred	**-0,95274**	0,04726	Pearson	*	25
Landscape	SemiNatural150	Exch. K	**-0,65186**	0,029755	Pearson	*	
Landscape	SemiNatural150	Chrysopidae	**-0,79008**	0,034506	Pearson	*	2
Landscape	SemiNatural500	Cotton N % degrad	**-0,75001**	0,012475	Spearman	*	
Landscape	SemiNatural500	Silk ctrl % degrad	**-0,68904**	0,027533	Spearman	*	
Landscape	SemiNatural500	Taxa_S_Earthw	**-0,70901**	0,021688	Spearman	*	
Landscape	SemiNatural500	Evenness_e^H/S_Earthw	**0,7744**	0,008543	Spearman	**	
Landscape	SemiNatural500	Nabidae	**-0,81832**	0,038095	Spearman	*	5
Landscape	Urban1000	Silt	**0,93518**	2,40E-05	Pearson	***	
Landscape	Urban1000	SO4--	**-0,92383**	0,002951	Pearson	**	
Landscape	Urban1000	Sand	**-0,68897**	0,019034	Pearson	*	
Landscape	Urban1000	Taxa_S_FARISA	**-0,68591**	0,019796	Pearson	*	4
Landscape	Urban150	Taxa_S_B16S	**-0,84414**	0,004211	Pearson	**	
Landscape	Urban150	Silt	**0,74276**	0,008827	Pearson	**	
Landscape	Urban150	Dominance_D_Phyt	**0,85998**	0,013049	Pearson	*	
Landscape	Urban150	Simpson_1-D_Phyt	**-0,85998**	0,013049	Pearson	*	
Landscape	Urban150	Shannon_H_Wf	**0,73828**	0,023118	Pearson	*	
Landscape	Urban150	Araneae	**-0,78802**	**0,03532**	Pearson	*	
Landscape	Urban150	Equitability_J_Wf	**0,70008**	0,03574	Pearson	*	
Landscape	Urban150	Sand	**-0,61671**	0,043286	Pearson	*	
Landscape	Urban150	Equitability_J_Carab	**-0,67531**	0,045921	Pearson	*	
Landscape	Urban150	Nabidae	**-0,7627**	0,046146	Pearson	*	10
Landscape	Urban500	Silt	**0,73615**	0,009792	Pearson	**	
Landscape	Urban500	Cicadellidae	**0,85101**	0,015161	Pearson	*	
Landscape	Urban500	Taxa_S_B16S	**-0,71629**	0,029945	Pearson	*	
Landscape	Urban500	Evenness_e^H/S_Wm	**-0,64174**	0,033292	Pearson	*	
Landscape	Urban500	Na+	**0,77789**	0,039457	Pearson	*	
Landscape	Urban500	Simpson_1-D_Carab	**-0,83055**	0,040636	Pearson	*	6
Mesof	Dominance_D_Mesof	AMF	**-0,71199**	0,047567	Pearson	**	
Mesof	Dominance_D_Mesof	Taxa_S_Phyt	**-0,98565**	0,000307	Pearson	***	
Mesof	Dominance_D_Mesof	NO2-	**0,98608**	0,000289	Pearson	***	
Mesof	Dominance_D_Mesof	Fructose	**-0,93433**	0,006327	Pearson	**	
Mesof	Dominance_D_Mesof	PO4---	**0,91151**	0,011398	Pearson	*	
Mesof	Dominance_D_Mesof	NH4+	**0,86002**	0,028019	Pearson	*	
Mesof	Dominance_D_Mesof	Cotton ctrl % degrad	**-0,7581**	0,029278	Pearson	*	
Mesof	Dominance_D_Mesof	QBS-ar	**-0,74754**	0,032994	Pearson	*	
Mesof	Dominance_D_Mesof	N	**0,84282**	0,035115	Pearson	*	
Mesof	Dominance_D_Mesof	S.I.R.	**-0,73975**	0,035913	Pearson	*	
Mesof	Dominance_D_Mesof	Tot N dm	**-0,73849**	0,036401	Pearson	*	11
Mesof	Equitability_J_Mesof	Lygus sp.	**-0,83048**	0,040671	Pearson	*	
Mesof	Equitability_J_Mesof	Taxa_S_FITS	**0,88727**	0,007706	Pearson	**	

Mesof	Equitability_J_Mesof	C.S.C.	**-0,71111**	0,047969	Pearson	*	3
Mesof	Evenness_e^H/S_Mesof	Aleyrodidae	**0,87299**	0,023172	Pearson	*	
Mesof	Evenness_e^H/S_Mesof	Taxa_S_BARISA	**-0,76109**	0,036905	Spearman	*	
Mesof	Evenness_e^H/S_Mesof	Taxa_S_FITS	**0,89533**	0,00643	Pearson	**	
Mesof	Evenness_e^H/S_Mesof	Ascorbic acid	**-0,8516**	0,031402	Pearson	*	4
Mesof	Shannon_H_Mesof	Lygus sp.	**-0,92667**	0,007869	Pearson	**	
Mesof	Shannon_H_Mesof	Syrphidae	**0,84151**	0,035687	Pearson	*	
Mesof	Shannon_H_Mesof	Taxa_S_paras	**-0,91684**	0,010085	Pearson	*	
Mesof	Shannon_H_Mesof	C.S.C.	**-0,85316**	0,007069	Pearson	**	
Mesof	Shannon_H_Mesof	Taxa_S_FITS	**0,82448**	0,022499	Pearson	*	
Mesof	Shannon_H_Mesof	Electric. Cond.	**0,70695**	0,049898	Pearson	*	6
Mesof	Simpson_1-D_Mesof	AMF	**0,71199**	0,047567	Pearson	*	
Mesof	Simpson_1-D_Mesof	Taxa_S_Phyt	**0,98565**	0,000307	Pearson	***	
Mesof	Simpson_1-D_Mesof	NO2-	**-0,98608**	0,000289	Pearson	***	
Mesof	Simpson_1-D_Mesof	Fructose	**0,93433**	0,006327	Pearson	**	
Mesof	Simpson_1-D_Mesof	PO4---	**-0,91151**	0,011398	Pearson	*	
Mesof	Simpson_1-D_Mesof	NH4+	**-0,86002**	0,028019	Pearson	*	
Mesof	Simpson_1-D_Mesof	Cotton ctrl % degrad	**0,7581**	0,029278	Pearson	*	
Mesof	Simpson_1-D_Mesof	QBS-ar	**0,74754**	0,032994	Pearson	*	
Mesof	Simpson_1-D_Mesof	N	**-0,84282**	0,035115	Pearson	*	
Mesof	Simpson_1-D_Mesof	S.I.R.	**0,73975**	0,035913	Pearson	*	
Mesof	Simpson_1-D_Mesof	Tot N dm	**0,73849**	0,036401	Pearson	*	11
Mesof	Taxa_S_Mesof	Equitability_J_Pred	**0,98973**	0,010266	Pearson	*	
Mesof	Taxa_S_Mesof	Staphylinidae	**0,87064**	0,010768	Pearson	*	
Mesof	Taxa_S_Mesof	Shannon_H_Pred	**0,98007**	0,019927	Pearson	*	
Mesof	Taxa_S_Mesof	Evenness_e^H/S_BARISA	**-0,63537**	0,048369	Pearson	*	
Mesof	Taxa_S_Mesof	QBS-ar	**0,72939**	0,016668	Pearson	*	
Mesof	Taxa_S_Mesof	Equitability_J_B16S	**0,7301**	0,025522	Pearson	*	
Mesof	Taxa_S_Mesof	Evenness_e^H/S_B16S	**0,71793**	0,029395	Pearson	*	
Mesof	Taxa_S_Mesof	Silk N % degrad	**-0,67198**	0,03331	Pearson	*	
Mesof	Taxa_S_Mesof	P (Olsen)	**0,6718**	0,033375	Pearson	*	
Mesof	Taxa_S_Mesof	Shannon_H_B16S	**0,70382**	0,034344	Pearson	*	
Mesof	Taxa_S_Mesof	Ca++	**0,77798**	0,03942	Pearson	*	11
Paras	Equitability_J_paras	NO3-	**-0,8093**	0,027445	Pearson	*	
Paras	Equitability_J_paras	Lepidoptera	**-0,85992**	0,013061	Pearson	*	
Paras	Equitability_J_paras	Taxa_S_Wm	**0,84935**	0,015575	Pearson	*	
Paras	Equitability_J_paras	Arable150	**0,76036**	0,047226	Pearson	*	4
Paras	Evenness_e^H/S_paras	Water resp.	**0,82751**	0,021579	Pearson	*	
Paras	Evenness_e^H/S_paras	QBS-ar	**0,77649**	0,040051	Pearson	*	
Paras	Evenness_e^H/S_paras	Ca++	**0,7821**	0,037708	Pearson	*	
Paras	Evenness_e^H/S_paras	Fructose	**0,82563**	0,022148	Pearson	*	
Paras	Evenness_e^H/S_paras	Lepidoptera	**-0,76509**	0,045055	Pearson	*	
Paras	Evenness_e^H/S_paras	Formicidae	**0,76016**	0,04732	Pearson	*	
Paras	Evenness_e^H/S_paras	Syrphidae	**0,79737**	0,031721	Pearson	*	
Paras	Evenness_e^H/S_paras	Taxa_S_Phyt	**0,76923**	0,0432	Pearson	*	
Paras	Evenness_e^H/S_paras	Arable150	**0,84862**	0,015757	Pearson	*	9
Paras	Shannon_H_paras	pH in H2O	**0,83882**	0,018329	Pearson	*	
Paras	Shannon_H_paras	Electric. Cond.	**-0,79459**	0,032768	Pearson	*	
Paras	Shannon_H_paras	Mineral. Coeff.	**-0,77522**	0,040593	Pearson	*	
Paras	Shannon_H_paras	Lygus sp.	**0,78129**	0,03804	Pearson	*	
Paras	Shannon_H_paras	Taxa_S_pred	**-0,9796**	0,020401	Pearson	*	5
Paras	Taxa_S_paras	Mineral. Coeff.	**-0,78784**	0,035391	Pearson	*	
Paras	Taxa_S_paras	Water resp.	**-0,75903**	0,047849	Pearson	*	
Paras	Taxa_S_paras	Ca++	**-0,82944**	0,021003	Pearson	*	
Paras	Taxa_S_paras	Shannon_H_Mesof	**-0,91684**	0,010085	Pearson	*	
Paras	Taxa_S_paras	Lygus sp.	**0,7671**	0,044149	Pearson	*	5
Phyt_abund	Agromyzidae	Simpson_1-D_Wm	**-0,86932**	0,028571	Spearman	*	
Phyt_abund	Agromyzidae	Dominance_D_FITS	**0,9277**	0,007652	Pearson	**	
Phyt_abund	Agromyzidae	Simpson_1-D_FITS	**-0,9277**	0,007652	Pearson	**	
Phyt_abund	Agromyzidae	Shannon_H_FITS	**-0,88174**	0,020152	Pearson	*	

Phyt_abund	Agromyzidae	Equitability_J_FITS	**-0,87518**	0,022396	Pearson	*	
Phyt_abund	Agromyzidae	Evenness_e^H/S_FITS	**-0,85085**	0,031708	Pearson	*	6
Phyt_abund	Aleyrodidae	Exch. K	**0,94743**	0,001183	Pearson	**	
Phyt_abund	Aleyrodidae	Ascorbic acid	**-0,94131**	0,001553	Pearson	**	
Phyt_abund	Aleyrodidae	Simpson_1-D_B16S	**-0,84399**	0,016945	Pearson	*	
Phyt_abund	Aleyrodidae	Dominance_D_B16S	**0,84391**	0,016966	Pearson	*	
Phyt_abund	Aleyrodidae	Evenness_e^H/S_Mesof	**0,87299**	0,023172	Pearson	*	5
Phyt_abund	Aphididae	Equitability_J_BARISA	**-0,80843**	0,027746	Pearson	*	
Phyt_abund	Aphididae	Pulmonata	**0,86692**	0,028571	Spearman	*	
Phyt_abund	Aphididae	Shannon_H_BARISA	**-0,76622**	0,044547	Pearson	*	
Phyt_abund	Aphididae	Evenness_e^H/S_BARISA	**-0,76138**	0,046755	Pearson	*	
Phyt_abund	Aphididae	Piro	**0,93043**	0,007092	Pearson	**	
Phyt_abund	Aphididae	Ester	**0,91824**	0,009755	Pearson	**	
Phyt_abund	Aphididae	SO4--	**0,87318**	0,010263	Pearson	*	
Phyt_abund	Aphididae	acP	**0,91375**	0,010837	Pearson	*	
Phyt_abund	Aphididae	alkP	**0,87304**	0,023153	Pearson	*	
Phyt_abund	Aphididae	Taxa_S_Earthw	**0,81157**	0,026671	Pearson	*	
Phyt_abund	Aphididae	dry matter	**-0,80358**	0,029451	Pearson	*	
Phyt_abund	Aphididae	Shannon_H_Earthw	**0,77218**	0,041903	Pearson	*	12
Phyt_abund	Cicadellidae	Evenness_e^H/S_BARISA	**0,95114**	0,000987	Pearson	***	
Phyt_abund	Cicadellidae	Shannon_H_BARISA	**0,93191**	0,002239	Pearson	**	
Phyt_abund	Cicadellidae	Equitability_J_BARISA	**0,92988**	0,002408	Pearson	**	
Phyt_abund	Cicadellidae	Syrphidae	**-0,86772**	0,011368	Pearson	*	
Phyt_abund	Cicadellidae	Urban500	**0,85101**	0,015161	Pearson	*	
Phyt_abund	Cicadellidae	Leu	**-0,89233**	0,016764	Pearson	*	
Phyt_abund	Cicadellidae	Gluc	**-0,84508**	0,034139	Pearson	*	
Phyt_abund	Cicadellidae	NH4+	**0,76573**	0,044765	Pearson	*	
Phyt_abund	Cicadellidae	SO4--	**-0,76431**	0,045409	Pearson	*	9
Phyt_abund	Lepidoptera	Evenness_e^H/S_paras	**-0,76509**	0,045055	Pearson	*	
Phyt_abund	Lepidoptera	Equitability_J_paras	**-0,85992**	0,013061	Pearson	*	
Phyt_abund	Lepidoptera	Dominance_D_Wm	**0,86988**	0,010922	Pearson	*	
Phyt_abund	Lepidoptera	Shannon_H_Wm	**-0,81848**	0,024389	Pearson	*	
Phyt_abund	Lepidoptera	Taxa_S_Wm	**-0,76714**	0,044131	Pearson	*	
Phyt_abund	Lepidoptera	NO3-	**0,93809**	0,001771	Pearson	**	
Phyt_abund	Lepidoptera	NH4+	**0,86498**	0,011949	Pearson	*	
Phyt_abund	Lepidoptera	Dominance_D_Earthw	**0,77029**	0,042732	Pearson	*	
Phyt_abund	Lepidoptera	Simpson_1-D_Earthw	**-0,77029**	0,042732	Pearson	*	9
Phyt_abund	Lygus sp.	Taxa_S_paras	**0,7671**	0,044149	Pearson	*	
Phyt_abund	Lygus sp.	Shannon_H_paras	**0,78129**	0,03804	Pearson	*	
Phyt_abund	Lygus sp.	Shannon_H_Mesof	**-0,92667**	0,007869	Pearson	**	
Phyt_abund	Lygus sp.	Taxa_S_FITS	**-0,87095**	0,023905	Pearson	*	
Phyt_abund	Lygus sp.	Equitability_J_Mesof	**-0,83048**	0,040671	Pearson	*	5
Phyt_abund	Pentatomidae	Dominance_D_Earthw	**-0,96362**	0,002381	Spearman	**	
Phyt_abund	Pentatomidae	Simpson_1-D_Earthw	**0,96362**	0,002381	Spearman	**	
Phyt_abund	Pentatomidae	Dominance_D_FITS	**0,98561**	0,005556	Spearman	**	
Phyt_abund	Pentatomidae	Simpson_1-D_FITS	**-0,98561**	0,005556	Spearman	**	
Phyt_abund	Pentatomidae	Cl-	**-0,81537**	0,038095	Spearman	*	
Phyt_abund	Pentatomidae	Equitability_J_FITS	**-0,84067**	0,044444	Spearman	*	
Phyt_abund	Pentatomidae	Evenness_e^H/S_FITS	**-0,84067**	0,044444	Spearman	*	
Phyt_abund	Pentatomidae	Shannon_H_FITS	**-0,84067**	0,044444	Spearman	*	8
Phyt_abund	Phyllotreta sp.	Thripidae	**-0,90633**	0,028571	Spearman	*	
Phyt_abund	Phyllotreta sp.	Silk ctrl % degrad	**-0,79704**	0,031844	Pearson	*	
Phyt_abund	Phyllotreta sp.	F	**-0,83845**	0,037041	Pearson	*	
Phyt_abund	Phyllotreta sp.	Equitability_J_Carab	**-0,97386**	0,001016	Pearson	**	
Phyt_abund	Phyllotreta sp.	Evenness_e^H/S_Carab	**-0,97186**	0,001177	Pearson	**	
Phyt_abund	Phyllotreta sp.	Shannon_H_Carab	**-0,95532**	0,00295	Pearson	**	
Phyt_abund	Phyllotreta sp.	Equitability_J_Phyt	**-0,90644**	0,004888	Pearson	**	
Phyt_abund	Phyllotreta sp.	Dominance_D_Phyt	**0,89743**	0,00612	Pearson	**	
Phyt_abund	Phyllotreta sp.	Simpson_1-D_Phyt	**-0,89743**	0,00612	Pearson	**	
Phyt_abund	Phyllotreta sp.	Evenness_e^H/S_Phyt	**-0,88855**	0,007494	Pearson	**	

Phyt_abund	Phyllotreta sp.	Shannon_H_Phyt	**-0,88055**	0,008873	Pearson	**	
Phyt_abund	Phyllotreta sp.	Evenness_e^H/S_Wf	**0,80496**	0,028959	Pearson	*	12
Phyt_abund	Pulmonata	Taxa_S_FITS	**0,94112**	0,016667	Spearman	*	
Phyt_abund	Pulmonata	dry matter	**-0,90633**	0,028571	Spearman	*	
Phyt_abund	Pulmonata	Aphididae	**0,86692**	0,028571	Spearman	*	3
Phyt_abund	Thripidae	acP	**0,94112**	0,016667	Spearman	*	
Phyt_abund	Thripidae	AryS	**0,94112**	0,016667	Spearman	*	
Phyt_abund	Thripidae	Ester	**0,94112**	0,016667	Spearman	*	
Phyt_abund	Thripidae	Gluc	**0,94112**	0,016667	Spearman	*	
Phyt_abund	Thripidae	Leu	**0,94112**	0,016667	Spearman	*	
Phyt_abund	Thripidae	NH4+	**-0,86692**	0,028571	Spearman	*	
Phyt_abund	Thripidae	NO2-	**-0,86692**	0,028571	Spearman	*	
Phyt_abund	Thripidae	Phyllotreta sp.	**-0,90633**	0,028571	Spearman	*	
Phyt_abund	Thripidae	QBS-ar	**0,86692**	0,028571	Spearman	*	
Phyt_abund	Thripidae	P (Olsen)	**0,86692**	0,028571	Spearman	*	10
Phyt	Dominance_D_Phyt	AMF	**-0,79393**	0,033019	Pearson	*	
Phyt	Dominance_D_Phyt	Equitability_J_Carab	**-0,93646**	0,005929	Pearson	**	
Phyt	Dominance_D_Phyt	Evenness_e^H/S_Carab	**-0,92197**	0,008895	Pearson	**	
Phyt	Dominance_D_Phyt	Evenness_e^H/S_Wf	**0,87756**	0,009422	Pearson	**	
Phyt	Dominance_D_Phyt	Urban150	**0,85998**	0,013049	Pearson	*	
Phyt	Dominance_D_Phyt	Shannon_H_Carab	**-0,89552**	0,015802	Pearson	*	
Phyt	Dominance_D_Phyt	Equitability_J_Wf	**0,81461**	0,02565	Pearson	*	
Phyt	Dominance_D_Phyt	Phyllotreta sp.	**0,89743**	0,00612	Pearson	**	
Phyt	Dominance_D_Phyt	Gluc	**-0,92841**	0,007504	Pearson	**	
Phyt	Dominance_D_Phyt	F	**-0,92375**	0,0085	Pearson	**	
Phyt	Dominance_D_Phyt	Nabidae	**-0,86924**	0,011054	Pearson	*	
Phyt	Dominance_D_Phyt	dsDNA	**-0,90326**	0,013584	Pearson	*	
Phyt	Dominance_D_Phyt	Araneae	**-0,84536**	0,016589	Pearson	*	
Phyt	Dominance_D_Phyt	AryS	**-0,88857**	0,017934	Pearson	*	
Phyt	Dominance_D_Phyt	Leu	**-0,88807**	0,01809	Pearson	*	
Phyt	Dominance_D_Phyt	Taxa_S_B16S	**-0,791**	0,03415	Pearson	*	
Phyt	Dominance_D_Phyt	Evenness_e^H/S_Earthw	**0,76663**	0,044358	Pearson	*	17
Phyt	Equitability_J_Phyt	Equitability_J_Carab	**0,98797**	0,000216	Pearson	***	
Phyt	Equitability_J_Phyt	Shannon_H_Carab	**0,97675**	0,000805	Pearson	***	
Phyt	Equitability_J_Phyt	Evenness_e^H/S_Carab	**0,97673**	0,000806	Pearson	***	
Phyt	Equitability_J_Phyt	Evenness_e^H/S_Wf	**-0,82827**	0,02135	Pearson	*	
Phyt	Equitability_J_Phyt	Arable500	**0,77839**	0,039247	Pearson	*	
Phyt	Equitability_J_Phyt	F	**0,97332**	0,001058	Pearson	**	
Phyt	Equitability_J_Phyt	Gluc	**0,95057**	0,003604	Pearson	**	
Phyt	Equitability_J_Phyt	Phyllotreta sp.	**-0,90644**	0,004888	Pearson	**	
Phyt	Equitability_J_Phyt	Leu	**0,91945**	0,00947	Pearson	**	
Phyt	Equitability_J_Phyt	AryS	**0,91667**	0,010127	Pearson	*	
Phyt	Equitability_J_Phyt	Nabidae	**0,86844**	0,011219	Pearson	*	
Phyt	Equitability_J_Phyt	Araneae	**0,83618**	0,01906	Pearson	*	
Phyt	Equitability_J_Phyt	Silk ctrl % degrad	**0,83178**	0,020316	Pearson	*	
Phyt	Equitability_J_Phyt	dsDNA	**0,87238**	0,023392	Pearson	*	
Phyt	Equitability_J_Phyt	QBS-e	**0,81736**	0,024751	Pearson	*	
Phyt	Equitability_J_Phyt	Evenness_e^H/S_Earthw	**-0,80288**	0,029704	Pearson	*	
Phyt	Equitability_J_Phyt	Taxa_S_B16S	**0,78025**	0,038473	Pearson	*	
Phyt	Equitability_J_Phyt	Taxa_S_Earthw	**0,77934**	0,038852	Pearson	*	
Phyt	Equitability_J_Phyt	Silk P % degrad	**0,76576**	0,044754	Pearson	*	19
Phyt	Evenness_e^H/S_Phyt	Equitability_J_Carab	**0,97233**	0,001138	Pearson	**	
Phyt	Evenness_e^H/S_Phyt	Evenness_e^H/S_Carab	**0,96808**	0,001512	Pearson	**	
Phyt	Evenness_e^H/S_Phyt	Shannon_H_Carab	**0,95235**	0,003352	Pearson	**	
Phyt	Evenness_e^H/S_Phyt	Arable500	**0,77393**	0,041146	Pearson	*	
Phyt	Evenness_e^H/S_Phyt	Evenness_e^H/S_Wf	**-0,77008**	0,042824	Pearson	*	
Phyt	Evenness_e^H/S_Phyt	F	**0,98733**	0,00024	Pearson	***	
Phyt	Evenness_e^H/S_Phyt	Gluc	**0,97747**	0,000756	Pearson	***	
Phyt	Evenness_e^H/S_Phyt	Leu	**0,9507**	0,003585	Pearson	**	
Phyt	Evenness_e^H/S_Phyt	Phyllotreta sp.	**-0,88855**	0,007494	Pearson	**	

Phyt	Evenness_e^H/S_Phyt	AryS	**0,92319**	0,008623	Pearson	**	
Phyt	Evenness_e^H/S_Phyt	QBS-e	**0,8691**	0,011082	Pearson	*	
Phyt	Evenness_e^H/S_Phyt	Nabidae	**0,86585**	0,011762	Pearson	*	
Phyt	Evenness_e^H/S_Phyt	dsDNA	**0,88651**	0,018588	Pearson	*	
Phyt	Evenness_e^H/S_Phyt	Evenness_e^H/S_Earthw	**-0,83349**	0,019824	Pearson	*	
Phyt	Evenness_e^H/S_Phyt	Taxa_S_Earthw	**0,82431**	0,022551	Pearson	*	
Phyt	Evenness_e^H/S_Phyt	Silk ctrl % degrad	**0,80953**	0,027364	Pearson	*	
Phyt	Evenness_e^H/S_Phyt	Araneae	**0,7964**	0,032086	Pearson	*	
Phyt	Evenness_e^H/S_Phyt	Silk P % degrad	**0,78795**	0,035345	Pearson	*	
Phyt	Evenness_e^H/S_Phyt	Taxa_S_B16S	**0,75536**	0,049584	Pearson	*	19
Phyt	Shannon_H_Phyt	AMF	**0,83795**	0,01857	Pearson	*	
Phyt	Shannon_H_Phyt	Evenness_e^H/S_Carab	**0,9627**	0,002061	Pearson	**	
Phyt	Shannon_H_Phyt	Equitability_J_Carab	**0,95312**	0,003245	Pearson	**	
Phyt	Shannon_H_Phyt	Shannon_H_Carab	**0,94819**	0,003957	Pearson	**	
Phyt	Shannon_H_Phyt	Evenness_e^H/S_Wf	**-0,84373**	0,017012	Pearson	*	
Phyt	Shannon_H_Phyt	Taxa_S_Pred	**0,96059**	0,039409	Pearson	*	
Phyt	Shannon_H_Phyt	F	**0,95765**	0,002653	Pearson	**	
Phyt	Shannon_H_Phyt	AryS	**0,95145**	0,003478	Pearson	**	
Phyt	Shannon_H_Phyt	Araneae	**0,88755**	0,00766	Pearson	**	
Phyt	Shannon_H_Phyt	Gluc	**0,92458**	0,008317	Pearson	**	
Phyt	Shannon_H_Phyt	Phyllotreta sp.	**-0,88055**	0,008873	Pearson	**	
Phyt	Shannon_H_Phyt	Leu	**0,91166**	0,011361	Pearson	*	
Phyt	Shannon_H_Phyt	Nabidae	**0,85853**	0,013378	Pearson	*	
Phyt	Shannon_H_Phyt	dsDNA	**0,88646**	0,018606	Pearson	*	
Phyt	Shannon_H_Phyt	Formicidae	**0,82454**	0,022479	Pearson	*	
Phyt	Shannon_H_Phyt	QBS-e	**0,78869**	0,035056	Pearson	*	
Phyt	Shannon_H_Phyt	N	**-0,78445**	0,036747	Pearson	*	
Phyt	Shannon_H_Phyt	Shannon_H_Earthw	**0,77916**	0,038927	Pearson	*	
Phyt	Shannon_H_Phyt	Taxa_S_Earthw	**0,77105**	0,042396	Pearson	*	
Phyt	Shannon_H_Phyt	Silk ctrl % degrad	**0,76657**	0,044388	Pearson	*	20
Phyt	Simpson_1-D_Phyt	AMF	**0,79393**	0,033019	Pearson	*	
Phyt	Simpson_1-D_Phyt	Equitability_J_Carab	**0,93646**	0,005929	Pearson	**	
Phyt	Simpson_1-D_Phyt	Evenness_e^H/S_Carab	**0,92197**	0,008895	Pearson	**	
Phyt	Simpson_1-D_Phyt	Evenness_e^H/S_Wf	**-0,87756**	0,009422	Pearson	**	
Phyt	Simpson_1-D_Phyt	Urban150	**-0,85998**	0,013049	Pearson	*	
Phyt	Simpson_1-D_Phyt	Shannon_H_Carab	**0,89552**	0,015802	Pearson	*	
Phyt	Simpson_1-D_Phyt	Equitability_J_Wf	**-0,81461**	0,02565	Pearson	*	
Phyt	Simpson_1-D_Phyt	Phyllotreta sp.	**-0,89743**	0,00612	Pearson	**	
Phyt	Simpson_1-D_Phyt	Gluc	**0,92841**	0,007504	Pearson	**	
Phyt	Simpson_1-D_Phyt	F	**0,92375**	0,0085	Pearson	**	
Phyt	Simpson_1-D_Phyt	Nabidae	**0,86924**	0,011054	Pearson	*	
Phyt	Simpson_1-D_Phyt	dsDNA	**0,90326**	0,013584	Pearson	*	
Phyt	Simpson_1-D_Phyt	Araneae	**0,84536**	0,016589	Pearson	*	
Phyt	Simpson_1-D_Phyt	AryS	**0,88857**	0,017934	Pearson	*	
Phyt	Simpson_1-D_Phyt	Leu	**0,88807**	0,01809	Pearson	*	
Phyt	Simpson_1-D_Phyt	Taxa_S_B16S	**0,791**	0,03415	Pearson	*	
Phyt	Simpson_1-D_Phyt	Evenness_e^H/S_Earthw	**-0,76663**	0,044358	Pearson	*	17
Phyt	Taxa_S_Phyt	AMF	**0,77521**	0,040597	Pearson	*	
Phyt	Taxa_S_Phyt	Dominance_D_Mesof	**-0,98565**	0,000307	Pearson	***	
Phyt	Taxa_S_Phyt	Simpson_1-D_Mesof	**0,98565**	0,000307	Pearson	***	
Phyt	Taxa_S_Phyt	Fructose	**0,95158**	0,000965	Pearson	***	
Phyt	Taxa_S_Phyt	NO2-	**-0,90527**	0,005039	Pearson	**	
Phyt	Taxa_S_Phyt	Staphylinidae	**0,84366**	0,017031	Pearson	*	
Phyt	Taxa_S_Phyt	PO4---	**-0,83472**	0,019472	Pearson	*	
Phyt	Taxa_S_Phyt	P (Olsen)	**0,82606**	0,022017	Pearson	*	
Phyt	Taxa_S_Phyt	N	**-0,82534**	0,022234	Pearson	*	
Phyt	Taxa_S_Phyt	Glucose	**0,81301**	0,026185	Pearson	*	
Phyt	Taxa_S_Phyt	Shannon_H_Earthw	**0,81091**	0,026894	Pearson	*	
Phyt	Taxa_S_Phyt	S.I.R.	**0,77833**	0,039275	Pearson	*	
Phyt	Taxa_S_Phyt	Cotton ctrl % degrad	**0,77711**	0,03979	Pearson	*	

Phyt	Taxa_S_Phyt	QBS-ar	**0,76402**	0,045542	Pearson	*	
Phyt	Taxa_S_Phyt	Evenness_e^H/S_paras	**0,76923**	0,0432	Pearson	*	15
Predat_abund	Araneae	AMF	**0,85236**	0,014832	Pearson	*	
Predat_abund	Araneae	Evenness_e^H/S_Wf	**-0,93036**	0,002367	Pearson	**	
Predat_abund	Araneae	Nabidae	**0,89045**	0,007186	Pearson	**	
Predat_abund	Araneae	Shannon_H_Phyt	**0,88755**	0,00766	Pearson	**	
Predat_abund	Araneae	Equitability_J_Wf	**-0,85891**	0,013291	Pearson	*	
Predat_abund	Araneae	Taxa_S_Wm	**0,85833**	0,013424	Pearson	*	
Predat_abund	Araneae	Dominance_D_Phyt	**-0,84536**	0,016589	Pearson	*	
Predat_abund	Araneae	Simpson_1-D_Phyt	**0,84536**	0,016589	Pearson	*	
Predat_abund	Araneae	Equitability_J_Phyt	**0,83618**	0,01906	Pearson	*	
Predat_abund	Araneae	Evenness_e^H/S_Carab	**0,86918**	0,024553	Pearson	*	
Predat_abund	Araneae	Arable500	**0,80586**	0,028641	Pearson	*	
Predat_abund	Araneae	Evenness_e^H/S_Phyt	**0,7964**	0,032086	Pearson	*	
Predat_abund	Araneae	Urban150	**-0,78802**	**0,03532**	Pearson	*	
Predat_abund	Araneae	Equitability_J_Carab	**0,83282**	0,039588	Pearson	*	
Predat_abund	Araneae	Shannon_H_Carab	**0,82926**	0,041238	Pearson	*	
Predat_abund	Araneae	Formicidae	**0,76623**	0,04454	Pearson	*	
Predat_abund	Araneae	N	**-0,87563**	0,009788	Pearson	**	
Predat_abund	Araneae	Basal resp.	**0,86385**	0,012192	Pearson	*	
Predat_abund	Araneae	S.I.R.	**0,85749**	0,013618	Pearson	*	
Predat_abund	Araneae	AryS	**0,89243**	0,016734	Pearson	*	
Predat_abund	Araneae	dsDNA	**0,89066**	0,017278	Pearson	*	
Predat_abund	Araneae	Fructose	**0,84201**	0,017468	Pearson	*	
Predat_abund	Araneae	Shannon_H_Earthw	**0,80322**	0,029582	Pearson	*	
Predat_abund	Araneae	F	**0,83062**	0,040603	Pearson	*	
Predat_abund	Araneae	alkP	**0,81447**	0,04844	Pearson	*	25
Predat_abund	Chrysopidae	SemiNatural150	**-0,79008**	0,034506	Pearson	*	
Predat_abund	Chrysopidae	Equitability_J_B16S	**0,87845**	0,009256	Pearson	**	
Predat_abund	Chrysopidae	Evenness_e^H/S_B16S	**0,87588**	0,009739	Pearson	**	
Predat_abund	Chrysopidae	Shannon_H_B16S	**0,86425**	0,012106	Pearson	*	
Predat_abund	Chrysopidae	NO3-	**-0,8027**	0,029768	Pearson	*	
Predat_abund	Chrysopidae	Equitability_J_Earthw	**0,78437**	0,036781	Pearson	*	6
Predat_abund	Formicidae	Evenness_e^H/S_paras	**0,76016**	0,04732	Pearson	*	
Predat_abund	Formicidae	Shannon_H_Phyt	**0,82454**	0,022479	Pearson	*	
Predat_abund	Formicidae	Evenness_e^H/S_FITS	**-0,91667**	0,010127	Pearson	*	
Predat_abund	Formicidae	Equitability_J_FITS	**-0,90531**	0,013025	Pearson	*	
Predat_abund	Formicidae	Fructose	**0,8528**	0,014725	Pearson	*	
Predat_abund	Formicidae	Ca++	**0,85262**	0,01477	Pearson	*	
Predat_abund	Formicidae	N	**-0,82474**	0,022418	Pearson	*	
Predat_abund	Formicidae	Caffeic acid	**0,77011**	0,042813	Pearson	*	
Predat_abund	Formicidae	Araneae	**0,76623**	0,04454	Pearson	*	
Predat_abund	Formicidae	Exch. Mg	**0,75913**	0,047803	Pearson	*	10
Predat_abund	Nabidae	AMF	**0,75463**	0,049934	Pearson	*	
Predat_abund	Nabidae	SemiNatural500	**-0,81832**	0,038095	Spearman	*	
Predat_abund	Nabidae	dsDNA	**0,98876**	0,000189	Pearson	***	
Predat_abund	Nabidae	alkP	**0,94316**	0,004755	Pearson	**	
Predat_abund	Nabidae	Basal resp.	**0,90427**	0,005169	Pearson	**	
Predat_abund	Nabidae	AryS	**0,94016**	0,005264	Pearson	**	
Predat_abund	Nabidae	acP	**0,93837**	0,005581	Pearson	**	
Predat_abund	Nabidae	Araneae	**0,89045**	0,007186	Pearson	**	
Predat_abund	Nabidae	F	**0,92839**	0,007507	Pearson	**	
Predat_abund	Nabidae	Evenness_e^H/S_Earthw	**-0,88413**	0,008239	Pearson	**	
Predat_abund	Nabidae	Taxa_S_Earthw	**0,87563**	0,009787	Pearson	**	
Predat_abund	Nabidae	Gluc	**0,91136**	0,011437	Pearson	*	
Predat_abund	Nabidae	Leu	**0,90473**	0,013182	Pearson	*	
Predat_abund	Nabidae	Silk ctrl % degrad	**0,79843**	0,031329	Pearson	*	
Predat_abund	Nabidae	Org. matter	**0,79648**	0,032054	Pearson	*	
Predat_abund	Nabidae	T.O.C.	**0,79256**	0,033545	Pearson	*	
Predat_abund	Nabidae	QBS-e	**0,77929**	0,03887	Pearson	*	

Predat_abund	Nabidae	Tot N dm	**0,77476**	0,040788	Pearson	*	
Predat_abund	Nabidae	Shannon_H_Earthw	**0,76817**	0,04367	Pearson	*	
Predat_abund	Nabidae	Arable500	**0,93956**	0,00167	Pearson	**	
Predat_abund	Nabidae	Evenness_e^H/S_Carab	**0,9382**	0,005611	Pearson	**	
Predat_abund	Nabidae	Dominance_D_Phyt	**-0,86924**	0,011054	Pearson	*	
Predat_abund	Nabidae	Simpson_1-D_Phyt	**0,86924**	0,011054	Pearson	*	
Predat_abund	Nabidae	Equitability_J_Phyt	**0,86844**	0,011219	Pearson	*	
Predat_abund	Nabidae	Evenness_e^H/S_Pred	**-0,98867**	0,011326	Pearson	*	
Predat_abund	Nabidae	Evenness_e^H/S_Phyt	**0,86585**	0,011762	Pearson	*	
Predat_abund	Nabidae	Evenness_e^H/S_Wf	**-0,86129**	0,012754	Pearson	*	
Predat_abund	Nabidae	Shannon_H_Phyt	**0,85853**	0,013378	Pearson	*	
Predat_abund	Nabidae	Equitability_J_Carab	**0,8833**	0,019635	Pearson	*	
Predat_abund	Nabidae	Shannon_H_Carab	**0,85615**	0,029552	Pearson	*	
Predat_abund	Nabidae	Equitability_J_Wf	**-0,78785**	0,035386	Pearson	*	
Predat_abund	Nabidae	Arable1000	**0,78023**	0,038481	Pearson	*	
Predat_abund	Nabidae	Urban150	**-0,7627**	0,046146	Pearson	*	
Predat_abund	Nabidae	Taxa_S_FARISA	**0,75743**	0,048603	Pearson	*	34
Predat_abund	Staphylinidae	AMF	**0,78405**	0,036913	Pearson	*	
Predat_abund	Staphylinidae	Shannon_H_Pred	**0,98902**	0,010979	Pearson	*	
Predat_abund	Staphylinidae	Taxa_S_Phyt	**0,84366**	0,017031	Pearson	*	
Predat_abund	Staphylinidae	Syrphidae	**0,79412**	0,032949	Pearson	*	
Predat_abund	Staphylinidae	Equitability_J_Pred	**0,9663**	0,033699	Pearson	*	
Predat_abund	Staphylinidae	P (Olsen)	**0,9719**	0,00025	Pearson	***	
Predat_abund	Staphylinidae	Taxa_S_Mesof	**0,87064**	0,010768	Pearson	*	
Predat_abund	Staphylinidae	Ca++	**0,81063**	0,02699	Pearson	*	
Predat_abund	Staphylinidae	Fructose	**0,80839**	0,027758	Pearson	*	
Predat_abund	Staphylinidae	C.S.C.	**-0,77816**	0,039344	Pearson	*	
Predat_abund	Staphylinidae	QBS-ar	**0,76001**	0,047391	Pearson	*	11
Predat_abund	Syrphidae	Evenness_e^H/S_BARISA	**-0,82289**	0,022993	Pearson	*	
Predat_abund	Syrphidae	Shannon_H_BARISA	**-0,8039**	0,029337	Pearson	*	
Predat_abund	Syrphidae	Equitability_J_BARISA	**-0,76035**	0,047231	Pearson	*	
Predat_abund	Syrphidae	Evenness_e^H/S_paras	**0,79737**	0,031721	Pearson	*	
Predat_abund	Syrphidae	Ca++	**0,89273**	0,006826	Pearson	**	
Predat_abund	Syrphidae	Cicadellidae	**-0,86772**	0,011368	Pearson	*	
Predat_abund	Syrphidae	Staphylinidae	**0,79412**	0,032949	Pearson	*	
Predat_abund	Syrphidae	Shannon_H_Mesof	**0,84151**	0,035687	Pearson	*	
Predat_abund	Syrphidae	QBS-ar	**0,76457**	0,045291	Pearson	*	9
Predat	Dominance_D_Pred	Arable500	**0,99945**	0,000553	Pearson	***	
Predat	Dominance_D_Pred	Evenness_e^H/S_Wm	**0,97766**	0,022338	Pearson	*	
Predat	Dominance_D_Pred	Arable1000	**0,95236**	0,047638	Pearson	*	
Predat	Dominance_D_Pred	Folin	**-0,9847**	0,015298	Pearson	*	
Predat	Dominance_D_Pred	Mg++	**-0,98142**	0,018576	Pearson	*	
Predat	Dominance_D_Pred	Exch. Ca	**0,96352**	0,036477	Pearson	*	6
Predat	Equitability_J_Pred	Evenness_e^H/S_Wm	**-0,9871**	0,0129	Pearson	*	
Predat	Equitability_J_Pred	Arable500	**-0,95274**	0,04726	Pearson	*	
Predat	Equitability_J_Pred	Taxa_S_Mesof	**0,98973**	0,010266	Pearson	*	
Predat	Equitability_J_Pred	C.S.C.	**-0,98136**	0,018638	Pearson	*	
Predat	Equitability_J_Pred	Staphylinidae	**0,9663**	0,033699	Pearson	*	
Predat	Equitability_J_Pred	Ca++	**0,96218**	0,03782	Pearson	*	
Predat	Equitability_J_Pred	pH in H2O	**-0,95241**	0,04759	Pearson	*	7
Predat	Evenness_e^H/S_Pred	Dominance_D_Carab	**-0,95512**	0,044885	Pearson	*	
Predat	Evenness_e^H/S_Pred	Caffeic acid	**0,9986**	0,001405	Pearson	**	
Predat	Evenness_e^H/S_Pred	Tot N dm	**-0,99685**	0,003152	Pearson	**	
Predat	Evenness_e^H/S_Pred	Nabidae	**-0,98867**	0,011326	Pearson	*	
Predat	Evenness_e^H/S_Pred	alkP	**-0,99861**	0,033627	Pearson	*	
Predat	Evenness_e^H/S_Pred	Sinapic acid	**0,96588**	0,034125	Pearson	*	
Predat	Evenness_e^H/S_Pred	Glucose	**0,96044**	0,039561	Pearson	*	
Predat	Evenness_e^H/S_Pred	Exch. Mg	**0,95291**	0,047086	Pearson	*	8
Predat	Shannon_H_Pred	Evenness_e^H/S_Wm	**-0,95827**	0,041734	Pearson	*	
Predat	Shannon_H_Pred	Equitability_J_Wm	**-0,95221**	0,047795	Pearson	*	

Predat	Shannon_H_Pred	Staphylinidae	**0,98902**	0,010979	Pearson	*	
Predat	Shannon_H_Pred	C.S.C.	**-0,98161**	0,018385	Pearson	*	
Predat	Shannon_H_Pred	Taxa_S_Mesof	**0,98007**	0,019927	Pearson	*	
Predat	Shannon_H_Pred	P (Olsen)	**0,95772**	0,042283	Pearson	*	
Predat	Shannon_H_Pred	Basal resp.	**-0,95542**	0,044577	Pearson	*	
Predat	Shannon_H_Pred	Sand	**-0,95264**	0,047364	Pearson	*	8
Predat	Simpson_1-D_Pred	Arable500	**-0,99949**	0,000509	Pearson	***	
Predat	Simpson_1-D_Pred	Evenness_e^H/S_Wm	**-0,9778**	0,022196	Pearson	*	
Predat	Simpson_1-D_Pred	Arable1000	**-0,95274**	0,047257	Pearson	*	
Predat	Simpson_1-D_Pred	Folin	**0,98482**	0,015184	Pearson	*	
Predat	Simpson_1-D_Pred	Mg++	**0,9816**	0,018396	Pearson	*	
Predat	Simpson_1-D_Pred	Exch. Ca	**-0,96298**	0,037015	Pearson	*	6
Predat	Taxa_S_Pred	Clay	**0,97996**	0,020042	Pearson	*	
Predat	Taxa_S_Pred	NO2-	**-0,97601**	0,023992	Pearson	*	
Predat	Taxa_S_Pred	Shannon_H_Phyt	**0,96059**	0,039409	Pearson	*	
Predat	Taxa_S_pred	Shannon_H_paras	**-0,9796**	0,020401	Pearson	*	4
QBS-ar	QBS-ar	AMF	**0,8834**	0,000701	Pearson	***	
QBS-ar	QBS-ar	Shannon_H_BARISA	**-0,79334**	0,006166	Pearson	**	
QBS-ar	QBS-ar	Evenness_e^H/S_BARISA	**-0,79005**	0,00654	Pearson	**	
QBS-ar	QBS-ar	Equitability_J_BARISA	**-0,78614**	0,007006	Pearson	**	
QBS-ar	QBS-ar	Taxa_S_Mesof	**0,72939**	0,016668	Pearson	*	
QBS-ar	QBS-ar	Fructose	**0,82127**	0,0235	Pearson	*	
QBS-ar	QBS-ar	Thripidae	**0,86692**	0,028571	Spearman	*	
QBS-ar	QBS-ar	Dominance_D_Mesof	**-0,74754**	0,032994	Pearson	*	
QBS-ar	QBS-ar	Simpson_1-D_Mesof	**0,74754**	0,032994	Pearson	*	
QBS-ar	QBS-ar	Simpson_1-D_Wm	**0,67273**	0,033041	Spearman	*	
QBS-ar	QBS-ar	Syrphidae	**0,76457**	0,045291	Pearson	*	
QBS-ar	QBS-ar	Taxa_S_Phyt	**0,76402**	0,045542	Pearson	*	
QBS-ar	QBS-ar	Staphylinidae	**0,76001**	0,047391	Pearson	*	
QBS-ar	QBS-ar	Evenness_e^H/S_paras	**0,77649**	0,040051	Pearson	*	
QBS-ar	QBS-ar	Water resp.	**0,85272**	0,001716	Pearson	**	
QBS-ar	QBS-ar	Exch. K	**0,75222**	0,012077	Pearson	*	
QBS-ar	QBS-ar	Tot N dm	**0,72979**	0,01658	Pearson	*	
QBS-ar	QBS-ar	alkP	**0,87163**	0,023662	Pearson	*	
QBS-ar	QBS-ar	dsDNA	**0,86008**	0,027995	Pearson	*	
QBS-ar	QBS-ar	Ester	**0,85768**	0,028943	Pearson	*	
QBS-ar	QBS-ar	AryS	**0,83711**	0,037638	Pearson	*	
QBS-ar	QBS-ar	acP	**0,81705**	0,047142	Pearson	*	22
QBS-e	QBS-e	Taxa_S_Earthw	**0,92916**	0,000101	Pearson	***	
QBS-e	QBS-e	Evenness_e^H/S_Phyt	**0,8691**	0,011082	Pearson	*	
QBS-e	QBS-e	Equitability_J_Phyt	**0,81736**	0,024751	Pearson	*	
QBS-e	QBS-e	SO4--	**0,81237**	0,026401	Pearson	*	
QBS-e	QBS-e	Equitability_J_BARISA	**-0,68949**	0,02739	Pearson	*	
QBS-e	QBS-e	Na+	**-0,80473**	0,029043	Pearson	*	
QBS-e	QBS-e	Shannon_H_Phyt	**0,78869**	0,035056	Pearson	*	
QBS-e	QBS-e	Evenness_e^H/S_Earthw	**-0,66683**	0,035203	Pearson	*	
QBS-e	QBS-e	Shannon_H_Earthw	**0,66608**	0,035486	Pearson	*	
QBS-e	QBS-e	Shannon_H_BARISA	**-0,66093**	0,037463	Pearson	*	
QBS-e	QBS-e	Nabidae	**0,77929**	0,03887	Pearson	*	
QBS-e	QBS-e	Dominance_D_FITS	**0,72937**	0,040039	Pearson	*	
QBS-e	QBS-e	Simpson_1-D_FITS	**-0,72937**	0,040039	Pearson	*	
QBS-e	QBS-e	F	**0,91101**	0,004323	Pearson	**	
QBS-e	QBS-e	Leu	**0,94235**	0,00489	Pearson	**	
QBS-e	QBS-e	Gluc	**0,92617**	0,007974	Pearson	**	
QBS-e	QBS-e	AryS	**0,843**	0,03504	Pearson	*	
QBS-e	QBS-e	acP	**0,82606**	0,042751	Pearson	*	
QBS-e	QBS-e	dsDNA	**0,81156**	0,049918	Pearson	*	19
Resp_rate	Basal resp.	Nabidae	**0,90427**	0,005169	Pearson	**	
Resp_rate	Basal resp.	Evenness_e^H/S_Wf	**-0,86222**	0,005881	Pearson	**	
Resp_rate	Basal resp.	Araneae	**0,86385**	0,012192	Pearson	*	

Resp_rate	Basal resp.	dsDNA	**0,89223**	0,016796	Pearson	*	
Resp_rate	Basal resp.	Equitability_J_Wf	**-0,78885**	0,019966	Pearson	*	
Resp_rate	Basal resp.	Taxa_S_B16S	**0,72143**	0,028244	Pearson	*	
Resp_rate	Basal resp.	alkP	**0,85547**	0,029825	Pearson	*	
Resp_rate	Basal resp.	AryS	**0,8534**	0,030662	Pearson	*	
Resp_rate	Basal resp.	N	**-0,78927**	0,034825	Pearson	*	
Resp_rate	Basal resp.	Shannon_H_Carab	**0,69035**	0,039544	Pearson	*	
Resp_rate	Basal resp.	Arable500	**0,65001**	0,041894	Pearson	*	
Resp_rate	Basal resp.	Shannon_H_Pred	**-0,95542**	0,044577	Pearson	*	
Resp_rate	Basal resp.	Taxa_S_Wm	**0,64086**	0,045871	Pearson	*	
Resp_rate	Basal resp.	Evenness_e^H/S_FARISA	**-0,6383**	0,047024	Spearman	*	
Resp_rate	Basal resp.	S.I.R.	**0,8057**	0,004896	Pearson	**	
Resp_rate	Basal resp.	Org. matter	**0,72756**	0,017082	Pearson	*	
Resp_rate	Basal resp.	T.O.C.	**0,72077**	0,01868	Pearson	*	
Resp_rate	Basal resp.	F	**0,76587**	0,044703	Pearson	*	18
Resp_rate	S.I.R.	AMF	**0,71129**	0,02108	Pearson	*	
Resp_rate	S.I.R.	N	**-0,97527**	0,000182	Pearson	***	
Resp_rate	S.I.R.	PO4---	**-0,93053**	0,002353	Pearson	**	
Resp_rate	S.I.R.	Basal resp.	**0,8057**	0,004896	Pearson	**	
Resp_rate	S.I.R.	Fructose	**0,87**	0,010899	Pearson	*	
Resp_rate	S.I.R.	Araneae	**0,85749**	0,013618	Pearson	*	
Resp_rate	S.I.R.	Evenness_e^H/S_Wf	**-0,80212**	0,01661	Pearson	*	
Resp_rate	S.I.R.	NO2-	**-0,81506**	0,025503	Pearson	*	
Resp_rate	S.I.R.	Dominance_D_Mesof	**-0,73975**	0,035913	Pearson	*	
Resp_rate	S.I.R.	Simpson_1-D_Mesof	**0,73975**	0,035913	Pearson	*	
Resp_rate	S.I.R.	Taxa_S_Phyt	**0,77833**	0,039275	Pearson	*	
Resp_rate	S.I.R.	Org. matter	**0,66158**	0,037208	Pearson	*	
Resp_rate	S.I.R.	T.O.C.	**0,65965**	0,037963	Pearson	*	
Resp_rate	S.I.R.	F	**0,75918**	0,047777	Pearson	*	14
Resp_rate	Water resp.	AMF	**0,73097**	0,016316	Pearson	*	
Resp_rate	Water resp.	QBS-ar	**0,85272**	0,001716	Pearson	**	
Resp_rate	Water resp.	Arable150	**0,74531**	0,013359	Pearson	*	
Resp_rate	Water resp.	Equitability_J_Wf	**-0,78746**	0,020338	Pearson	*	
Resp_rate	Water resp.	Evenness_e^H/S_Wf	**-0,71872**	0,04456	Pearson	*	
Resp_rate	Water resp.	Taxa_S_paras	**-0,75903**	0,047849	Pearson	*	
Resp_rate	Water resp.	Evenness_e^H/S_paras	**0,82751**	0,021579	Pearson	*	
Resp_rate	Water resp.	Exch. K	**0,79032**	0,006509	Pearson	**	8
Soil An	C.S.C.	Shannon_H_Mesof	**-0,85316**	0,007069	Pearson	**	
Soil An	C.S.C.	Shannon_H_Pred	**-0,98161**	0,018385	Pearson	*	
Soil An	C.S.C.	Equitability_J_Pred	**-0,98136**	0,018638	Pearson	*	
Soil An	C.S.C.	Staphylinidae	**-0,77816**	0,039344	Pearson	*	
Soil An	C.S.C.	Taxa_S_B16S	**0,6785**	0,044519	Pearson	*	
Soil An	C.S.C.	Equitability_J_Mesof	**-0,71111**	0,047969	Pearson	*	6
Soil An	C/N	Mineral. Coeff.	**-0,90909**	0,000106	Spearman	***	
Soil An	C/N	Tot C dm	**0,90909**	0,000106	Spearman	***	
Soil An	C/N	Tot. Calc.	**0,9**	0,00016	Spearman	***	
Soil An	C/N	In C dm	**0,89294**	0,000215	Spearman	***	
Soil An	C/N	Electric. Cond.	**-0,82727**	0,001677	Spearman	**	
Soil An	C/N	C/N (Humific.)	**0,81818**	0,002083	Spearman	**	
Soil An	C/N	Exch. Mg	**-0,62727**	0,038845	Spearman	*	
Soil An	C/N	Org. matter	**0,60909**	0,046696	Spearman	*	
Soil An	C/N	T.O.C.	**0,60909**	0,046696	Spearman	*	9
Soil An	C/N (Humific.)	C/N	**0,81818**	0,002083	Spearman	**	
Soil An	C/N (Humific.)	Mineral. Coeff.	**-0,70998**	0,014374	Pearson	*	
Soil An	C/N (Humific.)	Arable500	**0,69038**	0,018692	Pearson	*	
Soil An	C/N (Humific.)	Dominance_D_Carab	**0,74297**	0,021811	Pearson	*	
Soil An	C/N (Humific.)	Arable1000	**0,67696**	0,022139	Pearson	*	
Soil An	C/N (Humific.)	Org. matter	**0,6227**	0,040726	Pearson	*	
Soil An	C/N (Humific.)	Evenness_e^H/S_BARISA	**0,62226**	0,040908	Pearson	*	
Soil An	C/N (Humific.)	T.O.C.	**0,62548**	0,039573	Pearson	*	

Soil An	C/N (Humific.)	Sand	**0,61924**	0,042191	Pearson	*	9
Soil An	Clay	Taxa_S_B16S	**-0,83877**	0,004715	Pearson	**	
Soil An	Clay	Taxa_S_Pred	**0,97996**	0,020042	Pearson	*	
Soil An	Clay	Silk P % degrad	**-0,7011**	0,023889	Pearson	*	
Soil An	Clay	Equitability_J_Carab	**-0,72568**	0,026887	Pearson	*	
Soil An	Clay	Shannon_H_Carab	**-0,72108**	0,028358	Pearson	*	
Soil An	Clay	Simpson_1-D_Carab	**-0,82682**	0,042392	Pearson	*	
Soil An	Clay	Sand	**-0,97182**	5,95E-07	Pearson	***	7
Soil An	Electric. Cond.	In C dm	**-0,86105**	0,000663	Spearman	***	
Soil An	Electric. Cond.	Tot. Calc.	**-0,84545**	0,001045	Spearman	**	
Soil An	Electric. Cond.	Tot C dm	**-0,83636**	0,001333	Spearman	**	
Soil An	Electric. Cond.	Mineral. Coeff.	**0,82814**	0,001642	Pearson	**	
Soil An	Electric. Cond.	C/N	**-0,82727**	0,001677	Spearman	**	
Soil An	Electric. Cond.	pH in H2O	**-0,67496**	0,022687	Pearson	*	
Soil An	Electric. Cond.	Shannon_H_Mesof	**0,70695**	0,049898	Pearson	*	
Soil An	Electric. Cond.	Shannon_H_paras	**-0,79459**	0,032768	Pearson	*	8
Soil An	Exch. Ca	Shannon_H_FARISA	**0,73636**	0,00976	Spearman	**	
Soil An	Exch. Ca	Taxa_S_FARISA	**0,70788**	0,014798	Pearson	*	
Soil An	Exch. Ca	Shannon_H_Wm	**0,64933**	0,030613	Pearson	*	
Soil An	Exch. Ca	Dominance_D_Pred	**0,96352**	0,036477	Pearson	*	
Soil An	Exch. Ca	Simpson_1-D_Pred	**-0,96298**	0,037015	Pearson	*	
Soil An	Exch. Ca	Cotton N % degrad	**0,66061**	0,037588	Spearman	*	
Soil An	Exch. Ca	Equitability_J_Wm	**0,60999**	0,046284	Pearson	*	
Soil An	Exch. Ca	Simpson_1-D_Wm	**0,60909**	0,046696	Spearman	*	8
Soil An	Exch. K	Aleyrodidae	**0,94743**	0,001183	Pearson	**	
Soil An	Exch. K	Simpson_1-D_Wm	**0,81818**	0,002083	Spearman	**	
Soil An	Exch. K	Water resp.	**0,79032**	0,006509	Pearson	**	
Soil An	Exch. K	QBS-ar	**0,75222**	0,012077	Pearson	*	
Soil An	Exch. K	Exch. Na	**0,68431**	0,020199	Pearson	*	
Soil An	Exch. K	Taxa_S_Wm	**0,68243**	0,020683	Pearson	*	
Soil An	Exch. K	SemiNatural150	**-0,65186**	0,029755	Pearson	*	
Soil An	Exch. K	Ascorbic acid	**-0,80131**	0,030273	Pearson	*	
Soil An	Exch. K	Dominance_D_Wm	**-0,62317**	0,040531	Pearson	*	9
Soil An	Exch. Mg	Caffeic acid	**0,93058**	0,002349	Pearson	**	
Soil An	Exch. Mg	FRAP	**0,89278**	0,006819	Pearson	**	
Soil An	Exch. Mg	Folin	**0,84751**	0,016036	Pearson	*	
Soil An	Exch. Mg	Sinapic acid	**0,81167**	0,026637	Pearson	*	
Soil An	Exch. Mg	Taxa_S_Carab	**0,70785**	0,032878	Pearson	*	
Soil An	Exch. Mg	Equitability_J_FITS	**-0,74256**	0,034842	Pearson	*	
Soil An	Exch. Mg	Simpson_1-D_Carab	**0,83758**	0,037429	Pearson	*	
Soil An	Exch. Mg	C/N	**-0,62727**	0,038845	Spearman	*	
Soil An	Exch. Mg	Evenness_e^H/S_FITS	**-0,71977**	0,044102	Pearson	*	
Soil An	Exch. Mg	Evenness_e^H/S_Pred	**0,95291**	0,047086	Pearson	*	
Soil An	Exch. Mg	Formicidae	**0,75913**	0,047803	Pearson	*	11
Soil An	Exch. Na	Taxa_S_Wm	**0,76638**	0,00594	Pearson	**	
Soil An	Exch. Na	Dominance_D_Carab	**-0,80484**	0,008882	Pearson	**	
Soil An	Exch. Na	Dominance_D_Wf	**0,8**	0,010769	Spearman	*	
Soil An	Exch. Na	Simpson_1-D_Wf	**-0,8**	0,010769	Spearman	*	
Soil An	Exch. Na	Evenness_e^H/S_BARISA	**-0,67988**	0,021352	Pearson	*	
Soil An	Exch. Na	Equitability_J_Wf	**-0,72297**	0,027748	Pearson	*	
Soil An	Exch. Na	Shannon_H_BARISA	**-0,63388**	0,036236	Pearson	*	
Soil An	Exch. Na	Equitability_J_BARISA	**-0,63207**	0,036937	Pearson	*	
Soil An	Exch. Na	Simpson_1-D_Wm	**0,62727**	0,038845	Spearman	*	
Soil An	Exch. Na	Exch. K	**0,68431**	0,020199	Pearson	*	10
Soil An	In C dm	Tot. Calc.	**0,99772**	7,46E-12	Spearman	***	
Soil An	In C dm	C/N	**0,89294**	0,000215	Spearman	***	
Soil An	In C dm	Taxa_S_BARISA	**0,7206**	0,01236	Spearman	*	
Soil An	In C dm	Tot C dm	**0,9795**	1,44E-07	Spearman	***	
Soil An	In C dm	Electric. Cond.	**-0,86105**	0,000663	Spearman	***	5
Soil An	Mineral. Coeff.	C/N	**-0,90909**	0,000106	Spearman	***	

Soil An	Mineral. Coeff.	Taxa_S_BARISA	**-0,7374**	0,009604	Spearman	**	
Soil An	Mineral. Coeff.	Dominance_D_Carab	**-0,74448**	0,0214	Pearson	*	
Soil An	Mineral. Coeff.	Folin	**0,77205**	0,04196	Pearson	*	
Soil An	Mineral. Coeff.	Dominance_D_BARISA	**0,61977**	0,041964	Pearson	*	
Soil An	Mineral. Coeff.	Simpson_1-D_BARISA	**-0,6194**	0,042121	Pearson	*	
Soil An	Mineral. Coeff.	Taxa_S_paras	**-0,78784**	0,035391	Pearson	*	
Soil An	Mineral. Coeff.	Shannon_H_paras	**-0,77522**	0,040593	Pearson	*	
Soil An	Mineral. Coeff.	Electric. Cond.	**0,82814**	0,001642	Pearson	**	
Soil An	Mineral. Coeff.	C/N (Humific.)	**-0,70998**	0,014374	Pearson	*	10
Soil An	Org. matter	T.O.C.	**0,99991**	3,19E-18	Pearson	***	
Soil An	Org. matter	Dominance_D_B16S	**0,83539**	0,005052	Pearson	**	
Soil An	Org. matter	Simpson_1-D_B16S	**-0,83535**	0,005057	Pearson	**	
Soil An	Org. matter	Arable500	**0,74465**	0,008565	Pearson	**	
Soil An	Org. matter	Arable1000	**0,72724**	0,011211	Pearson	*	
Soil An	Org. matter	Basal resp.	**0,72756**	0,017082	Pearson	*	
Soil An	Org. matter	Nabidae	**0,79648**	0,032054	Pearson	*	
Soil An	Org. matter	S.I.R.	**0,66158**	0,037208	Pearson	*	
Soil An	Org. matter	Evenness_e^H/S_FARISA	**-0,61818**	0,042646	Spearman	*	
Soil An	Org. matter	alkP	**0,82012**	0,045624	Pearson	*	
Soil An	Org. matter	C/N	**0,60909**	0,046696	Spearman	*	
Soil An	Org. matter	C/N (Humific.)	**0,6227**	0,040726	Pearson	*	12
Soil An	P (Olsen)	Staphylinidae	**0,9719**	0,00025	Pearson	***	
Soil An	P (Olsen)	Shannon_H_Earthw	**0,74213**	0,013979	Pearson	*	
Soil An	P (Olsen)	Taxa_S_Wf	**0,7618**	0,01705	Pearson	*	
Soil An	P (Olsen)	Taxa_S_Phyt	**0,82606**	0,022017	Pearson	*	
Soil An	P (Olsen)	Fructose	**0,81044**	0,027053	Pearson	*	
Soil An	P (Olsen)	Thripidae	**0,86692**	0,028571	Spearman	*	
Soil An	P (Olsen)	Taxa_S_Mesof	**0,6718**	0,033375	Pearson	*	
Soil An	P (Olsen)	Shannon_H_Pred	**0,95772**	0,042283	Pearson	*	
Soil An	P (Olsen)	AryS	**0,82634**	0,042619	Pearson	*	
Soil An	P (Olsen)	Ca++	**0,76636**	0,044483	Pearson	*	
Soil An	P (Olsen)	NO2-	**-0,76293**	0,046042	Pearson	*	
Soil An	P (Olsen)	Dominance_D_Carab	**-0,67257**	0,047151	Pearson	*	
Soil An	P (Olsen)	Taxa_S_Wm	**0,60733**	0,047511	Pearson	*	13
Soil An	pH in H2O	Equitability_J_Pred	**-0,95241**	0,04759	Pearson	*	
Soil An	pH in H2O	Shannon_H_paras	**0,83882**	0,018329	Pearson	*	
Soil An	pH in H2O	Electric. Cond.	**-0,67496**	0,022687	Pearson	*	3
Soil An	Sand	Clay	**-0,97182**	5,95E-07	Pearson	***	
Soil An	Sand	Taxa_S_B16S	**0,87407**	0,002059	Pearson	**	
Soil An	Sand	Urban1000	**-0,68897**	0,019034	Pearson	*	
Soil An	Sand	Equitability_J_Carab	**0,75044**	0,01983	Pearson	*	
Soil An	Sand	Silk P % degrad	**0,7131**	0,020607	Pearson	*	
Soil An	Sand	F	**0,7728**	0,024551	Pearson	*	
Soil An	Sand	Shannon_H_Carab	**0,71065**	0,031884	Pearson	*	
Soil An	Sand	Silt	**-0,63078**	0,037444	Pearson	*	
Soil An	Sand	C/N (Humific.)	**0,61924**	0,042191	Pearson	*	
Soil An	Sand	Urban150	**-0,61671**	0,043286	Pearson	*	
Soil An	Sand	Shannon_H_Pred	**-0,95264**	0,047364	Pearson	*	11
Soil An	Silt	Urban1000	**0,93518**	2,40E-05	Pearson	***	
Soil An	Silt	SO4--	**-0,89872**	0,005934	Pearson	**	
Soil An	Silt	Ferulic acid	**0,92857**	0,006746	Spearman	**	
Soil An	Silt	Urban150	**0,74276**	0,008827	Pearson	**	
Soil An	Silt	Urban500	**0,73615**	0,009792	Pearson	**	
Soil An	Silt	Sand	**-0,63078**	0,037444	Pearson	*	6
Soil An	T.O.C.	Dominance_D_B16S	**0,83548**	0,005044	Pearson	**	
Soil An	T.O.C.	Simpson_1-D_B16S	**-0,83543**	0,005049	Pearson	**	
Soil An	T.O.C.	Arable500	**0,74311**	0,008778	Pearson	**	
Soil An	T.O.C.	Arable1000	**0,72644**	0,011344	Pearson	*	
Soil An	T.O.C.	Basal resp.	**0,72077**	0,01868	Pearson	*	
Soil An	T.O.C.	Nabidae	**0,79256**	0,033545	Pearson	*	

Soil An	T.O.C.	S.I.R.	**0,65965**	0,037963	Pearson	*	
Soil An	T.O.C.	C/N (Humific.)	**0,62548**	0,039573	Pearson	*	
Soil An	T.O.C.	Evenness_e^H/S_FARISA	**-0,61818**	0,042646	Spearman	*	
Soil An	T.O.C.	alkP	**0,81795**	0,046695	Pearson	*	
Soil An	T.O.C.	C/N	**0,60909**	0,046696	Spearman	*	
Soil An	T.O.C.	Org. matter	**0,99991**	3,19E-18	Pearson	***	12
Soil An	Tot C dm	In C dm	**0,9795**	1,44E-07	Spearman	***	
Soil An	Tot C dm	Tot. Calc.	**0,97273**	5,14E-07	Spearman	***	
Soil An	Tot C dm	C/N	**0,90909**	0,000106	Spearman	***	
Soil An	Tot C dm	Taxa_S_BARISA	**0,6314**	0,037202	Spearman	*	
Soil An	Tot C dm	Electric. Cond.	**-0,83636**	0,001333	Spearman	**	5
Soil An	Tot N dm	Evenness_e^H/S_Pred	**-0,99685**	0,003152	Pearson	**	
Soil An	Tot N dm	Piro	**0,91705**	0,010037	Pearson	*	
Soil An	Tot N dm	QBS-ar	**0,72979**	0,01658	Pearson	*	
Soil An	Tot N dm	Evenness_e^H/S_BARISA	**-0,69298**	0,018072	Pearson	*	
Soil An	Tot N dm	Shannon_H_BARISA	**-0,68279**	0,020589	Pearson	*	
Soil An	Tot N dm	alkP	**0,858**	0,028812	Pearson	*	
Soil An	Tot N dm	Equitability_J_BARISA	**-0,64125**	0,033472	Pearson	*	
Soil An	Tot N dm	Dominance_D_Mesof	**-0,73849**	0,036401	Pearson	*	
Soil An	Tot N dm	Simpson_1-D_Mesof	**0,73849**	0,036401	Pearson	*	
Soil An	Tot N dm	Nabidae	**0,77476**	0,040788	Pearson	*	
Soil An	Tot N dm	acP	**0,82316**	0,044145	Pearson	*	
Soil An	Tot N dm	Taxa_S_Earthw	**0,6359**	0,048127	Pearson	*	
Soil An	Tot N dm	NO2-	**-0,75505**	0,049734	Pearson	*	13
Soil An	Tot. Calc.	C/N	**0,9**	0,00016	Spearman	***	
Soil An	Tot. Calc.	Taxa_S_BARISA	**0,72818**	0,011054	Spearman	*	
Soil An	Tot. Calc.	In C dm	**0,99772**	7,46E-12	Spearman	***	
Soil An	Tot. Calc.	Tot C dm	**0,97273**	5,14E-07	Spearman	***	
Soil An	Tot. Calc.	Electric. Cond.	**-0,84545**	0,001045	Spearman	**	5
Weeds_f	Dominance_D_Wf	Exch. Na	**0,8**	0,010769	Spearman	*	
Weeds_f	Dominance_D_Wf	Shannon_H_Wm	**0,73333**	0,031123	Spearman	*	2
Weeds_f	Equitability_J_Wf	Arable1000	**-0,73899**	0,022917	Pearson	*	
Weeds_f	Equitability_J_Wf	Arable150	**-0,73746**	0,023354	Pearson	*	
Weeds_f	Equitability_J_Wf	Arable500	**-0,70671**	0,033287	Pearson	*	
Weeds_f	Equitability_J_Wf	Urban150	**0,70008**	0,03574	Pearson	*	
Weeds_f	Equitability_J_Wf	Araneae	**-0,85891**	0,013291	Pearson	*	
Weeds_f	Equitability_J_Wf	Basal resp.	**-0,78885**	0,019966	Pearson	*	
Weeds_f	Equitability_J_Wf	Water resp.	**-0,78746**	0,020338	Pearson	*	
Weeds_f	Equitability_J_Wf	Dominance_D_Phyt	**0,81461**	0,02565	Pearson	*	
Weeds_f	Equitability_J_Wf	Simpson_1-D_Phyt	**-0,81461**	0,02565	Pearson	*	
Weeds_f	Equitability_J_Wf	Exch. Na	**-0,72297**	0,027748	Pearson	*	
Weeds_f	Equitability_J_Wf	Nabidae	**-0,78785**	0,035386	Pearson	*	11
Weeds_f	Evenness_e^H/S_Wf	Arable500	**-0,73608**	0,023751	Pearson	*	
Weeds_f	Evenness_e^H/S_Wf	Araneae	**-0,93036**	0,002367	Pearson	**	
Weeds_f	Evenness_e^H/S_Wf	Basal resp.	**-0,86222**	0,005881	Pearson	**	
Weeds_f	Evenness_e^H/S_Wf	Dominance_D_Phyt	**0,87756**	0,009422	Pearson	**	
Weeds_f	Evenness_e^H/S_Wf	Simpson_1-D_Phyt	**-0,87756**	0,009422	Pearson	**	
Weeds_f	Evenness_e^H/S_Wf	Nabidae	**-0,86129**	0,012754	Pearson	*	
Weeds_f	Evenness_e^H/S_Wf	S.I.R.	**-0,80212**	0,01661	Pearson	*	
Weeds_f	Evenness_e^H/S_Wf	Shannon_H_Phyt	**-0,84373**	0,017012	Pearson	*	
Weeds_f	Evenness_e^H/S_Wf	Equitability_J_Phyt	**-0,82827**	0,02135	Pearson	*	
Weeds_f	Evenness_e^H/S_Wf	Phyllotreta sp.	**0,80496**	0,028959	Pearson	*	
Weeds_f	Evenness_e^H/S_Wf	F	**-0,8045**	0,029123	Pearson	*	
Weeds_f	Evenness_e^H/S_Wf	N	**0,77206**	0,041959	Pearson	*	
Weeds_f	Evenness_e^H/S_Wf	Evenness_e^H/S_Phyt	**-0,77008**	0,042824	Pearson	*	
Weeds_f	Evenness_e^H/S_Wf	Water resp.	**-0,71872**	0,04456	Pearson	*	
Weeds_f	Evenness_e^H/S_Wf	Silk ctrl % degrad	**-0,71203**	0,047548	Pearson	*	15
Weeds_f	Shannon_H_Wf	Urban150	**0,73828**	0,023118	Pearson	*	
Weeds_f	Shannon_H_Wf	Arable1000	**-0,67566**	0,045765	Pearson	*	
Weeds_f	Shannon_H_Wf	Taxa_S_B16S	**-0,74505**	0,033912	Pearson	*	3

Weeds_f	Simpson_1-D_Wf	Exch. Na	**-0,8**	0,010769	Spearman	*	
Weeds_f	Simpson_1-D_Wf	Shannon_H_Wm	**-0,73333**	0,031123	Spearman	*	2
Weeds_f	Taxa_S_Wf	P (Olsen)	**0,7618**	0,01705	Pearson	*	
Weeds_f	Taxa_S_Wf	Glucose	**0,84347**	0,017081	Pearson	*	
Weeds_f	Taxa_S_Wf	Cotton ctrl % degrad	**0,75689**	0,02969	Pearson	*	3
Weeds_m	Dominance_D_Wm	Arable150	**-0,66066**	0,026905	Pearson	*	
Weeds_m	Dominance_D_Wm	Lepidoptera	**0,86988**	0,010922	Pearson	*	
Weeds_m	Dominance_D_Wm	Na+	**0,80587**	0,028637	Pearson	*	
Weeds_m	Dominance_D_Wm	NO3-	**0,80466**	0,029066	Pearson	*	
Weeds_m	Dominance_D_Wm	NH4+	**0,79284**	0,033437	Pearson	*	
Weeds_m	Dominance_D_Wm	Exch. K	**-0,62317**	0,040531	Pearson	*	
Weeds_m	Dominance_D_Wm	Dominance_D_FARISA	**0,62287**	0,040653	Pearson	*	
Weeds_m	Dominance_D_Wm	Simpson_1-D_FARISA	**-0,62287**	0,040653	Pearson	*	8
Weeds_m	Equitability_J_Wm	Dominance_D_FARISA	**-0,73932**	0,009321	Pearson	**	
Weeds_m	Equitability_J_Wm	Simpson_1-D_FARISA	**0,73932**	0,009321	Pearson	**	
Weeds_m	Equitability_J_Wm	Exch. Ca	**0,60999**	0,046284	Pearson	*	
Weeds_m	Equitability_J_Wm	Shannon_H_Pred	**-0,95221**	0,047795	Pearson	*	4
Weeds_m	Evenness_e^H/S_Wm	Urban500	**-0,64174**	0,033292	Pearson	*	
Weeds_m	Evenness_e^H/S_Wm	Dominance_D_FARISA	**-0,8102**	0,002497	Pearson	**	
Weeds_m	Evenness_e^H/S_Wm	Simpson_1-D_FARISA	**0,8102**	0,002497	Pearson	**	
Weeds_m	Evenness_e^H/S_Wm	Equitability_J_Pred	**-0,9871**	0,0129	Pearson	*	
Weeds_m	Evenness_e^H/S_Wm	Simpson_1-D_Pred	**-0,9778**	0,022196	Pearson	*	
Weeds_m	Evenness_e^H/S_Wm	Dominance_D_Pred	**0,97766**	0,022338	Pearson	*	
Weeds_m	Evenness_e^H/S_Wm	Shannon_H_Pred	**-0,95827**	0,041734	Pearson	*	7
Weeds_m	Shannon_H_Wm	Arable150	**0,6609**	0,026829	Pearson	*	
Weeds_m	Shannon_H_Wm	Dominance_D_Wf	**0,73333**	0,031123	Spearman	*	
Weeds_m	Shannon_H_Wm	Simpson_1-D_Wf	**-0,73333**	0,031123	Spearman	*	
Weeds_m	Shannon_H_Wm	Na+	**-0,8299**	0,020865	Pearson	*	
Weeds_m	Shannon_H_Wm	Lepidoptera	**-0,81848**	0,024389	Pearson	*	
Weeds_m	Shannon_H_Wm	Exch. Ca	**0,64933**	0,030613	Pearson	*	
Weeds_m	Shannon_H_Wm	NO3-	**-0,76657**	0,044389	Pearson	*	
Weeds_m	Shannon_H_Wm	NH4+	**-0,76201**	0,046464	Pearson	*	8
Weeds_m	Simpson_1-D_Wm	Exch. K	**0,81818**	0,002083	Spearman	**	
Weeds_m	Simpson_1-D_Wm	Taxa_S_B16S	**0,76667**	0,02139	Spearman	*	
Weeds_m	Simpson_1-D_Wm	Agromyzidae	**-0,86932**	0,028571	Spearman	*	
Weeds_m	Simpson_1-D_Wm	Dominance_D_FARISA	**-0,64545**	0,031963	Spearman	*	
Weeds_m	Simpson_1-D_Wm	Simpson_1-D_FARISA	**0,64545**	0,031963	Spearman	*	
Weeds_m	Simpson_1-D_Wm	QBS-ar	**0,67273**	0,033041	Spearman	*	
Weeds_m	Simpson_1-D_Wm	Exch. Na	**0,62727**	0,038845	Spearman	*	
Weeds_m	Simpson_1-D_Wm	Exch. Ca	**0,60909**	0,046696	Spearman	*	8
Weeds_m	Taxa_S_Wm	Dominance_D_Carab	**-0,72848**	0,026018	Pearson	*	
Weeds_m	Taxa_S_Wm	Equitability_J_paras	**0,84935**	0,015575	Pearson	*	
Weeds_m	Taxa_S_Wm	Exch. Na	**0,76638**	0,00594	Pearson	**	
Weeds_m	Taxa_S_Wm	Shannon_H_Earthw	**0,74767**	0,012909	Pearson	*	
Weeds_m	Taxa_S_Wm	Araneae	**0,85833**	0,013424	Pearson	*	
Weeds_m	Taxa_S_Wm	Exch. K	**0,68243**	0,020683	Pearson	*	
Weeds_m	Taxa_S_Wm	N	**-0,81758**	0,024677	Pearson	*	
Weeds_m	Taxa_S_Wm	Dominance_D_Earthw	**-0,68961**	0,027353	Pearson	*	
Weeds_m	Taxa_S_Wm	Simpson_1-D_Earthw	**0,68961**	0,027353	Pearson	*	
Weeds_m	Taxa_S_Wm	Lepidoptera	**-0,76714**	0,044131	Pearson	*	
Weeds_m	Taxa_S_Wm	Basal resp.	**0,64086**	0,045871	Pearson	*	
Weeds_m	Taxa_S_Wm	Na+	**-0,76228**	0,04634	Pearson	*	
Weeds_m	Taxa_S_Wm	P (Olsen)	**0,60733**	0,047511	Pearson	*	13

Tab. LXIV: List of significant correlations found between all biotic and functional indicators measured in this work. AMF: Arbuscular Mycorrhizal Fungi; B16S: bacteria analysed by 16S sequencing; B_ARISA: bacteria analysed by A.R.I.S.A. technique; Carab: carabids; Crop NP: crop nutritional properties; dsDNA: double-stranded DNA; Earthw: earthworms; Enzym Act: soil enzymatic activities; F_ARISA: fungi analysed by A.R.I.S.A. technique; FDA: Fluorescein Diacetate Hydrolysis test; F: Fluorescein quantity; Fertim: fertimeter yarn degradation percentage; FITS:

fungi analysed by ITS sequencing; Landscape: landscape structure; Mesof: mesofauna; Paras: parasitoids; Phyt_abund: abundance of different phytophagous groups; Phyt: phytophagous agents; Predat_abund: abundance of different predator groups; Predat: predators; QBS-ar: Soil Biological Quality Index based on arthropods; QBS-e: Soil Biological Quality Index based on earthworms; Resp_rate: soil respiration rate; Soil An: soil chemical-physical analyses; Weeds_f: weeds in the area of crop field; Weeds_m: weeds in the grassy margin. Significance: ***: p value<0.001; **: p value<0.01; *: p value<0.05.