

A range of low molecular weight compounds have recently been identified that stimulate plant growth. They do not fall into the usually recognized classes of plant hormones and are produced by bacteria in the rhizosphere, fungi or even other plants. Their mode of action is complex as they trigger other physiological processes such as induced systemic pathogenic resistance. *Sinorhizobium meliloti* bacteria produce a signal molecule called lumichrome that has been shown to promote plant growth in various plant species. Little is known about how exactly the growth promotion takes place and which genes and proteins play a pivotal role. The mechanism remains to be clarified; therefore our aim is to elucidate the molecular mechanism behind the growth stimulation. Lumichrome applied at nanomolar concentrations elicited growth in *Medicago sativa*, *Lotus japonicus* and *Lycopersicon esculentum*. Growth promotion was observed in the shoots as well as in the roots but displayed the most promising results in the roots. Large scale profiling of gene expression, proteins and metabolites in lumichrome treated and untreated plants has been completed. DNA microarray analysis revealed interesting genes that were differentially expressed in *Lotus japonicus* as well as in *Lycopersicon esculentum* roots. On the protein level, two-dimensional (2D) gel electrophoresis was utilized to analyze the differential protein expression of *Lotus japonicus* and *Lycopersicon esculentum* in lumichrome treated and untreated roots. For *Lotus japonicus*, 10 spots displaying significant changes in protein expression levels were identified. Further analysis is underway to identify key proteins in *Lycopersicon esculentum* roots. In addition, gas chromatography mass spectrometry (GC-MS) analysis showed significant differences in metabolite levels of lumichrome treated and untreated plants. In understanding the molecular mechanism and by identifying a small number of genes involved in mediating these processes, these genes could in future be used to engineer crops for enhanced vigour and productivity.

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Carbon sequestration following a biome switch from mesic savanna to forest

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Bush-encroachment is becoming a world-wide phenomenon in savannas potentially leading to their replacement by forests with cascading ecosystem consequences. One would expect woody invasion to increase carbon sequestration but American studies show decreasing sequestration with increasing rainfall resulting in net carbon losses from invaded grasslands in mesic areas. We compared carbon sequestration in mesic savannas with forests in Hluhluwe Game Reserve, KwaZulu-Natal to determine whether woody invasion also resulted in net carbon losses. We compared soil- and above-ground carbon stocks in

three paired sites of grassland vs. forest and grassland vs. newly-invaded thicket. Total carbon was found to be highest in forests ($485.3 \pm 70.65 \text{ Mg C ha}^{-1}$), second highest in thickets ($397.5 \pm 21.27 \text{ Mg C ha}^{-1}$) and lowest in grasslands ($283.7 \pm 53.36 \text{ Mg C ha}^{-1}$). All woody sites showed higher total carbon levels than their adjacent grassy sites, regardless of whether they were forest or thicket. $\delta^{13}\text{C}$ profiles in the soil indicated that all sites were ancient grasslands, invaded at different times by forest. Though woody invasion leads to increased carbon sequestered in this area, the costs of the biome switch include a loss in biodiversity, and possible reduction in streamflow.

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Botryosphaeriaceae as endophytes and pathogens of trees in South Africa

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Endophytes are microorganisms such as bacteria and fungi that live asymptotically in plants without causing obvious disease symptoms. These endophytes have different beneficial to adverse functions within plants, or have an effect when plant parts senesce or die off. Some endophytes may also represent latent plant pathogens that have an endophytic stage in their life cycle. The fungal family Botryosphaeriaceae represents a large group of fungi with a cosmopolitan host range and that occur globally in many different habitats. Many of the species in this family are endophytes, and represent an important group of latent pathogens, with some species causing serious diseases on native and non-native trees as well as other types of plants and crops. Due to the cryptic nature of these latent pathogens, they thus represent a serious quarantine threat to the health of native plants as well as commercial crops. Recent and ongoing studies on members of the Botryosphaeriaceae in South Africa also show that this family is a good indicator group that represents part of the biodiversity of fungi and the large amount of new species still to be discovered in southern Africa. Due to the wide occurrence and host range of the Botryosphaeriaceae, this group thus represents an excellent model to study mycological processes within plants, such as cross-infections between related and unrelated hosts as well as native and non-native plants, and to learn about the distribution and speciation of fungi in southern Africa.

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