

Soil microorganisms: Allelopathy and a wide mutualistic interaction.

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Abstract

Plants are part of a complex ecosystem in their natural habitat, which includes a wide variety of soil microbes. Some of these microorganisms, such as mycorrhizal fungi and nitrogen-fixing symbiotic bacteria, have long been recognised for their importance in plant performance by increasing mineral nutrition. However, only lately has the complete range of plant-associated microorganisms and their potential to replace synthetic agricultural inputs been discovered. The understanding of the composition and behaviour of rhizospheric microbiomes has advanced significantly over the last few years. Plants shape microbiome structures, most likely through root exudates, and bacteria have evolved numerous adaptations to flourish in the rhizospheric niche, according to research. The mechanisms underlying these interactions, as well as the processes that cause microbiome changes, are, however, largely unexplored. The present information in numerous study domains that can converge to increase our understanding of the molecular mechanisms supporting this phenomenon is summarised in this review, which focuses on the interaction of plants and root related bacteria increasing plant mineral nutrition.

Keywords: Soil, Microorganisms, Ecosystem, Bacteria.

Introduction

One of the factors driving the invasion success of exotic plant species is allelopathy, which has been extensively researched. Many abiotic and biotic factors influence the synthesis, release, accumulation, destiny, and functioning of allelochemicals, making allelopathic interactions between organisms complicated. Allelopathy appears to be a context-dependent feature rather than a species-wide trait, according to a rising number of studies. For example, soil samples taken over two growing seasons from *Centaurea maculosa*-infested areas revealed just a low level of catechin, the primary allelochemical, obtained from one location in one season [1].

The findings are intriguing because allelopathy has long been assumed to improve *maculosa*. Allelopathy may vary spatially and temporally due to variances in soil conditions and allelochemical output across invasive populations. However, the actual mechanisms driving allelopathy's context-dependency remain unknown. *Ageratina adenophora* Spreng is a poisonous invasive perennial weed native to Central America that has spread to Asia, Africa, Oceania, and Hawaii [2]. It was initially discovered in China in the 1940s and has since spread to six provinces in Southwest China. In petri-dish laboratory trials and pot experiments, it has showed considerable allelopathic potential. *Adenophora adenophora* has also been shown to accumulate allelochemicals at phytotoxic levels in soil samples in Lancang County, Yunnan Province, Southwest China [3].

In particular, two major allelochemicals, 9-Oxo-10, 11-dehydroageraphorone (DTD) and 9-hydroxyageraphorone (HHO), have been discovered in the *A. adenophora* leaf leachate and root exudate. Yang discovered that the quantities of DTD and HHO in soils taken from some sites were sufficient to prevent native species seedling growth, but not in soils collected from other sites [4]. *Adenophora* has no allelopathic effects in a common garden trial in Xishuangbanna, Yunnan, Southwest China. These findings indicate that *A. adenophora*'s allelopathic effects are context-dependent. DTD and HHO decomposed faster in live soil than in sterile soil in two recent experiments, implying that soil microbes minimise allelopathic effects [5].

Conclusion

We initially conducted a competition experiment utilising soils collected from six invaded and six non-invaded sites to assess the effects of soil microbes on the allelopathic effects of the invasive species. The invasive species' allelopathic effects were reduced using activated carbon. Using soils taken from sites with varied abundances of *A. adenophora*, we studied the effects of *A. adenophora* abundance on the allelopathic effects of its leaf leachate, the degradation of DTD and HHO, and the allelochemical-degrading soil microorganisms. Finally, we isolated allelochemical-degrading bacteria from invaded and non-invaded soils and investigated their impacts on DTD and HHO degradation, as well as the invasive species' allelopathic effects. We hypothesised that I in soils from invaded sites, the allelopathic effects of *A. adenophora* would be lower, DTD and HHO degradation would be faster, and activity of

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allelochemical-degrading soil microbes would be higher than in soils from non-invaded sites; and (ii) with growing abundance of *A. adenophora*, activity of allelochemical-degrading soil microorganisms would increase, promoting allele.

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