

# Biocontrol of Plant Interactions Using *Streptomyces*

## Plant-Microbe Interactions and Their Effect on Plant Health

The overwhelming majority of eukaryotes, including plants, interact extensively with a various community of microorganisms. In plants, interactions particularly emerge at the interface between the plant roots and therefore the soil environment, whereby bacteria from the soil abundantly colonize the soil layer, referred to as the “Rhizosphere”, that’s immediately surrounding and influenced by the plant root age. Several microbial species also are capable of attaching to the basis surface (a region called “the rhizoplane”) and a little subset of the soil community additionally enter the plant root tissue. The latter group of microorganisms are adapted to survive within the inter or intracellular spaces within the plant roots, which are collectively referred to as the “endophytic compartment”. Advances in next generation sequencing (NGS) techniques have facilitated deeper probing into the microbial ecology of the plant root microbiome. Although abiotic factors like soil characteristics appear to influence the composition of the microbiome, it’s also clear that host genetics play a key role in root microbiome assembly and plants are likely to pick beneficial species from their environment. Factors like differences in root architecture can influence this assembly and selection process, for instance by influencing soil characteristics, also because the organisations and structure of root cells. Additionally, around 20–40 you look after photo-synthetically fixed carbon is exuded from plants into the Rhizosphere; these exudates include a broad range of organic compounds which will be utilized by microorganisms and should help to pick certain species from the soil community.

It has been known for a few times that both soil and plant-associated microbes can contribute to plant health, since the presence of certain microbial species may result during a reduction in disease incidence and severity. Additionally, specific isolates from the plant root microbiome produce a variety of secondary metabolites which will inhibit plant pathogens both in vitro and in vivo. Especially, the potential of a Gram positive genus of Actinobacteria, called *Streptomyces*, has drawn the eye of the many within the scientific and industrial communities. *Streptomyces* are saprotrophic organisms, best known for his or her role as producers of clinically useful antibiotics, of which they’re liable for approximately 55%. This genus is characterised by their polar filamentous growth, their spore-forming capabilities, and particularly, their extensive secondary metabolism. These secondary metabolites are known to possess a various range of activities and are used for a good range of applications, including as anti-bacteria’s, antifungals, anti-cancer and anti-helminthic drugs. Since *Streptomyces* are abundant in soil and are shown to suppress a variety of phyto-pathogenic organisms both in vitro and in vivo, these organisms are gaining interest as potential bio-control agents that would be utilized in place of conventional chemical treatment. During this review, we specifically specialise in reviewing research that investigates the role that *Streptomyces* can play in inhibiting pathogens of cereal crops, particularly fungal pathogenic species. We specialise in this especially, thanks to the worldwide importance of cereal crops, the massive socioeconomic impacts of yield losses caused by fungal disease and therefore the lack of other alternatives for controlling

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many of those pathogens. Several excellent reviews have discussed the overall potential of *Streptomyces* as bio-control agents or their application to at least one specific crop species and that we extend this literature by specifically that specialize in cereal crops.

#### Streptomyces-Plant Interactions

The evolution of the primary true *Streptomyces*'s approximately 450 million years ago is assumed to possess been largely stimulated by the transition of plants ashore, approximately 550 million years ago. Many years of plant-streptomycete interactions may explain why *Streptomyces* are often found to be abundant within the rhizosphere and roots of a spread of various plant species. For instance, *Streptomyces* are shown to be enriched within the roots and rhizosphere of *Arabidopsis thaliana*, also as in important crop species, like potatoes, rice, and wheat and oilseed rap. An extended period of coevolution with plants may additionally have resulted in several aspects of the expansion and metabolism of this genus. for instance, selective pressures to interrupt down material are thought to possess driven the evolution of a saprotrophic and filamentous lifestyle, which might have enabled early streptomycetes to penetrate living and dead material so as to access otherwise unavailable nutrients stored in complex molecules, like cellulose. This might have eventually led to an endophytic lifestyle, and indeed, fluorescent microscopy has shown that streptomycetes can exist endophytically within the roots of several different plant species, including lettuce, wheat and pea, which they'll be ready to penetrate plant roots by entering openings that occur at the bases of root hairs and lateral roots. *Streptomyces* also are capable of manufacturing an array of cellulolytic and hydrolytic enzymes which may allow forced entry into material by breaking down the skin cell walls and middle lamellae between

plant cells. Their ability to supply a various array of antimicrobial secondary metabolites may additionally allow them to compete for niche space and therefore the carbon-rich resources that are exuded by plants.

Given their ability to colonize plant roots and produce potent antimicrobial secondary metabolites and the genus *Streptomyces* are getting an increasingly obvious choice when trying to find novel bio-control agents. This is often particularly the case, as additionally to contributing to plant protection, members of this genus are frequently found to contribute to plant growth promotion (PGP) under both ambient and stressful environmental conditions, like high salinity; these additional benefits could form the idea for highly desirable bio-control agents which will both enhance plant growth and protect against disease.

It is important for us to notice that, although many *Streptomyces* are either beneficial or passive colonizers of the plant microbiome, certain species have evolved a phytopathogenic lifestyle. Perhaps the foremost well-studied example is *Streptomyces scabies*, the causative agent of common potato scab. Several virulence factors are found to be related to this disease-causing lifestyle, including small molecules like coronafacic acid and thaxtomin, the latter of which is found on a pathogenicity island within the genome of plant-pathogenic strains. Only a couple of *Streptomyces* species have these genes, and it's suggested that their acquisition was a singular event and doesn't represent the interactions that are characteristic of plant-*Streptomyces* relationships. Indeed, out of over 500 isolated *Streptomyces* species, only 10 are deemed to be pathogenic. Thus, there's an enormous diversity of strains that would be screened for his or her potential to act as beneficial bio control agents.