

Gene Expression Studies of Plant Microbes

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Editorial Note

We have investigated the impacts of 63 different low-molecular-weight compounds, most of them plant derived, on the in vitro expression of two antifungal biosynthetic genes by the plant-protecting rhizobacterium *Pseudomonas fluorescens* CHA0. The majority of the compounds tested affected the expression of one or both antifungal genes. This suggests that biocontrol activity in plant-beneficial pseudomonads is modulated by plant-bacterium signaling. Beneficial plant-associated bacteria play an important role in promoting growth and preventing disease in plants. The application of Plant Growth-Promoting Rhizobacteria (PGPR) as biofertilizers or biocontrol agents has become an effective alternative to the use of conventional fertilizers and can increase crop productivity at low cost. Plant-microbe interactions depend upon host plant-secreted signals and a reaction hereon by their associated bacteria. However, the molecular mechanisms of how beneficial bacteria respond to their associated plant-derived signals are not fully understood.

Rhizobacteria Factor

Assessing the transcriptomic response of bacteria to root exudates is a powerful approach to determine the bacterial

gene expression and regulation under rhizospheric conditions. Such knowledge is necessary to understand the underlying mechanisms involved in plant-microbe interactions. This paper describes a detailed protocol to study the transcriptomic response of *B. mycooides* EC18, a strain isolated from the potato endosphere, to potato root exudates. With the help of recent high-throughput sequencing technology, this protocol can be performed in several weeks and produce massive datasets. First, we collect the root exudates under sterile conditions, after which they are added to *B. mycooides* cultures. The RNA from these cultures is isolated using a phenol/chloroform method combined with a commercial kit and subjected to quality control by an automated electrophoresis instrument. After sequencing, data analysis is performed with the web-based T-REx pipeline and a group of differentially expressed genes is identified. This method is a useful tool to facilitate new discoveries on the bacterial genes involved in plant-microbe interactions. Plants may exude up to 20% of the carbon fixed during photosynthesis through roots into the rhizosphere, i.e., the narrow zone of soil near the roots. Due to the higher nutrient availability, the rhizosphere is a suitable habitat for diverse microorganisms, including plant-growth promoting bacteria. The root exudates contain a range of inorganic compounds like ions, inorganic acids, oxygen, and water. However, the majority of the root exudates is formed by organic materials, which can be divided into low molecular weight compounds and high molecular weight compounds. The low molecular weight compounds include amino acids, organic acids, sugars, phenolic compounds, fatty acids, and an array of secondary metabolites. The high molecular weight compounds consist of mucilage and proteins.

Rhizosphere microorganisms can use some of these compounds as an energy source for growth and development. The root exudates play an important role in shaping the rhizobacterial community since the plant-produced compounds in the exudates can influence the behavior of rhizosphere-associated bacteria by affecting the expression of specific genes. Understanding the bacterial response to root exudates is a key step in deciphering plant-microbe interaction mechanisms. As the bacterial response to plant-microbe interactions is the product of differential gene expression, it can be studied by transcriptome analysis.