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Commentary

Utilizing Microbial Potential: Enhancing Plant Health, Environmental Restoration and Pathogen Control

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DESCRIPTION

Plants can be colonized by endophytic bacteria, which are able to build symbiotic relationships with them and strengthen plant immune responses. In addition to promoting plant growth, endophytic bacteria have the ability to regulate phytopathogenic fungi. Here, the techniques by which phytopathogenic fungi control plant growth and the ways by which various major species of beneficial endophytic bacteria include *Bacillus, Paenibacillus, and Pseudomonas,* have been shown to enhance plant growth. More analysis is necessary on these endophytic bacteria, as most of the strains analyzed in these genera originated from soils and the rhizosphere. To identify appropriate endophytic bacteria for a range of applications, it is critical to comprehend the basic biocontrol and plant growth-promoting activities. Also, an efficient screening strategy must be developed. To promote sustainable agriculture, endophytic bacteria with beneficial biocontrol and growth-promoting properties for plants must be developed.

Salinity has a variety of complex biological impacts and is an essential environmental component of marine habitats. It is unclear, meanwhile, how salinity fluctuations affect the ecological roles and diversity of High-Nucleic Acid and Low-Nucleic Acid (HNA and LNA) bacteria, metagenomic sequencing analysis and 16s rRNA sequencing to uncover the response of the HNA and LNA communities of bacteria to the drop in salinity from 26°C to 16°C, as well as their ecological roles. The findings showed that salinity variations had a major impact on the distribution of HNA and LNA bacteria in communities.

A strong association was observed between salinity and relative abundance in 14 groups of LNA bacteria. Some bacteria can move from HNA bacteria to LNA bacteria as a result of salinity variations. With decreasing salinity, the complexity in the network between the HNA and LNA bacterial populations progressively decreased in the structure of the network connection. Salinity affected the amount of some genes involved in the cycling of nitrogen and carbon in HNA and LNA bacteria. The findings indicate that salinity has a significant role in controlling the populations and activities of HNA and LNA bacteria, as well as its effects on biodiversity and ecological functions.

Although carbon-fixing bacteria serve as an important functional category in soil carbon fixing processes, it is unknown how they relate to soil multifunctionality in the context of vegetation regeneration in areas that have been eroded. This makes it more difficult for us to determine how much plant restoration actually affects soil ecosystem services. Thus, in a highly degraded area of southern China, we investigated the effects of three distinct vegetation communities (tree-shrub, tree-grass, and tree-shrub-grass) on the community of carbon-fixing bacteria in the soil within the same small watershed. Vegetation restoration locations included higher numbers of carbon-fixing bacterial species, more complex networks of these bacteria, and stronger relationships between them than eroded regions did. The predominant carbon-fixing bacteria in the eroded areas changed from Rhodovastum to Nocardia due to the structure of the vegetation community.

In comparison to the control group, the relative abundance of Rhodovastum dropped by 90.11%, 96.76%, and 95.37% among the tree-shrub, tree-grass, and tree-shrub-grass patterns, respectively. This suggests that patterns of vegetation communities may be able to cause the predominant autotrophic (strict) carbon-fixing bacteria to become facultative autotrophs. The modifications in soil multifunctionality brought about by vegetation restoration are intimately linked to the changes in the properties of the carbon-fixing bacterial community. These findings show that vegetation communities significantly improve the soil's ability to fix carbon.

Incessantly resurfacing or evolving pathogenic microorganisms have posed serious threats to worldwide public health throughout human history. On the other hand, people are always investigating the potential uses for microbes. For relevant studies and applications involving bacteria, such as their inhibition, imaging, and anchoring, a thorough grasp of their surface chemical-biological data is crucial. Using a fresh categorizes the mechanisms of bacteria recognition by different units of recognition, including the following: non-targeted-based non-specific identification (modified nanomaterials, dyes, etc.),

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specific target-based broad specific recognition (natural components, antibiotics, etc.), and screening technology-based high-specific identification (different kinds of antibodies, aptamers, and bacteriophage, etc.).

This classification contributes to improving our comprehension of the bacterial adhesion mechanism and provides new insights in the flow of biochemical data from the surface of harmful bacteria. Furthermore, applications for bacterial imaging, tracking, control, and advantageous use that rely on various recognition systems are discussed. In order to achieve the successful control and even exploitation of pathogenic bacteria, this review seeks to provide fresh perspectives for the application of bacteria detection elements in upcoming diagnostics and vaccines. Ultimately, "turning waste into treasure" is anticipated, necessitating communication and multidisciplinary collaboration among all parties involved. The systematic "bacteria identification-control-utilization" strategy that is the basis of this review will be crucial for preserving the microbial world's natural equilibrium and removing microbial risks.