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SEL DIGEST

Coming of age for the rhizosphere microbiome transplantation

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Abstract Microbiome transplants have the potential to disrupt agriculture and medicine by transferring the microbial genetic pool (and hence capabilities) from one host to another. Yet, for this technology to become reality, we need to understand the drivers shaping the success of microbiome transplant. We highlight here recent findings by Dr. Gaofei Jiang and colleagues. Using disease suppression as a model function, they highlight the microbiome characteristics making a successful transplant possible. We see this study is a seminal work making microbiome transplant an informed process that will replace the current error-prone trial procedures. We anticipate that the insights may catalyse a paradigm shift in microbiome management in agriculture and medicine.

Keywords Microbiome transplant, Coalescence, Ralstonia, Biodiversity, Crop health

1 Background

The plant microbiome is the undisputed guardian of plant health. The billions of bacteria, fungi and other microbes attributed to plant microbiome form together an enormous genetic pool that, when properly addressed, naturally ward off pathogens. The prospects of the microbiome engineering in agriculture are huge as beneficial plant-associated microorganisms can in ideal cases ward off pathogens, preserving yield without pesticides.

The potential role of microbiome as driver of plant health dates back to the late the 19th century and was formalized in the 1970s (Schlatter et al., 2017). Yet, microbiota structure in soil and plant is however difficult to dissect and redesign to improve functionality. Even after decades of research, most attempts made to identify and apply microorganisms as biological control agents have proven unreliable at best (Niu et al., 2020). During the last ten years, a paradigm shift has been consequently taking place, approaching disease suppression as resulting from the concerted interactions of dozens to hundreds of species (Wei et al., 2019). In fact, a substantial fraction of all soil-dwelling bacteria naturally inhibits pathogens (Gu et al., 2020). Instead of invading the microbiome with alien species, microbiome-mediated plant protection might be best harnessed at a community level. But this complexity also brought new challenges, both from a scientific and applied perspective.

Microbiome transplant may be an ideal technique to embrace the complexity of plant-associated microbial communities at the service of a better plant health. Transferring a whole or synthetic minimal microbiome can efficiently restore plant protection (Kwak et al., 2018; Choi et al., 2020) and provide insights into the species sets underlying protective abilities (Duran et al., 2018). However, one key obstacle must be overcome. Microbiome transplants have been up to date a trial-and-error process prone to failure (Choi et al., 2020), likely due to unforeseeable coalescence processes (Rillig et al., 2016) with the existing microbiome or an incompatibility with the host. Resolving the mechanisms underlying compatibility between donor and receiver microbiomes is thus an essential next step.

2 Main section

A recent work by Dr. Jiang and colleagues at Nanjing Agricultural University (Jiang et al., 2022) brings this much needed breakthrough towards a systematic and reliable use of microbiome transplants. By systematically assessing the characteristics of successful and failed rhizosphere microbiome transplants, they identified key microbiome

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characteristics allowing for a successful deployment of plant resistance to bacterial wilt, a major disease affecting more than 200 crops globally (Jiang et al., 2017). Microbiome success was evaluated as its ability to retain its plant-protective ability in the receiver plants. As to be expected, most microbiomes transfer failed. Yet, and this is the brilliance of this work, Dr. Jiang and colleagues were able to discover characteristics that were robustly associated with successful transplantation. Those successful transplants were from the beginning on enriched in highly connected species forming cohesive ecological units, confirming the importance of ecological networks as determinant of microbiome function. Further, successful transplants were enriched in antagonistic species able to inhibit the target pathogen. Their composition was also tilted towards *Proteobacteria* and *Bacteroidetes*, two taxonomic groups well-known for their broad plant protective capacities.

3 Conclusions

We anticipate that this work will pave the way for a novel strategy to enhance microbiomes by informed microbiome transplant. By combining these insights with recent data science advances, it may soon become straight forward to automatically select the donor microbiome characteristics and design adapted biotechnology processes to produce it in massive quantities. This may encompass self-regulating synthetic communities or microbiome cultivation in mass hydroponic systems.

Together, these advances will enable an agriculture that is both highly productive and requires only minimal agrochemical inputs. Given the high similarities in microbiome dynamics across hosts, we further expect that these insights may help design more targeted and successful microbiome transplantation strategies for medical purposes such as Crohn disease management.

Conflict of interest

The authors declare that they have no conflict of interest.

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Prof. Dr. Alexandre Jousset is a microbial ecologist working on the assembly mechanisms of the plant microbiome. He combines in his research community ecology with plant-microbe interactions to design high-performance microbiomes protecting plants against biotic and abiotic stressors. He is founder and managing director of the AgriFood company Blossom Microbial Technologies B.V. and holds a professor position at the Nanjing Agricultural University.

Prof. Dr. Seon-Woo Lee is an applied microbiologist working on novel technologies promoting microbiome function. He is the Principal investigator of Molecular Plant Pathology/Microbiology Lab at Dong-A University, Korea. His group uses metagenomics to study plant-microbe interactions at a microbiome level and is developing a range of microbiome-based technologies including minimal synthetic microbiomes and phage modulation of the native microbiome.

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