Research demonstrates microbiome transmissibility in perennial ryegrass

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Ian Tannenbaum, first author of paper. Credit: Ian Tannenbaum

Scientist Ian Tannenbaum has spent most of his career working in clinical microbiology but was excited to transition to agricultural microbiology when he was offered a chance to conduct the first assessment of the perennial ryegrass microbiome and how it changes during plant maturation and seed production.

"The concepts of the project were very interesting to me and unlike anything I'd previously worked on," said Tannenbaum, who is affiliated

with the Centre for AgriBioscience and La Trobe University in Victoria, Australia. "This was my first series of experiments aimed at understanding the natural bacterial assembly of a plant microbiome."

Tannenbaum's most surprising discovery? Finding a stable bacterial microbiome within surface-sterilized ryegrass seeds that almost disappears when the plant matures but returns in a new generation of seed.

"Our findings suggest that a portion of microbiome recruited by the parent plant was inherited by the following generation of seed, which demonstrates microbiome transmissibility," Tannenbaum explained. "The microbiome of the mature plant can be used as a snapshot of the following seed generations."

Working alongside a team of researchers, Tannenbaum found that the microbiome within perennial ryegrass seeds was predominantly comprised of a class of bacteria known as *Gammaproteobacteria*. In germinated seeds, the bacterial population was influenced by the presence of a resident fungal endophyte, which appeared to impact the abundance of some bacteria strongly enough to result in different seed microbiome between those with the fungal endophyte and those without.

They also compared the impact of soil by studying plants grown in potting mix and a sand/vermiculite mixture. Both soil types were strong determiners of the mature plant microbiomes. Many bacterial species were shared between the two soil types but differed greatly in their relative abundance.

Finally, the team assessed the microbiome of the following generation of seed generated from the plants grown in either mixture. The microbiome profile of the new seed was more reflective of the seed microbiome of the parent. However, additional classes were observed and determined to

have been recruited from the growth environment by the parent plant and transmitted to the seed.

More information: Ian Tannenbaum et al, Profiling the Lolium perenne Microbiome: From Seed to Seed, *Phytobiomes Journal* (2020). DOI: 10.1094/PBIOMES-03-20-0026-R

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