

Perennial ryegrass microbiomes: manipulating microbial communities for enhanced pasture performance

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It is well recognised that the plant microbiome plays a critical role in plant health, productivity, and resilience to environmental stresses. Recent research has suggested the two disciplines of plant breeding and microbiome engineering should be integrated at an early stage of crop development and this will enhance plant performance via the promotion of beneficial plant-microbe interactions. Achieving this goal requires a greater understanding of key factors that shape the plant microbiome. Perennial ryegrass (*Lolium perenne*), the most common pastoral forage species utilised in New Zealand, was used as a model system. The microbiome associated with different plant zones (including the rhizosphere, root and shoot) was assessed from plants collected from multiple field trials across the North and South Islands of New Zealand. Results indicate that plant

zone, geographic location and plant growth stage were the strongest drivers of ryegrass microbiome structure as analysed by amplicon sequencing of 16S and ITS genes for bacteria and fungi, respectively. In contrast, ryegrass cultivar and the presence of agriculturally beneficial strains of *Epichloë* endophyte had minor impacts on the ryegrass microbiome but significantly shaped the ryegrass seed microbiome. Current research is focused on investigating the influence of diverse ryegrass genetics (>400 different families) on the plant microbiome to uncover host genetic contributions to microbial community assembly. This knowledge will provide a critical foundation for the development of novel forage crops with beneficial microbiome traits to enhance plant performance and promote sustainability.