Pan-Genome Analysis of Perennial Ryegrass Endophytes

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Neotyphodium species are fungal endophytes that form symbioses with agronomically important pasture grasses. \textit{N. lolii} is the predominant endophyte of perennial ryegrass (\textit{Lolium perenne} L.), but other non-\textit{N. lolii} taxa, such as LpTG-2, are also detected. Within- and between-taxon diversity provides a source of variation for production of secondary metabolites (in particular lolitrem B, ergot alkaloids and peramine) which are either toxic to grazing animals or reduce feeding by invertebrate herbivores. A selection of 23 perennial ryegrass endophytes was assembled in order to sample diversity across the range of variation for the various taxa, and high-throughput DNA sequencing technology has been performed on each strain. Furthermore, the genome of the commonly identified 'Standard Toxic' (ST) \textit{N. lolii} endophyte has been assembled into a reference genome, in order to facilitate this cross-taxon pan-genome analysis. Results from the analysis include: an enhanced understanding of the genomic variation amongst various perennial ryegrass endophytes; improved insights into mitochondrial and nuclear genomic changes that have occurred during the endophyte evolution; and an increased ability to associate genetic variation with phenotypic differences, such as presence and absence of key genes in alkaloid biosynthesis.

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