

Genetic variation in the perennial ryegrass fungal endophyte *Neotyphodium lolii*

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Introduction The common fungal endophytes (*Neotyphodium* species) of temperate pasture grasses are associated with improved tolerance to water and nutrient stress and resistance to insect pests, but are also the causal agents of animal toxicoses. Considerable variation exists among grass-endophyte associations for these beneficial and detrimental agronomic traits. The extent to which this variation may be attributed to the endophyte genotype, the host genotype or environmental interactions is currently unknown. The development of molecular genetic markers for endophytes based on simple sequence repeat (SSR) loci and the demonstration of the specific detection of endophytes *in planta* with these markers (van Zijll de Jong *et al.*, 2005) allows efficient assessment of endophyte diversity in grass populations.

Materials and methods To investigate the contribution of endophyte genotype to variation in endophyte-related traits in the perennial ryegrass-*N. lolii* association, 18 *in planta*-validated endophyte SSR markers were screened across 37 accessions of wild and cultivated perennial ryegrass from around the world. The incidence of endophyte in these accessions was variable, ranging from 2-100%.

Results Assessment of the genetic diversity of endophytes in 281 endophyte-positive genotypes detected low levels of genetic variation, with a single endophyte predominant in most accessions. The more divergent endophytes detected in some accessions probably belong to other taxonomic groupings such as *N. occultans*. The geographical pattern of diversity in endophytes was non-random, showing similarities with both ancient and more recent routes of dispersion of perennial ryegrass.

Conclusions The low level of genetic variation within *N. lolii* suggests that variation in endophyte-related traits may be more associated with genotypic differences in perennial ryegrass. Further assessment (van Zijll de Jong *et al.*, 2005) of the genetic diversity of endophytes in perennial ryegrass, in plants collected from farms with variable incidence of endophyte-related livestock toxicosis as well as varieties containing endophyte strains with reduced toxicity effects, support the role of both endophyte and host genotype in the expression of endophyte-related traits. This study may be extended by assessment of variation in symbiosis-related genes through the development of functionally-associated single nucleotide polymorphism (SNP) markers.

Reference

Van Zijll de Jong, E., Smith, K.F., Spangenberg, G.C., Forster, J.W. (2005) Molecular genetic marker-based analysis of the forage grass host – *Neotyphodium* endophyte interaction. In: Roberts, C.A., West, C.P., Spiers, D.E. (eds.) *Neotyphodium* in Cool Season Grasses: Current Research and Applications, pp.123-133.

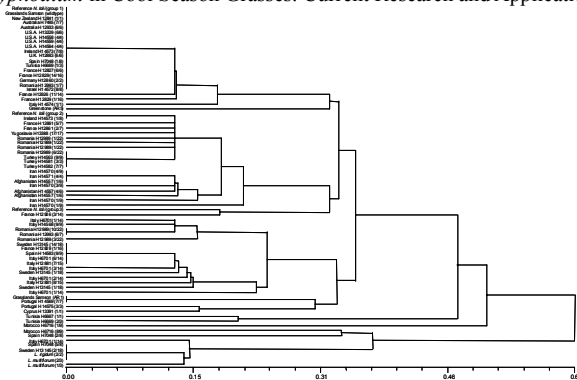


Figure 1 A phenogram of the genetic diversity of endophytes in *Lolium* accessions from around the world based on measurements of average taxonomic distance for 18 SSR loci and cluster analysis with unweighted pair group method of arithmetic averages (UPGMA).