

Population genetics of perennial ryegrass (*Lolium perenne* L.): differentiation of pasture and turf cultivars

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Introduction Cultivar differentiation using molecular markers to assess genetic variation may be of value in obtaining or protecting plant breeders rights. A knowledge of genetic variation and how it is structured within perennial ryegrass (*Lolium perenne* L.) populations will also help us understand the consequences to fitness and adaptation when implementing molecular breeding strategies. In a study of the population genetic structure of a number of perennial ryegrass varieties we examined the cultivar differentiation potential of marker technology.

Materials and methods We used 26 genomic DNA-derived simple sequence repeat (SSR) marker loci. Based on genetic mapping in the p150/112 reference population, these loci are distributed across each of the 7 linkage groups (chromosomes) of the perennial ryegrass genome. Two groups of populations were compared to assess the capacity to distinguish them using the SSR marker loci: pasture varieties derived from the Kangaroo Valley ecotype from New South Wales, Australia, and turf varieties from a range of sources.

Results An analysis of molecular variance (AMOVA) showed that 90% of the variation is located within the cultivars, 8% among cultivars within the pasture and turf groups and 2% between the pasture and turf groups. Individuals in this analysis could not reliably be allocated to their source cultivar or group (pasture or turf) on the basis of their 26 loci SSR genotype (Figure 1). Due to the obligate outbreeding nature of perennial ryegrass, relatively high levels of diversity are maintained within cultivars that have undergone selection in their development.

Definition and identification of cultivars based on molecular markers may depend on careful selection of markers, informed by the population structure and breeding history of the cultivars to be distinguished. This data has important implications for the design and selection of metapopulations for association genetics analyses in outbreeding grass species.

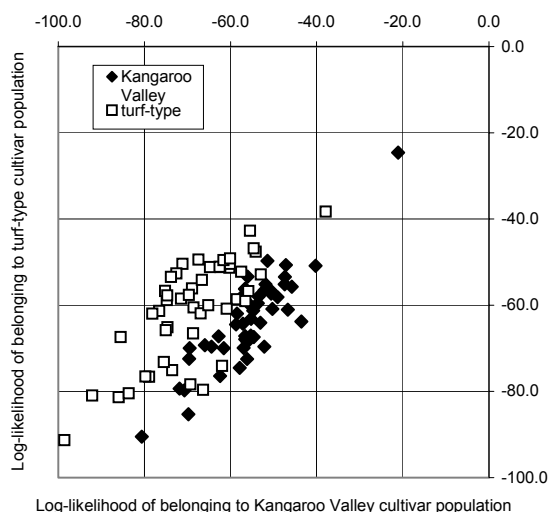


Figure 1 Log-log plot of the likelihood of a perennial ryegrass individual belonging to the population defined by the Kangaroo Valley-derived cultivars or the population defined by the turf-type cultivars. The probability that an individual is derived from the defined populations is calculated from the observed allele frequencies in the population excluding that individual if necessary, and assuming Hardy-Weinberg equilibrium and panmixia.