

Assessment of genetic diversity in *Lolium multiflorum* detected by microsatellite markers

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Annual ryegrass (*Lolium multiflorum* Lam.) is a cool-season annual grass native to southern Europe. It is an important short-duration grass with high palatability and digestibility. The capacity to tolerate trampling make this species highly valued for forage/livestock systems. In addition, the species has a good capacity to resprout. Embrapa currently conducts a breeding program for Annual ryegrass and the genetic diversity knowledge is useful to characterize individuals/accessions/cultivars allowing the identification of possible duplications in the germplasm collection and also to select parental genotypes in breeding programs. Molecular markers are largely used to access the genetic variability in the DNA level. Microsatellites (SSRs) are PCR based markers, consisting in tandemly repeated nucleotide sequences that require specific primers to anneal at the flanking regions. Therefore, SSRs can be used to obtain markers in genetic related species. The objective of this work was to estimate the genetic variability among populations of ryegrass belonging to Embrapa Dairy Cattle breeding program. The DNA was extracted from 628 individuals, belonging to 32 ryegrass populations and the microsatellite markers were obtained by cross-amplification of close related species. A dendrogram was generated by UPGMA algorithm, using the NTSYS software, by Dice similarity coefficient. Twenty five primer pairs (71.5%) showed cross-species amplification in *L. multiflorum* and 15 were chosen based on the polymorphisms detected. Once no genomic information is available for *L. multiflorum*, the use of markers previously described for closely related species was an efficient alternative for microsatellite markers identification. The similarity coefficient values ranged from 0.51 to 0.94. High genetic divergence among the populations was observed, indicating a high degree of diversity. The result is expected since *L. multiflorum* is an allogamous species and has a wide geographical distribution. The data will be useful helping breeders to select parents for crosses and as well as to evaluate the genetic diversity between populations during breeding programs.

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