Resumos do 57º Congresso Brasileiro de Genética • 30 de agosto a 2 de setembro de 2011
Centro de Convenções do Hotel Monte Real Resort • Águas de Lindóia • SP • Brasil
www.sbg.org.br - ISBN 978-85-89109-06-2

Genetic variability among genotypes of *Pennisetum purpureum* Schum. using microsatellite markers

Palla, PC1; Cunha ACLM1; Reis, DRL1; Machado, MA1; Lédo, FJS1; Azevedo, ALS1
1 Embrapa Gado de Leite, CNPGL, Juiz de Fora, MG
azevedo@cnpgl.embrapa.br

Key words: Forage, Genetic diversity, Pennisetum purpureum, Molecular markers

In Brazil, dairy farming is practiced by more than one million farmers who have grazing as the main or only source of feed for livestock. The low yield and poor quality of pastures have been related as one of the major causes of low productivity of milk, so one alternative to improve the dairy herd is the use of more capable and with a better quality forage. Among the grasses with that potential, we detach the elephant grass (Pennisetum purpureum) for being a tropical grass grown all over Brazil and highly valued for its quality, high biomass yield, pest resistance, palatability and perennial nature. Embrapa Dairy Cattle has an Active Germplasm Bank of elephant grass (BAGCE) that develops for more than a decade, a program of breeding in this specie. The study of genetic diversity in BAGCE is essential for the breeding program because it can help in the selection of contrasting individuals in order to obtain targeted intersections. The most common used marker in studies of molecular diversity is the microsatellite marker, which is widely spread in the genome and its principal property is the high polymorphism. Aiming to evaluate the genetic diversity and possible misidentification of BAGCE, we used 18 microsatellite markers on 107 genotypes from the bank. Four samples of pearl millet (Pennisetum glaucum) were used as outgroups. The DNA from each accession was extracted from 300mg of young leaves and the extraction product was quantified and qualified by nanospectrophotometry. The samples were amplified by PCR and its product subjected to capillary electrophoresis on MegaBACE 1000 (GE Healthcare).The Presence / Absence of fragments was scored for each individual. Dice's similarity was calculated for each pairwise combination using NTSYS Program. A total of 180 alleles were identified, yielding an average of 10 alleles per marker. The number of alleles ranged from four (M-44, F-48 and M-53) to 32 (M-39) and the genetic similarity between genotypes was 0.65, i.e., we observed a high genetic variability in the BAGCE. Moreover, identical accessions were identified where the similarity coefficient was equal to one: 20, 21 and 73, 27, 66 and 72, 84 and 93, 08 and 106. This result suggests the existence of misidentification of some accesses, i.e. identical accesses have different names. These errors probably occurred during the exchange of materials between different germplasm banks, which have separate IDs for the same access. The results from the study of genetic diversity will be used in the selection of contrasting accessions for breeding programs and also assists in correctly identifying the accesses and possible elimination of duplicates.

Acknowledgements
The authors want to thank CNPq, FAPEMIG and UNIPASTO for financial support.