

Molecular diversity of forage peanut using microsatellite markers

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Forage species of the genus *Arachis* are known as forage peanut, and they are widely used in mixed pastures. These legumes increase the profitability of production systems and even provide environmental benefits. There are only five cultivars currently available to producers. Microsatellite markers are abundant in eukaryote genomes, are characterized by short sequences repeated in tandem, multi-allelic and codominant. The characterization and evaluation of germplasm banks contribute to greater genetic knowledge, enabling the detection of possible genotypes to be used in breeding programs, identification of duplicates and maintenance of genetic variability. The objective of this study was to analyze the genetic diversity and molecular characterization of the germplasm bank of forage peanut using microsatellite markers. We analyzed 83 accessions and two cultivars of the genus *Arachis* (*A. pintoi*, *A. repens* and *A. glabrata*), located at Embrapa Acre germplasm bank. DNA extractions were performed at the Laboratory of Morphogenesis and Molecular Biology of Embrapa Acre. Twenty two microsatellite loci were tested. Amplification conditions previously described in the literature for each locus failed. Thus, new annealing temperatures and enzyme concentration were optimized. Ten loci were characterized and checked on agarose (3%). The amplification products were genotyped in denaturing polyacrylamide gel (5%) and silver nitrate stained. Estimates of expected (H_E) and observed (H_O) heterozygosity were analyzed in the software TFPGA. From the six selected loci, one was used for germplasm genotyping. The locus (Ah 11) was developed from *A. hypogea* sequences. The transferability was positive to *A. pintoi* e *A. glabrata*. Eighteen alleles were identified. The results show high levels of diversity, with $H_E=0.892$. The low level of observed heterozygosity ($H_O=0.304$) is related to the autogamy reproductive biology. It was also possible to characterize unique profiles for eight accessions and one cultivar (Amarillo), among the 85 genotypes analyzed. It demonstrated the potential of molecular studies to protect and identify cultivars, when phenotypic traits weren't available. The data obtained will be of great importance to assist breeding programs of forage peanut. Financial Support: Embrapa, FDCT Funtac, Capes and Unipasto