CHARACTERIZATION AND ANALYSIS OF MICROSATELLITE MARKERS IN PEANUT (*Arachis hypogaea* L.). Moretzsohn MC[1], Hopkins MS[2], Mitchell SE[3], Ferreira ME[4], Valls JFM[1], Kresovich S[3]. [1]Embrapa Recursos Genéticos e Biotecnologia, C.P. 02372, Brasília, DF 70.770-900; [2]USDA-ARS, Plant Genetic Resources Conservation Unit, 1109 Experiment Street, Griffin, GA 30223; 3Institute for Genomic Diversity, Cornell Univ. Ithaca, NY 14853. 4Universidade Católica de Brasília, SGAN 916, 70.790-160, Brasília-DF. marciocm@cenargen.embrapa.br

Microsatellite or SSR (Simple Sequence Repeat) markers are increasingly being used in plants for many genetic applications, including the assessment of genetic variability in germplasm collections and phylogenetic studies. Microsatellite markers have proven to be an ideal tool for such studies due to their high information content, as they are multiallelic and codominant. The objectives of the present work were to: (1)characterize microsatellite markers in cultivated peanut, (2)quantify genetic diversity among peanut accessions of the Brazilian germplasm collection, and (3)evaluate the transferability of SSR markers. Eight SSR primers were used for genetic variation analysis of 61 *A. hypogaea* accessions, representing both *A. hypogaea* spp. hypogaea and ssp. fastigiata, and their 6 varieties. Considerable variation was found at the 8 microsatellite loci analyzed. Between 3 to 18 alleles were found at each polymorphic locus, with an average of 8.0 alleles per locus. Gene diversity (h) values ranged from 0.463 to 0.921, with an average value of 0.683. Only six pairs of accessions could not be differentiated by using these primers. One SSR locus (A1-041) had alleles specific to the A and B genomes of diploid wild species. Similarity groups for cultivated peanut accessions and 33 samples representing 24 wild species of the section Arachis were established. Two main clusters were evident for *A. hypogaea* accessions. One group contained all fastigiata/fastigiata accessions, one hypogaea/hypogaea accession, and the only hypogaea/hirsuta accession included in the analysis. All 38 accessions of this group were heterozygous for alleles 292 and 280 of A1-041 locus ("AABB-genome"). The second group contained all the hypogaea/hypogaea accessions, the two fastigiata/aequatoriana accessions, and the only fastigiata/vulgaris accession. These 23 accessions were homozygous for the 292 allele ("AAAA-genome"). These data suggest that cultivated peanut had not a single origin and that *A. ipaënsis* and *A. duranensis* seem to be involved in its origin. Thirteen primers were also tested on 44 wild species of Arachis, representing the 9 sections of the genus. The transferability was up to 76% for section Arachis species, but only 38% for species from other Arachis sections. These primers will be very useful for several genetic studies with wild species of Arachis, such as comparative genome mapping, population genetic structure and phylogenetic relationships among species. The present study also provides important information for germplasm conservation and for the *A. hypogaea* breeding programs. Órgão Financiador : Embrapa Recursos Genéticos e Biotecnologia