

SP 19758L  
Id 31931

# Comparative mapping of the AA genome of *Arachis* with the model legumes *Lotus japonicus* and *Medicago truncatula*

Lustosa, FLF<sup>1</sup>; Gouvea, EG<sup>1</sup>; Santos, SP<sup>2</sup>; Marques, T<sup>2</sup>; Alves-Freitas, DMT<sup>1</sup>; Bertoli, DJ<sup>3</sup>; Moretzsohn, MC<sup>1\*</sup>

<sup>1</sup>Embrapa Recursos Genéticos e Biotecnologia, C.P. 02372, CEP 70.770-900, Brasília, DF; <sup>2</sup>Universidade Católica de Brasília, Campus I, QS 07, Lote 1, Águas Claras, CEP 71966-700, Brasília, DF; <sup>3</sup>Universidade de Brasília, Departamento de Genética, Campus Darcy Ribeiro, Brasília, DF.

\*marciocm@cenargen.embrapa.br

**Keywords:** peanut, linkage mapping, microsatellites, anchor markers, SNPs.

The genus *Arachis* is native to South America and contains 80 described species. Most of the section *Arachis* species, to which cultivated peanut (*Arachis hypogaea* L.) belongs, have an AA genome type, some species have a BB genome and one species (*A. glandulifera* Stalker) has a DD genome. Peanut is an allotetraploid (AABB), originated from a cross between two diploid species, with AA and BB genomes, followed by a spontaneous duplication of chromosomes. It is susceptible to several biotic and abiotic stresses, to which many of the wild species are resistant. Linkage maps and the mapping of genes of interest can accelerate the process of plant breeding. The objective of the present study was the construction of a genetic linkage map for the AA genome of *Arachis*, using anchor markers, microsatellites and SNPs and its comparison to the genomes of the model legumes *Lotus japonicus* and *Medicago truncatula*. The map was constructed using an F<sub>5</sub> population with 93 individuals, resulting from a cross between two diploid species with AA genome (*A. duranensis* and *A. stenosperma*). This population was obtained by single-seed descent through successive generations of inbreeding. Using a minimum LOD score of 4 and a maximum recombination fraction of 0,35, 76 anchor markers, 62 microsatellites and 18 SNPs identified in RGAs (resistance gene analogues) and other genes of interest were mapped into 10 linkage groups. This number was expected since *Arachis duranensis* and *A. stenosperma* are diploid species with 2n=20 chromosomes. About 54% of the markers showed distortion of the expected 1:1 proportion, mapping in seven of the 10 linkage groups. Comparative mapping showed that several groups had common markers and in the same order in the genomes of *Arachis*, *Lotus* and *Medicago*. Therefore, the utility of this map will be greatly enhanced by using the information of the near-complete genome sequences of *Lotus* and *Medicago*. Additional markers are being added to this map, aiming at a higher genome coverage and to obtain a reference map for *Arachis*. Resistance genes for biotic and abiotic stresses are currently being mapped in this population, as well as BB-genome and tetraploid populations, to implement marker-assisted selection in peanut breeding programs.

Financial support: Embrapa Recursos Genéticos e Biotecnologia, Generation Challenge Program e The European Union Grain Legume Integrated Project (GLIP e TLI).