THE AFRICAN ASSOCIATION OF INSECT SCIENTISTS
P. O. Box 59862, 00200 City Square
NAIROBI, KENYA

18ème Conférence de l'Association Africaine des Entomologistes
18th Conference of the African Association of Insect Scientists

Salle de Conférence du Ministère de l'Agriculture Ouaga 2000/ Conference room of the Ministry of Agriculture Ouaga 2000
OUAGADOUGOU, BURKINA FASO

16 - 20 Novembre / 16 – 20 November 2009

" Gestion des insectes ravageurs des cultures et vecteurs de maladies pour un environnement viable et une sécurité alimentaire en Afrique: Développements courants"

"Insect pest and vector management for sustainable environment and food security in Africa: Current developments"

Programme

S2-20

GENETIC MAPPING AND SYNTENY ANALYSIS ALLOWED THE IDENTIFICATION OF GENOME REARRANGEMENTS IN THE ALLOTETRAPLOID ARACHIS HYPOGAEA.

Daniel Foncéka (1), Hodo-Abalo Tossim (2), Ronan Rivallan (1), Brigitte Courtois (1), Jean-François Rami (1)

(1) Cirad: Centre de coopération internationale en recherche agronomique pour le développement. UMR Développement et Amélioration des plantes, TA A96/3, Avenue Agropolis, Montpellier, France
(2) ISRA-CERAAS: Institut Sénégalais de Recherches Agricoles, Centre d?Etude Régional pour l'Amélioration de l'Adaptation à la Sécheresse, Route de Khombole, BP 3320, Thiès, Sénégal

Cultivated peanut (Arachis hypogaea L.) is widely used as a food and cash crop around the world. It is considered to be an allotetraploid AABB (2n = 4x = 40) originated from a recent and single hybridization event between two wild diploids. Among the sixty wild species described, A. duranensis (AA) and A. ipaensis (BB) appeared to be the best candidates for the A and B genome donors, respectively. The combining effects of polyploidisation and domestication have greatly narrowed the genetic diversity and hampered the application of molecular approaches for the genetic analysis and the improvement of the cultivated peanut. Recently, the development of synthetic amphidiploids using wild diploid species allowed overcoming the reproductive barrier between wild diploids and the cultivated tetraploid species. This material is an important resource for genetic mapping, synteny analysis between the A and B genomes and molecular breeding.

The objectives of this study were to construct a wild x cultivated tetraploid genetic map using the co-dominant SSR markers, to assess the type of inheritance and the synteny between the A and B genomes.

A synthetic amphidiploid, obtained from the cross between the most probable wild progenitors of the cultivated peanut (A. duranensis, A ipaensis), was crossed to the Fleur11 variety. A population of 88 BC1F1 individuals was produced and genotyped with 277 polymorphic SSR markers.

We mapped 299 loci in 21 linkage groups (LGs), spanning a total map distance of 1843.7 cM. We determined the sub-genomic origin of the SSR alleles by comparison with the alleles of the wild diploid parents of the amphidiploid. This enabled us to confirm the disomic inheritance of all loci and to distinguish the A from the B genome linkage groups (LG). We have not observed LGs with mosaic A/B allele composition. This indicates that the chromosome pairing happened between "homologous" genomes and confirms the high affinity between the A/B genomes of the cultivated species and the A genome of A. duranensis and the B genome of A. ipaensis, respectively. We also identified the homeologous LGs with 53 SSR markers that mapped on both the A and B genomes. We observed an overall good collinearity between each pair of homeologous LGs. However, three inversions of chromosome segment were pointed out between homeologous LGs a01/b01, a03/b03 and a09/b09, as well as a major translocation involving the LGs b07 and b08. These rearrangement events are discussed regarding the divergence of the A and B genomes.

The result of this study contributes to the comprehension of the structure of the A and B genomes and the broadening of the gene pool of the cultivated peanut.