

3- Genomic resources, interspecific introgression and trait dissection in Groundnut

Daniel FONCEKA, Jean-Christophe GLASZMANN, Jean-François RAMI

from a collaboration between Cirad, Embrapa, ISRA, UCB and UNB

Cirad, UMR AGAP, F-34398 Cedex 5, Montpellier, France

Among the numerous interactions and collaborations between researchers from Brazil and from France, facilitated by the Labex under the CIBA consortium umbrella, the one on groundnut improvement has emblematic features.

This is a programme aimed at developing genome analysis and genetic improvement in a species of South American origin that has become very important for many economies and populations in Asia and Africa. It emerged from a single event of allotetraploidization that gave rise to a cultivated species with a limited whole range of variation. The research conducted encompassed two components: one consisted in developing genomic resources as a foundation for genome analysis; the other consisted in a base-broadening scheme development starting from a cross between a synthetic amphidiploid made at Embrapa and an improved groundnut variety cultivated in Senegal.

The first component involved a stay of scientists from Embrapa at Cirad in Montpellier for the production of large genomic segments in Bacterial Artificial Chromosomes (BAC); BAC libraries were produced from the ancestral species, which became a useful resource for a broader community within the GCP. It is still being used for basic genomic studies.

The second component, which will be described in more details, involved a PhD/postdoc work at Cirad and breeding activities conducted at ISRA/CERAAS in Sénégal. The hybrid between the synthetic amphidiploid and the cultivar was used to initiate a large marker assisted backcross scheme and develop a collection of chromosome segment substitution lines (CSSLs) that would globally incorporate the whole genome of the wild ancestors (the “donor”) as overlapping segments introgressed in the “recipient” cultivar. As such, they enable characterization of the specific phenotypic effect of allelic replacement on the substituted segment, considerably limiting the confusing effects of epistasis with the rest of the genome. Reciprocally, they enable characterization of the pleiotropic effect of donor genes (or stretches of genes). They enable the breeder to assess the value *per se* and to test various combinations of donor genome segments in the recipient genome. This has been very successful and is currently producing novel materials with high genetic resolution capacity and high breeding value.

These studies have received financial support from the Generation Challenge Programme (GCP).

References

- Guimarães PM, Garsmeur O, Proite K, Leal-Bertioli SCM, Seijo G, Chaine C, Bertioli DJ, D'Hont A. 2008. *BMC Plant biology*, 8 (14): 8 p.
- Foncéka D, Hodo-Abalo T, Rivallan R, Faye I, Ndoeye Sall M, Ndoeye O, Favero AP, Bertioli DJ, Glaszmann JC, Courtois B, Rami JF, 2009. *BMC Plant Biology*, 9:103.
- Fonckeka D, Tossim HA, Rivallan R, Faye I, Ndoeye Sall M, Ndoeye O, Fávéro AP, Bertioli DJ, Glaszmann JC, Courtois B, JF Rami. 2012. *BMC Plant Biology*: 12:26.
- Nielen S, Vidigal BS, Leal-Bertioli SCM, Ratnaparkhe MB, Paterson AH, Garsmeur O, D'Hont A, Guimarães PM, Bertioli DJ, 2012. *Molecular genetics and genomics*, 287 (1): 21-38.