Development of CSSLs from a cross between cultivated peanut and a wild synthetic amphidiploid

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Cultivated peanut (*Arachis hypogaea*) is considered to be a recent allotetraploid (2n = 4x = 40) derived from the hybridization of two wild diploids. The genetic basis of the cultivated peanut is very narrow as a result of the genetic bottleneck associated with the recent polyploidization event. In order to enlarge the genetic basis of the cultivated peanut, a synthetic amphidiploid obtained from a cross between two diploid wild species *A. ipaensis* (B genome) and *A. duranensis* (A genome) was crossed to Fleur 11, a local variety cultivated in Senegal. We report here our progress toward the development of a population of Chromosome Segment Substitution Lines (CSSLs).

1. Breeding scheme for the development of the CSSLs

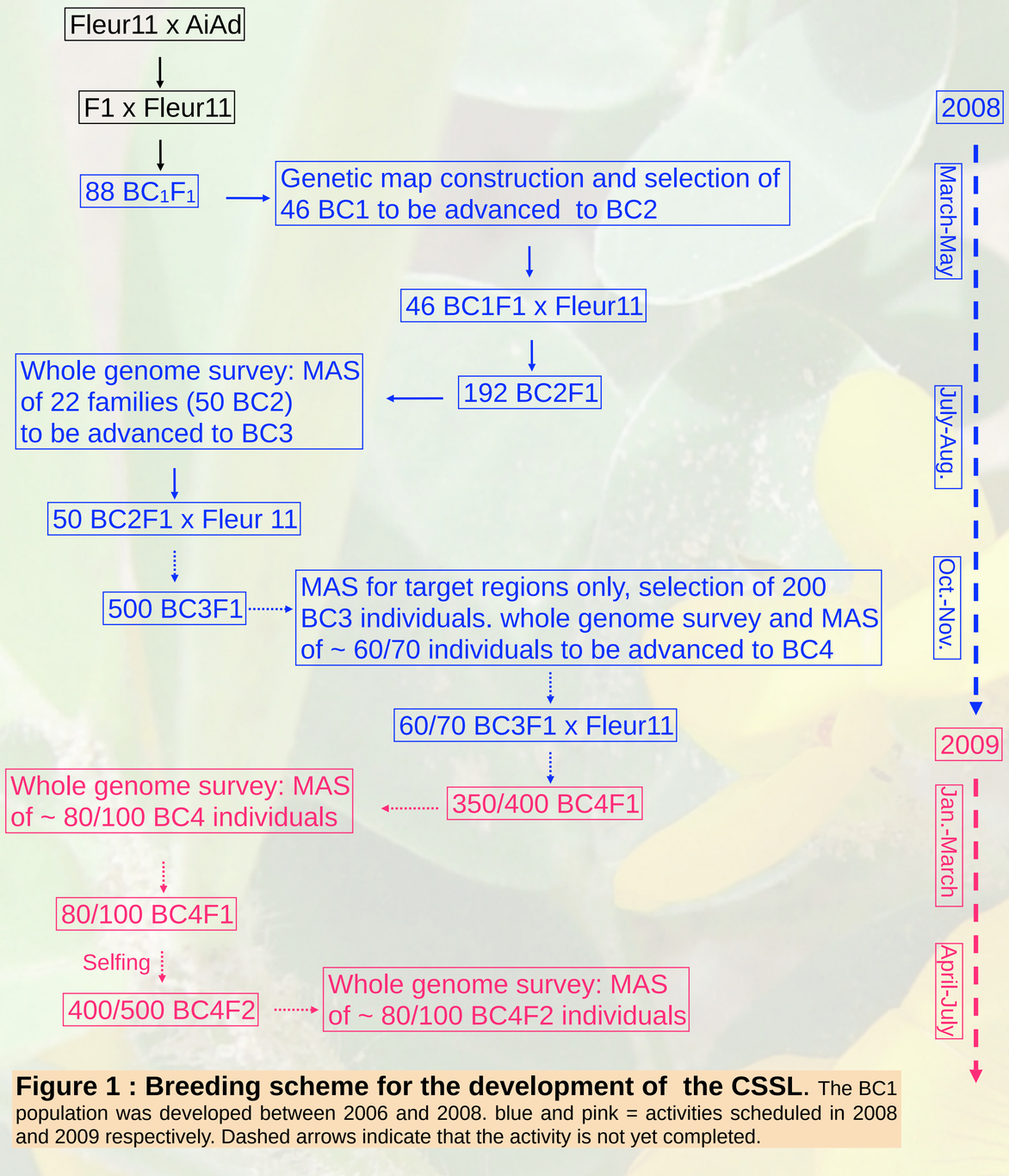

Figure 1 : Breeding scheme for the development of the CSSL. The BC1 population was developed between 2006 and 2008. blue and pink = activities scheduled in 2008 and 2009 respectively. Dashed arrows indicate that the activity is not yet completed.

2. Genetic map construction

A total of 406 SSR markers was screened for polymorphism against the amphidiploid (AiAd) and the cultivated Fleur 11 variety. Two hundred and eight (51.2%) markers were polymorphic and used to genotype the population of 88 BC1 individuals. Among the 208 polymorphic markers, 199 that showed a clear electrophoretic profile amplified 245 loci. Finally, 231 loci were mapped on 21 linkage groups with a total distance of 1515.5 cM (Kosambi) and an average distance between markers of 6.5 cM (Figure 2).

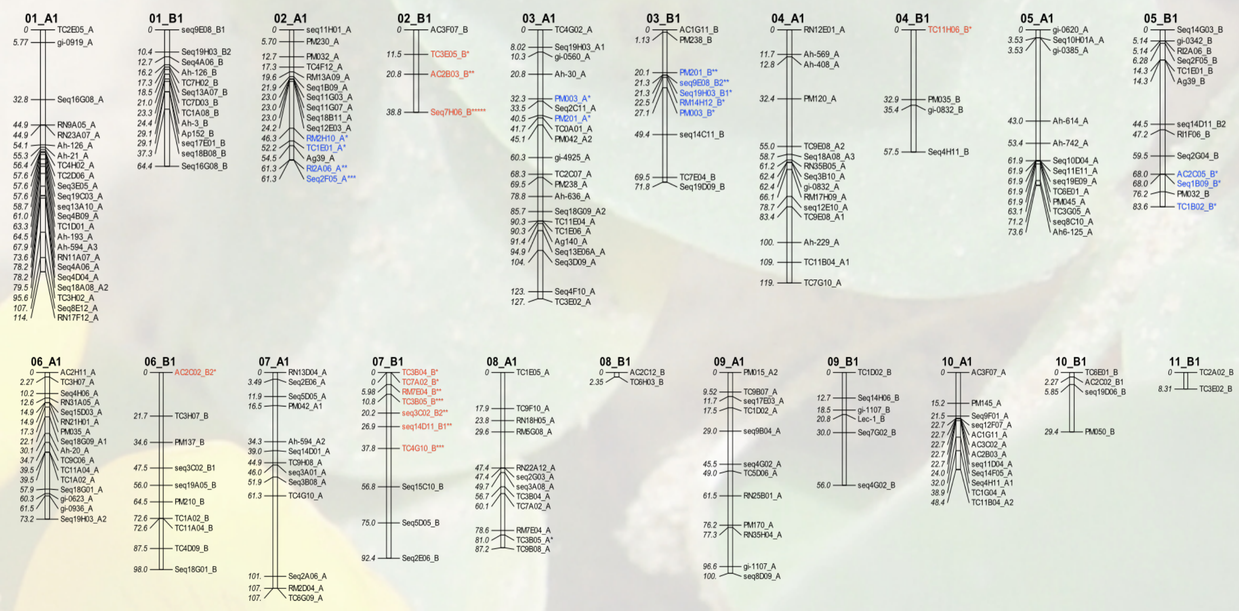

Figure 2 : Peanut genetic linkage map based on SSR markers. The map was constructed using the Mapdisto 1.7.0 software. A minimum LOD score of 4 and a maximum recombination fraction of 0.3 was used to build the linkage groups. Numbers on the left are Kosambi map distance. blue = markers skewed toward the cultivated parent, red = markers skewed toward the wild parent.

The level of polymorphism was different between the A and B genomes. As a result, among the 245 loci, only 81 (33,3%) were polymorphic for the B genome. Distortions of segregation have been observed for 28 markers (12%). Apart from 2 markers, all the distorted markers were concentrated on six different linkage groups (2A, 2B, 3A, 3B, 5B and 7B). For the A genome, the groups of distorted markers were skewed toward the cultivated parent. For the B genome, the distorted markers were skewed either toward the wild or the cultivated parent.

3. Colinearity between maps and synteny between genomes

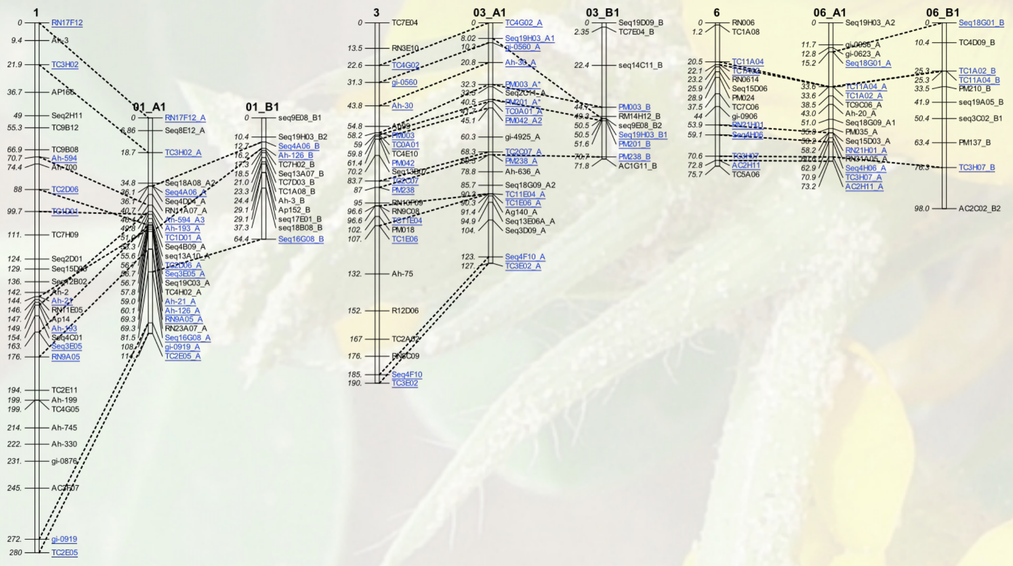

Figure 3 : Colinearity and synteny between linkage groups 1, 3 and 6. Common markers between the Moretzsohn LG 1, 3, and 6, and the LG 1, 3, and 6 of the A genome on the one hand and between the LG 1, 3 and 6 of the A genome and the homeologous LG 1, 3 and 6 of the B genome on the other hand are shown in blue in the map and are connected with the dashed lines.

An overall good colinearity was observed between the linkage group of our map and those from the map published by Moretzsohn et al. (2005) involving two wild diploids with A genome (*A. duranensis* x *A. sternosperma*). An example is shown in Figure 3. In addition, synteny has been observed between the A and B genomes. The A and B genomes of the present map shared 30 common markers allowing to distinguish 7 pairs of homeologous linkage groups. An example is shown in Figure 3.

4. Graphical genotypes of the BC1 and BC2 selected lines

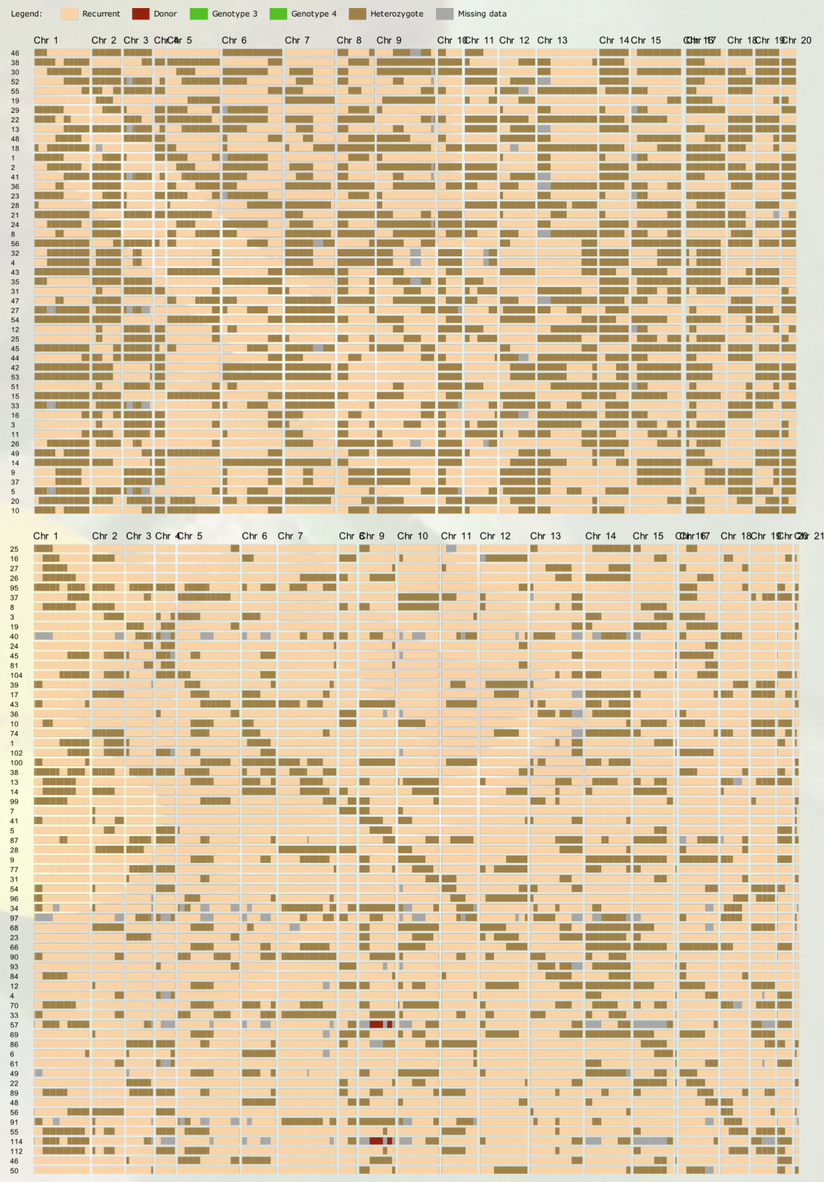

Figure 4 : Graphical genotypes of the BC1 and BC2 selected lines. The graphical genotypes of the BC1 and BC2 selected lines have been drawn using the CSSL-Finder 0.8b4 (qscsb) software. For the BC1 selected lines (up) the percentage of donor genome ranged from 32% to 62% (mean 48%). The overall lines offer a wide genome coverage with a minimum segment size of 2.3 cM and a maximum of 89.4 cM (mean 34.8 cM) . For the BC2 lines (down), the percentage of donor genome ranged from 6% to 38% (mean 21%). A complete genome coverage was obtained with segments size ranging from2.3 cM to 46.5 cM (mean 24.5 cM).

Conclusion

It is expected that a collection of about 100 Chromosome Segments Substitution Lines, targeting an average introgression size of 20 cM, will be available in 2009. Once fixed and multiplied, this material can be characterised in different environments for different traits of interest involved in biotic or abiotic stress response. Moreover, these lines can be used as a starting point toward gene cloning through derivation of near isogenic lines in QTL regions.

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