SNP discovery in pea: a powerful tool for academic research and breeding

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HAL Id: hal-01208702

https://hal.archives-ouvertes.fr/hal-01208702

Submitted on 2 Jun 2020

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Pea has a 4.3 Gb complex genome for which only limited genomic and sequencing resources are available to date. In order to answer to an increasing demand from French breeders for a breakthrough in Marker Assisted Selection, we carried out a massive development of markers in pea.

We sequenced eight cDNA normalized libraries from genotypes representative of modern pea breeding material, assembled a large set of 10,000 cDNA contigs, and identified over 35,000 reliable SNP markers. A SNP subset was genotyped with the Golden Gate assay to generate a high density reference composite genetic map covering 1255 cM and comprising 2070 markers including 1340 newly developed SNPs, anchored to the *M. truncatula* physical map. Developed SNPs furthermore showed efficiency in structuring diversity in a collection of pea cultivars, even using a proposed reduced subset of 297 most informative SNPs (Duarte *et al.*, 2014).

 A complementary approach of SNP ?genotyping by sequencing? ran on genomic DNA libraries from a 48 RILs mapping population. It has developed to date more than 100,000 SNPs, among which approximately 60,000 will undergo mapping (unpublished).

This work gives a comprehensive knowledge for the selection of choice subsets of SNP markers useful for polymorphism, mapping and hierarchical information purposes. These new resources publicly delivered by the PEAPOL project will thus help as tools in cumulating alleles at QTLs for traits of interest, directing the creation of new pea ideotypes adapted to various climates and cropping systems, with stabilized and high yields.

Duarte *et al.* (2014) *BMC Genomics* **15**:126