

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

Gilles Boutet, J. Duarte, Susete Alves Carvalho, Clément Lavaud, Raluca Uricaru, Pierre Peterlongo, Marie-Laure Nayel, Alain Baranger, Nathalie Riviere

► **To cite this version:**

Gilles Boutet, J. Duarte, Susete Alves Carvalho, Clément Lavaud, Raluca Uricaru, et al.. SNP discovery in pea: a powerful tool for academic research and breeding. 6. International Food Legumes Research Conference (IFLRC VI), Jul 2014, Saskatook, Canada. 2014. hal-01208702

**HAL Id: hal-01208702**

**<https://hal.archives-ouvertes.fr/hal-01208702>**

Submitted on 2 Jun 2020

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

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

Boutet, G.<sup>1\*</sup>, Duarte, J.<sup>2</sup>, Alves Carvalho, S.<sup>1</sup>, Lavaud, C.<sup>1</sup>, Uricaru, R.<sup>1,3</sup>, Peterlongo, P.<sup>3</sup>, Pilet-Nayel, M-L.<sup>1</sup>, Baranger, A.<sup>1</sup>, and Rivière, N.<sup>2</sup>. <sup>1</sup>UMR1349 IGEPP INRA AGROcampus-Ouest Université Rennes1, 35653 LE RHEU France; <sup>2</sup>BIOGEMMA, Upstream Genomics Team, 63720 CHAPPES France; <sup>3</sup>INRIA Rennes - Bretagne Atlantique/IRISA, EPI GenScale, Rennes, France. \*(gboutet@rennes.inra.fr)

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