

France: Grain legume collections

The center of grain legume genetic resources at INRA-Dijon

Gérard Duc, Jean-Bernard Magnin-Robert, Grégoire Aubert, Marianne Martinello, Céline Rond, Christine Le Signor, Judith Burstin
INRA-UMR LEG, BP 86510, 21065 Dijon cedex, France
Contact : duc@epoisses.inra.fr

The center of INRA genetic resources is located at INRA-Dijon since year 2004.

The INRA collection of *Pisum sativum* consists of two type of material: (i) spontaneous variability with ca 2800 accessions, mostly composed of old european cultivated forms (land races and cultivars) developed for diverse uses; passport and phenotypic data are registered on this collection, and (ii) mutagenized variability, with 5000 EMS mutants including symbiotic mutants.

INRA collection of *Vicia faba* contains ca 2000 accessions of wide geographic origin on which passport and phenotypic data are registered. This collection is maintained by selfing, but the allogamous status of this crop (Suso et al 2006) also offers a possibility of dynamic management of populations. 23 populations have been built pooling lines issued from breeding programs. The use of an existing dominant male sterility gene is proposed in order to develop new populations having increased within population inter-mating, and which may used as the basis of recurrent selection programs.

INRA collection of white lupin, *Lupinus albus*, contains ca 2200 accessions, mostly local populations of wide geographic origins.

Associated with this source of variability, a continuing enrichment in phenotypic data, and the development of molecular markers for genotyping, support three strategic directions:

- the structuration of collections, in order to define core collections;
- ECOTILLING and association genetics to reveal allelic variability and its phenotypic effects;
- marker assisted selection .

SSR markers and markers of genes of known function have been developed for pea (Loridon et al. 2005, Aubert et al. 2005). SSR markers for faba bean are under development in collaboration with ICARDA (generation challenge program). For example, markers helpful to breed low trypsin inhibitor activity seed (Page et al. 2002) and super-nodulating pea genotypes (Krussel et al. 2002) are available, while ECOTILLING or TILLING reverse genetics approaches on selected genes will help identifying interesting progenitors.

D. Page, G. Aubert, G. Duc, T. Welham, C. Domoney:2002 Combinatorial variation in coding and promoter sequences of genes at the Tri locus in *Pisum sativum* accounts for variation in trypsin inhibitor activity in seeds ***Mol Genet Genomics*** 267, 359-369

Krusel L., Madsen L.H., Sato S., Aubert G., Genua A., Szczygowski, Duc G., Tabata S., Bruijn F., Pajuelo E., Sandal N., Stougaard J., 2002 : Shoot control of nodule and root development is mediated by e serine/threonine receptor kinase. **Nature** 420,422-426

Loridon, K., McPhee, K., Morin, J., Dubreuil, P., Pilet-Nayel, M.L., Aubert, G., Rameau, C., Baranger, A., Coyne, C., Lejeune-Henaut, I. and Burstin, J. 2005: Microsatellite marker polymorphism and mapping in pea (*Pisum sativum* L.). **Theoretical and Applied Genetics** 111, 1022-1031.

Aubert, G., Morin, J., Jacquin, F., Loridon, K., Quillet, M.C., Petit, A., Rameau, C., Lejeune-Henaut, I., Huguet, T. and Burstin, J. 2006: Functional mapping in pea, as an aid to the candidate gene selection and for investigating syntenry with the model legume *Medicago truncatula*. **Theoretical and Applied Genetics** 112, 1024-1041.

Suso, M., Gilsanz, S., Duc, G., Marget, P. and Moreno, M.2006: Germplasm Management of Faba Bean (*Vicia faba* L.): Monitoring Intercrossing between Accessions with Inter-plot Barriers. **Genetic Resources and Crop Evolution** 13, 1427-1439.

LegumBase, a Genetic Resources Integrated Information System for Legumes

¹Vincent Savoys, ²Sophie Durand, ¹Christine Le Signor, ¹Françoise Moussy, ¹J-Bernard Magnin-Robert, ¹Gérard Duc, ¹Judith Burstin, ¹Richard Thompson

¹INRA-UMR LEG, BP 86510, 21065 Dijon cedex, France

²INRA URGI, 523 place des Terrasses de l'Agora, 91000 Evry, France

contact : vincent.savois@epoisses.inra.fr

UMR LEG and the group for Legumes of the department of Genetics and Plant Breeding of INRA have to face an ever increasing data volume with their different seed stock centres. In this way, after having evaluated the different existing solutions, they have decided to customize Drosobase (<http://drosobase.cnrs-gif.fr/DrosoBase/index.php>), an open source web application for drosophila stock management, to create LegumBase. LegumBase is today an application dedicated to manage legume genetic resources (pea, faba bean, and *M. truncatula* induced mutants) of heritage (wild and breeding genotypes) and scientific interest (RILs, mutants...). It has a double aim: at first to form connections between legumes collections and to speed up exchanges between labs but also to diffuse this data to the scientific community as a whole. To achieve this, LegumBase provides to curators a stock and commands management tool through a secured interface but also a tool to manage their data they offer. Curators remain owners of their data and choose their data publicity policy. So, they can decide whether the data should remain private or not. LegumBase is also built to offer an access to legumes collections. In this purpose, LegumBase also offers a genotype and annotation search tool which enable cross-species comparisons and an order interface for registered users. The database currently contains about 10,000 pea and *Medicago truncatula* genotypes. Most of them come from EMS mutant populations (TILLING platform sponsored by the GLIP project) of pea and *M. truncatula*. There are also several hundred accessions of a genetic resource centre for grain legumes of heritage value. All accessions are defined by passport data. About 25% are also characterized by annotation data. These annotations include mainly phenotypic data and pictures.

More legumes curators should join soon the project. LegumBase is now online at the following address: <http://www.inra.fr/legumbase>.