SL09 - Development of molecular markers for large-scale implementation for marker-assisted selection in lupin breeding

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Marker-assisted selection (MAS) in plant breeding requires that the markers to be closely linked to genes of interest, be cost-effective, and applicable to a wide range of breeding germplasm. We applied the DNA fingerprinting technology called "microsatellite-anchored fragment length polymorphisms (MFLP)", which has proved to be highly efficient in generating candidate markers linked to genes of interest, and the markers could be easily converted into sequence-specific PCR markers desirable for routine implementation. To ensure the markers applicable to a wide range of crosses, we developed a strategy of generating multiple candidate markers followed by a validation step to select the best marker before conversion to an implementable form. By applying these techniques, we have developed a number of molecular markers linked to key genes of agronomic interest in lupin, including anthracnose disease resistance, phomopsis disease resistance, low alkaloid gene, pod non-shattering gene and soft seeded gene. In the last five years, about 100,000 lupin plants were tested and selected by molecular markers, representing one of the very few examples in the world of large-scale practical molecular plant breeding on legume crops. Examples are presented to illustrate the molecular strategies by which we successfully developed the implementable markers both for single gene controlled traits and for polygenic controlled trait.

SL10 - EURIGEN: Characterization of European rice germplasm for stress response traits

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The general objective of the EU-funded EURIGEN project is the characterisation and exploitation of European rice genetic resources of the temperate rice growing area, to enhance competitiveness of Europe in rice production, and alleviation of biotic and abiotic constraints typical of the Mediterranean area. This goal is achievable by means of the acquisition, evaluation and conservation of existing rice accessions, and identification of new genetic materials targeted at sustainable agricultural systems, making use of the most updated genomic tools. The project has two major targets: i) identification and conservation of genetic resources and ii) identification of valuable sources of new genes and alleles for agronomic and quality traits relevant to breeding programs. The main platform of the project is the classification, maintenance and regeneration of the temperate rice germplasm bank. A panel of 455 rice accessions relevant for breeding programs in European growing areas were analysed at both phenotypic and genotypic level. A centralised seed bank of the collection was established and a DNA biorepository organised in bar-coded 96-well plates was created and made available to the EURIGEN partners. A core collection of 200 rice accessions was selected based upon phylogenetic analyses and phenotyped in the field and controlled conditions for adaptation to biotic and abiotic stresses including blast, reduced water availability and salinity. To identify molecular markers associated with the adaptation traits as well as alleles ensuring the best performance under stress, the 200 accessions were genotyped with 384 SNPs using the high-throughput ILLUMINA BeadExpress genotyping platform. The SNPs were selected in candidate genes involved in stress responses based on literature data and preliminary results from ongoing projects at international level. The integration of phenotypic and genotypic data will enable us to carry out association analyses and valorise the existing natural variation to devise novel strategies of rice improvement in EU countries. The EURIGEN actions pursue the general objectives in accordance with the assessments of the FAO International Treaty on Plant Genetic Resources for Food and Agriculture, and the Council Regulation (EC 870/2004) establishing a *Community Programme on the conservation, characterization, collection and utilization of genetic resources in agriculture*.