

Achievements from GLIP Functional Genomics Platforms

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Seeking to understand the genetic and molecular basis of key traits for improving the performance of legume crops, a complementary set of genomics tools has been developed in the European Grain Legumes Integrated Project (GLIP).

Because cultivated legume species are diverse, some being difficult to transform and regenerate, and others with large and complex genomes, the scientific community has focussed on model legumes that are more amenable to molecular genetics study: *Medicago truncatula* and *Lotus japonicus*. The EU-GLIP project selected *M. truncatula* because it is more closely related to European grain legume crop species.

With two-thirds of the gene space of *M. truncatula* sequenced (www.medicago.org/), the total number of *Medicago* genes is estimated at about 65,000. What do these 65,000 genes do? How do they contribute to important agricultural and biological traits?

GLIP provides three levels of answers: (1) Automated annotation by IMGAG (International *Medicago* Genome Annotation Group) provides hypothetical gene function. (2) Genome-wide expression profiling provides correlative evidence for the involvement of specific genes in specific functions. (3) Functional genomics platforms provide stronger evidence for gene function by analysing the phenotypic consequences of mutations in specific genes.

I will present an overview of the functional genomics platforms developed in GLIP for *M. truncatula* and *Pisum sativum*. Three types of platforms have been generated, based on the mode of disruption of gene function: chemical mutagenesis, Fast Neutron deletion and retrotransposon insertion. I will highlight the versatility and complementarity of the different platforms by featuring selected examples of the achievements of GLIP.