

# **The organisation of the genetic diversity in the complex of species *Medicago truncatula* - *Medicago littoralis*. Consequence for the efficient screening of natural allelic variation and installation of a biological center of resources.**

Jean-Marie Prosperi, Thomas Bataillon, Magalie Delalande and Joëlle Ronfort

Institut National de la Recherche Agronomique. SGAP – UMR1097. F34130 Mauguio. FRANCE

Classically the definition of gene function requires the phenotypic characterization of genetic variants. Currently, such analysis of genes is based largely on laboratory-induced mutants. An alternative complementary source of genetic variation is the naturally occurring variation among genetic resources. The multigenic nature of most of this variation has limited its application until now. However, the use of genetic methods developed to map quantitative trait loci, in combination with the characteristics and resources available for molecular biology, allow this variation to be exploited at the molecular level.

The Genetic Resources and Mediterranean *Medicago* Plant Breeding Laboratory INRA-Montpellier (French Gene Bank for *Medicago* species) has gathered over several years a collection including 650 accessions of the *M. truncatula* - *M. littoralis* species complex. One accession does not refer to one inbred line, but to a sample of seeds collected from one site, in most cases a set of different lines. A variable level of polymorphism remains in each accession. We built a core collection consisting of 131 natural populations sampled on their geographical distributions, environmental descriptions of the site and pod characteristics. This collection is being evaluated for several characteristics: morphological, agronomical and genetic markers. From these 650 accessions, 530 inbred lines were extracted. They are currently being characterized both at the morphological and the molecular level. We outline the methodology we use for the sampling of core collections aimed at maximizing allelic diversity (M strategy). A sub-set of 191 inbred lines genotyped for both SSR and allozymes is used to test the efficiency of our method. We show that SSR assisted sampling allows to improve allelic richness of core collection by 10%. This collection will be a great tool for genomic studies is currently being screened for symbiotic mutants or tolerance to diseases. Based on this method, we will build different sets (n=32, 64, 96...) of well characterized inbred lines -core collections- comprising a maximum of the diversity available in *natura*. These core collections will be freely distributed to the *M. truncatula* research community.

In parallel , several natural populations around Montpellier (South of France) have been studied in detail using genetic markers. With the availability of SSR markers, we were able to study the organization at a very fine spatial scale. We will present results on the amount of selfing occurring naturally in the populations and the patterns of gene flow. The implication of these findings for future screening of naturally occurring allelic variation will be discussed.

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