

# Genome of model legume *Medicago truncatula* sequenced

Nevin D. Young, Frédéric Debelle, Giles E. D. Oldroyd, et al. *The Medicago Genome Provides Insight into the Evolution of Rhizobial Symbioses.*



*Highly repeated sequences are located in the pericentromeric regions*

Scientists from LIPM (INRA-CNRS) in collaboration with Génoscope (CEA-Institut de Génomique), as part of an international consortium \*, have reported the genome sequence of a legume, *Medicago truncatula* (Mt) also known as Barrel Medic. This sequence provides easy access to the location of genes of interest in crop legumes (pea, field bean, lentil, alfalfa, clover) which will greatly facilitate breeding. Legumes have the capacity to fix atmospheric nitrogen; as a result legume crops do not require nitrogen fertilizers, which represents a

real asset for a sustainable and more environmentally friendly agriculture. Results are published in *Nature* on November 17th 2011.

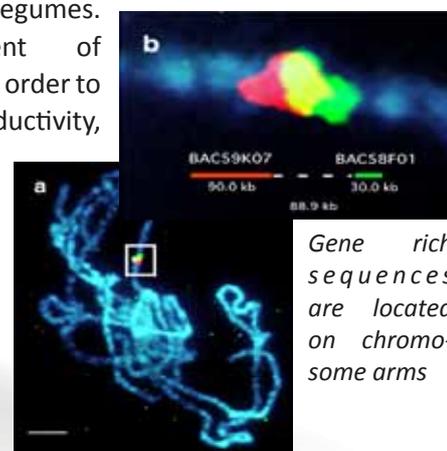
This fodder plant, proposed as a model legume by INRA in the 1980s, belongs to the Fabaceae family (formerly Legumes). Legumes play a major economic role: they are a substantial source of plant proteins for animals and humans, and their cultivation does not require nitrogen fertilizers, which is cost-effective and beneficial to the environment. Because they improve soil fertility, they play an important role in crop rotations. The world production is 300 million tonnes per year.

Legumes have the unique characteristic to fix atmospheric nitrogen which other cultivated plants cannot do. This characteristic is the result of a symbiosis with soil bacteria called rhizobia which form root nodules. Rhizobia produce an

enzyme missing in plants, nitrogenase, which allows them to fix atmospheric nitrogen inside the plant. In return, the plant provides an environment and nutrients that are necessary for the bacteria to develop and fix nitrogen.

Through their participation in an international collaboration, scientists from INRA have deciphered the genome sequence of Mt. The study has revealed that a duplication of the entire genome about 60 million years ago, when legumes appeared, has played a major role in the formation of the Mt genome and contributed to the evolution of symbiotic life with rhizobia. Genes that were involved in the symbiosis with mycorrhizal fungi have duplicated and one copy has evolved to control the nodulation process.

Mt is phylogenetically close to most of the legumes cultivated in Europe, such as pea, field bean, alfalfa and clover. There is a strong conservation of the order in which genes are located on chromosomes of these species (shared synteny). Knowledge of the genome sequence of Mt has allowed the order of the genes on its eight chromosomes to be determined. This knowledge should greatly ease the identification of important genes in cultivated legumes. Genetic improvement of legumes is necessary in order to increase their productivity, their use in crop rotation and to develop sustainable systems that require less chemical inputs, in particular nitrogen fertilizers whose production is very energy-consuming.



*Gene rich sequences are located on chromosome arms*

**Nature, November 17th 2011, DOI: 10.1038/nature10625**

\*Participants in the International Consortium include: University of Oklahoma, J. Craig Venter Institute, Genoscope (CEA Institut de Génomique), Wellcome Trust Sanger Institute, University of Minnesota, LIPM INRA/CNRS, John Innes Centre, Noble Foundation, University of Wageningen, MIPS, Ghent University, National Center for Genome Resources (NCGR), BIA INRA, CNRGV INRA. The French participation to the program, including sequencing of *M. truncatula* chromosome 5 was funded by the European Union Grain Legumes program (with equal funding from Genoscope and EU), the French ANR SEQMEDIC program, INRA, and CNRS.