

Importance of Legumes

- ✧ ≈ 650 genera, 18000 species

Soybean, pea, bean, alfalfa...

- ✧ Fertilizer saving

- ✧ Crop rotation (Soil improvement)

- ✧ Nutritional value (Food and Feed)



Economically and environmentally important crops



Medicago truncatula

*Medicago
truncatula*



+

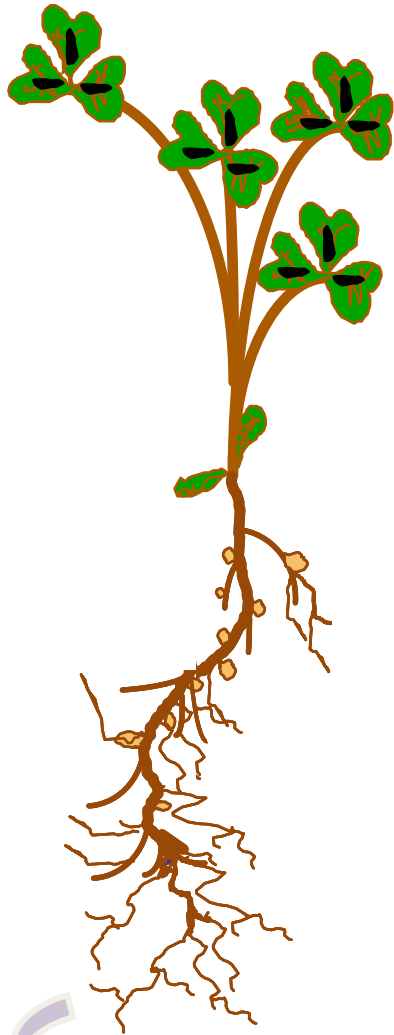
*Sinorhizobium
meliloti*



root nodules
N₂ fixation



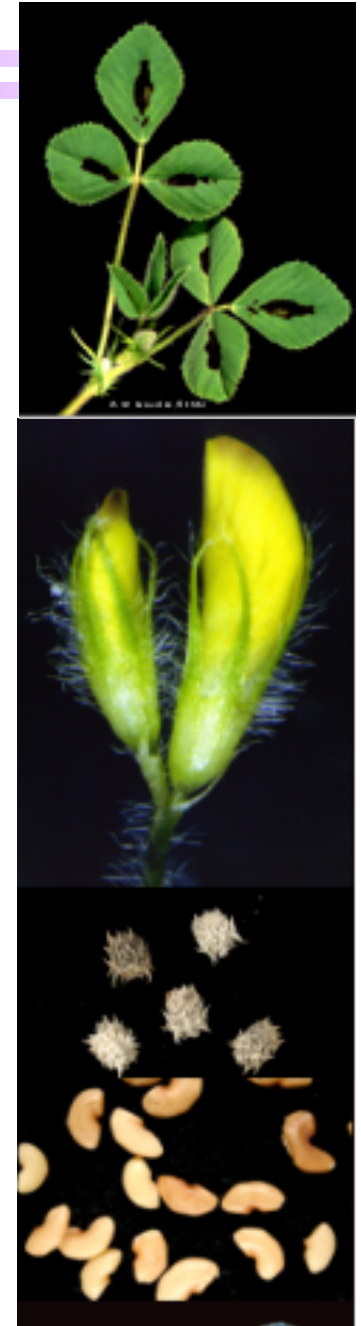
The Legume plant : *Medicago truncatula*



- ✧ Small plant
- ✧ Diploid plant
- ✧ Small genome (450 Mbp)
- ✧ Genome is assembled
- ✧ Lots of tools
Affymetrix Genechips,
Mutants library, Transformation...

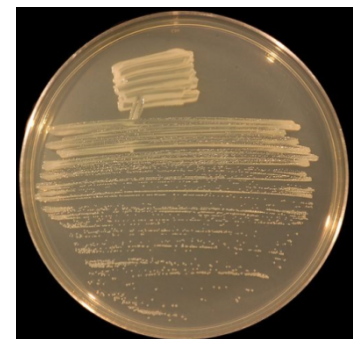
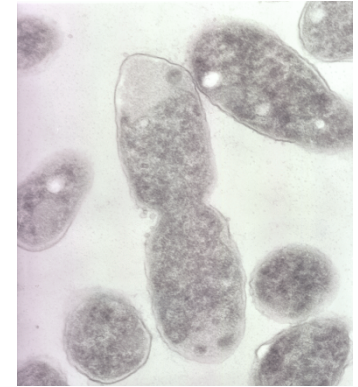
Young *et al.*, Nature, (2011)

Medicago truncatula is a model plant



The *M. truncatula* microsymbiont : *Sinorhizobium meliloti*

- ✧ Soil bacterium
- ✧ Sequenced genome
Galibert *et al*, Science (2001)
- ✧ Mutant library
- ✧ Nitrogen-fixing bacteria



M. truncatula – *S. meliloti* are able to establish a symbiosis

Genomic resources:

The *Medicago* genome provides insight into the evolution of rhizobial symbioses

Young, Debellé, Oldroyd et al., 2011. Nature.

<http://www.medicagohapmap.org/hapmap/about>

Briefly, **384 inbred lines spanning the range of *Medicago* diversity are being resequenced** using Illumina next generation technology. This provides a foundation for discovering single nucleotide polymorphisms (SNPs), insertions/deletions (INDELs) and copy number variants (CNV) at very high resolution among the *Medicago* lines. Thirty of these lines have been deeply resequenced (20X coverage or more), while the remainder are sequenced at least 5X coverage. The resulting database of sequence variants establishes a basis for describing population structure and identifying genome segments with shared ancestry (haplotypes) – and thereby creating a long-term, community-accessible genome-wide association (GWA) mapping resource.

Genetic resources:



INRA BRC-MTR : Biological Resource Centre

for the model species *Medicago truncatula* L.

Depending on their origin, *Medicago truncatula* resources can be split into two categories :

Natural Diversity

INRA Montpellier possess the world second largest collection of natural diversity of *Medicago truncatula*.

It is the only collection currently organised and managed so that it responds to the needs of scientists in the area of genomics, by offering:

- * Populations
- * Inbred lines
- * Recombinant Inbred Lines
- * F1 hybrids and progenies

The material is already being widely distributed to the international scientific community with more than 1,500 samples sent every year over the past six years.

This material is managed at INRA Montpellier

Contacts :

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Induced Mutations

Large mutagenesis programs have been developed on *Medicago truncatula*. This material has been obtained by using three techniques:

- * Gamma irradiation,
- * T-DNA mutagenesis
- * Tobacco Tnt1 mutagenesis.

More recently, INRA Dijon have developed a program of mutants production by using the tilling procedure.

Up to now such resources have not been widely distributed.

The material is managed at INRA-Dijon

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Location of 200 populations from the collection: between latitude 28° to 46°N, Longitude 17°W to 59°E, and altitude:0 to 1650 masl.



Genetic resources:

TILLING *Medicago truncatula* population

***Medicago truncatula* insertion mutants**

~16,000 *Tnt1* lines at the Noble Foundation (25 *Tnt1* inserts/line)

+ Pascal Ratet: CNRS / Gif sur Yvette

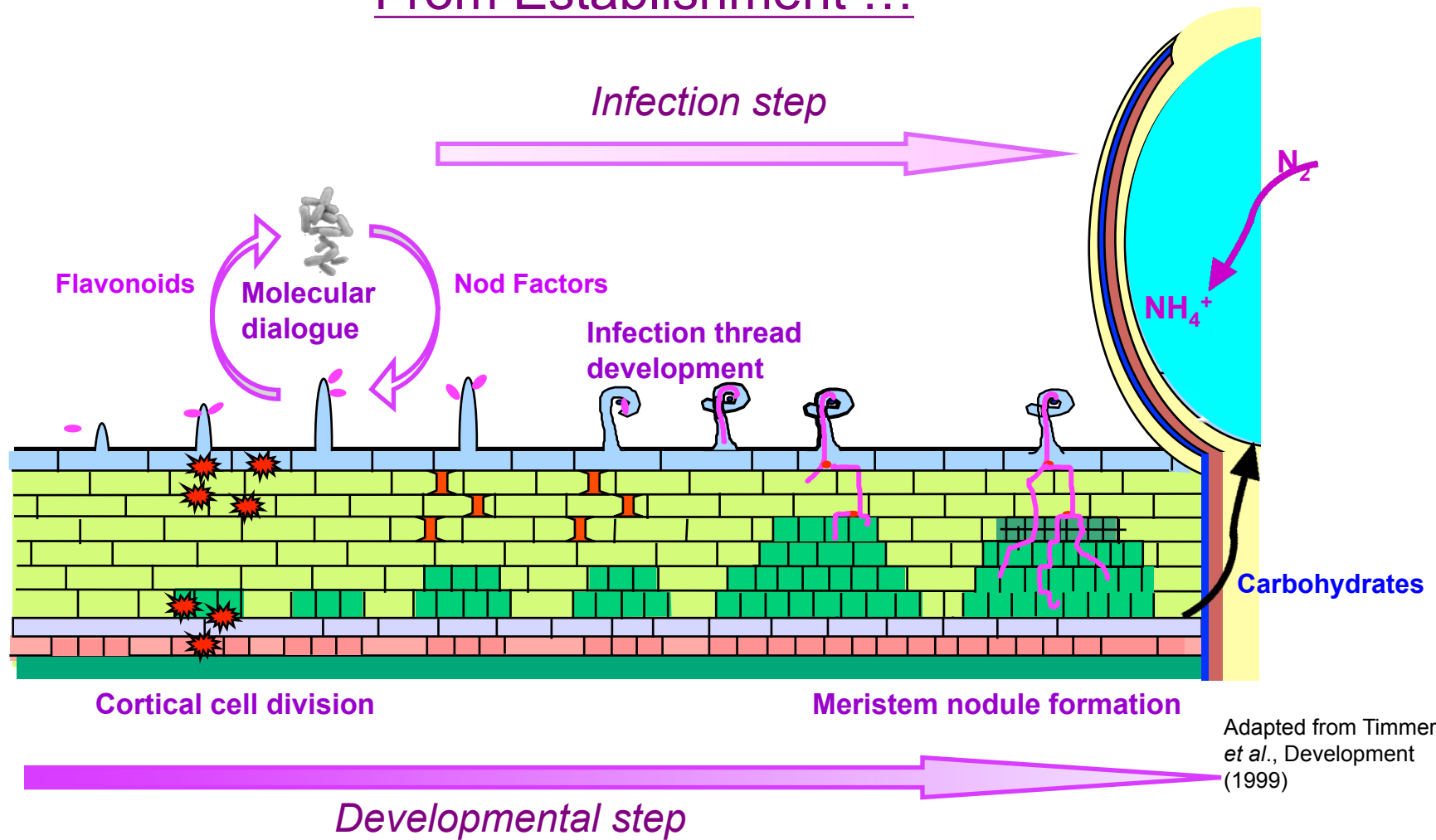
***Medicago truncatula* deletion mutants**

Fast Neutron Bombardment (FNB)-induced deletion mutants of *Medicago truncatula* Jemalong A17

M2 population from ~146,000 M1 lines

Medicago truncatula – *Sinorhizobium meliloti* symbiosis

From Establishment ...



Medicago truncatula – *Sinorhizobium meliloti* symbiosis

...to nodule functioning

