

## MUTANT COLLECTIONS FOR FORWARD AND REVERSE GENETICS IN *MEDICAGO TRUNCATULA*

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*Medicago truncatula* is considered the model species for genetic studies on forage legumes.

In the frame of the FIRB project, Post Genomic of Forage Legume, we have developed several tools for functional studies in this species.

An activation tagging approach based on four 35S enhancers as activating elements was used to produce a mutant collection which was screened for alteration in saponin production and accumulation. Line E25 showed an altered saponin pattern being incapable of accumulating hemolytic saponins.

A second collection of about 1000 lines was produced employing the Tnt retrotransposon as mobile element. The average number of Tnt copies per line was 15 and analysis of about several hundred Tnt flanking sequences demonstrated that this element has a strong preference for inserting into coding regions.

Phenotypic screening of the available collections were conducted for nodule number and morphology and for root architecture. In both cases several interesting mutants were observed.

The TILLING approach was used to generate a tool for reverse genetic studies. About 2300 individual plants, belonging to 1563 families, were grown and phenotypically evaluated; their genomic DNA was extracted and pooled and their M3 seeds were inventoried. Mutants for plant architecture and growth habit and for leaf shape, size and pigmentation were observed in M2 generation.

The three collections are being organized in a platform which will be available for studies of forward and reverse genetics.