

## POST-GENOMICS OF FORAGE LEGUMES: AN ITALIAN INITIATIVE TO SET UP GENETIC TOOLS TO IMPROVE FORAGE QUALITY AND ECO-COMPATIBILITY

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*Medicago truncatula* is a close relative of alfalfa (*Medicago sativa*), the most widely cultivated forage species in temperate regions. Alfalfa is considered the preferred nutritive source, both environment friendly and cost effective, for animal production because of the high nutritive value of its forage and its capacity to establish symbioses with nitrogen (N)-fixing rhizobia and with mycorrhizal fungi. However, the size and complexity of cultivated alfalfa genome impedes molecular genetic studies. Conversely, the small genome size (454-526 Mbp) of *Medicago truncatula*, its ploidy level (diploid), its autogamous reproductive system and the high level of synteny with *Medicago* spp and pea make *M. truncatula* the most suitable tool for genomic and post-genomic studies in legume biology.

Here we report the activities of a multiinstitutional Italian effort funded by the Italian Ministry of University and Research (MIUR) as part of a Post-Genome Initiative – FIRB (Funds for Investing in Fundamental Research) RBN018BHE. The project aimed at developing genomic tools and expertise on *Medicago truncatula* as model system for forage legumes and involved eight laboratories from different Italian Organizations (CNR, Universities, MiPAF-C.R.A.) to study different aspects of legume biology at genomic level.