## IDENTIFICATION OF A *MEDICAGO TRUNCATULA* GLUTATHIONE S-TRANSFERASE GENE ESSENTIAL FOR ANTHOCYANIN ACCUMULATION

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Anthocyanins and proanthocyanidins (PAs) are flavonoids that share large part of their biosynthetic pathways. In a screening of a *Tnt1* transposon tagged *Medicago truncatula* population two indipendent mutants lacking anthocyanin pigmentation in the leaves were identified. The observed phenotype co-segregated with an insertion in a glutathione S-transferase (*MtGST*) gene in R1 progenies derived from both mutants. Homozygous mutated plants did not show *MtGST* expression as per real time RT-PCR analysis.

The importance of GSTs for anthocyanins transport has been demonstrated in different plant species where mutations in the encoding genes led to the reduction in anthocyanins accumulation and pigment mislocalisation. Indeed, it has been proposed that GSTs either aid in cellular detoxification by catalysing the conjugation of glutathione to anthocyanins and other flavonoids or act as flavonoid-binding matrix to protect these compounds from oxidation and favour their long-distance transport. Nevertheless, GSTs are one of the molecular actors associated with vacuole sequestration of anthocyanins and PAs. In this regard, spectrophotometric assays highlighted the absence of anthocyanins in the homozygous mutated plants and a reduced accumulation in the heterozygous compared to the wild type. Conversely, no qualitative alteration in proanthocyanidins presence was detected by 0,2% DMACA staining of seeds and glandular trichomes in the mutants.

Using both molecular and computational approaches we show that MtGST is the ortholog of AN9 in Petunia and Bz2 in maize. Further studies are ongoing to estabilish MtGST role in anthocyanin transport and sequestration in  $Medicago\ truncatula$  as well as to assess its role, if any, in PAs accumulation.