**Gene-edited Medicago *Mtsoc1* or *Mting* mutants do not flower**

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Optimised flowering is a key trait for enhanced crop productivity. In the eudicot Arabidopsis, genetic pathways are known to converge on floral integrator genes like *FT* and *SOC1* to elevate their expression and lead to flower development. *Medicago truncatula* (Medicago), like winter annual Arabidopsis, is induced to flower by extended cold (vernalisation) followed by warm long day photoperiods. Interestingly Medicago lacks key Arabidopsis flowering regulators including CO and FLC. However, the *FT-like* gene *MtFTa1* is upregulated by floral inductive conditions and promotes flowering.

We analyse Medicago flowering using gene editing to knock out single Medicago candidate genes or multiple duplicated homologs simultaneously. Previously, a *SOC1-like* gene *MtSOC1a* was implicated as it was elevated by *MtFTa1* expression, while there was a moderate delay to flowering in the single mutant. We also showed that the novel *MtING2* gene, encoding an ING domain and a PHD finger, promotes growth and flowering in Medicago.

Here we present results of analysis of triple *soc1* mutants, or double *Mting* mutants. Both mutants have striking phenotypes - because they do not flower. We use RNA-seq to compare their differential gene expression to other non-flowering Medicago plants. We test if homologs of targets of Arabidopsis SOC1 are misexpressed in the *soc1* triple mutants. We ask if targets of the NuA4 histone acetyltransferase complex in Arabidopsis, which ING2 is part of, are misexpressed in the Medicago *ing* mutants. Our work provides insights into flowering regulation in legumes and points to increased forage production including by using non-flowering mutants.