

Comparative analysis of plant growth and development: use of *Medicago truncatula* as a bridge species.

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The diploid legume *Medicago truncatula* has been developed as a model experimental system and offers the prospect of accelerating the pace of discovery of genes involved in processes of interest to both basic as well as applied legume biologists. Using a forward genetic approach we have identified a set of *M. truncatula* mutants that affect many phases of plant growth and development. As expected for a model system, a limited amount of phenotypic screening in *M. truncatula* appears to have captured a significant portion of the mutant spectrum observed from mutant screens in crop legumes such as pea, despite the substantially longer history of breeding and genetics in the crop legumes.

With the goal of understanding traits unique to, or of special relevance to legume biology, we have initiated a comparative analysis of flower development in the legume model *M. truncatula*, the crop species *Pisum sativum*, and the model for general plant biology, *Arabidopsis thaliana*. Studies of floral ontogeny in pea suggest that while some aspects of flower development are similar between pea and Arabidopsis, significant differences are also evident between the two species, with such differences presumably being indicative of elaboration of the basic paradigm in legumes. Using floral homeotic mutants that feature interorgan conversion among sepal, petal, stamen and carpel, and candidate genes identified in *M. truncatula* and pea, we are examining how broadly inferences from Arabidopsis are likely to be applicable to legumes, with *M. truncatula* serving as a bridge species for comparison of crop legumes to Arabidopsis.