

# Transcriptomic inquiry into divergent Fabaceae

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The symbiotic interaction with rhizobia is a hallmark trait of Fabaceae family and confers a distinct adaptive advantage by facilitating atmospheric nitrogen fixation in specialized root nodule structures. However, while nodulation is characteristic of legumes, not all legumes are equally capable of nodulating. In general more than 80% of Mimosoideae and Papilionoideae legumes nodulate whereas less than 30% of the Caesalpinioideae species form nodules. Thus, this divergent offshoot represents a transition from non-nodulating to nodulating legumes and can help tease out the evolutionary origins of nodule formation.

In our work we hypothesize that the differential distribution of nodulating species in some early-diverging legume taxa is reflected in divergent or convergent gene family changes throughout the clade. Moreover, we consider the possibility that differential loss rather than gain of several genes together with previously reported whole genome duplication (WGD) might have been the driving force that contributed to genomic changes related to the evolution of symbiotic nitrogen fixation. Therefore we aim to characterize gene families susceptible to evolutionary selection pressure in the early-diverging lineages of legumes. Transcriptomic and genomic data from closely related genera of Caesalpinioideae legumes, and so called early diverging Papilionoideae as well as Mimosoideae will serve as basal research material in order to establish whether the changes have been gradual or punctuated. Comprehensive comparative analysis of transcriptome sequences of: *Adenolobus peuchelii*, *Albizia chevalierii*, *Cassia sturtii*, *Ceratonia siliqua*, *Chamaecrista mimosoides*, *Desmanthus velutinus*, *Dichrostachys cinerea*, *Gymnocladus dioicus*, *Faidherbia albida*, *Peptadenia stipulacea*, and *Senna obtusifolia* was performed to indicate these potential determinants.