**Unusual mergers, acquisitions, and diversity in the legume family**

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The legume family, with approximately 770 genera and close to 20,000 species, is one of the largest and most diverse plant families. Following the family’s origin around 70 million years ago, it diverged into six lineages—the largest of these in terms of species count being the Papilionoideae, with close to two thirds of the family’s species, and the smallest being Duparquetioideae, containing the single eponymous genus Duparquetia. Among those six subfamilies, symbiotic nitrogen fixation (SNF) is present in most genera in the Papilionoideae but is found in only a scattered minority of genera in the second largest subfamily, the Caesalpinioideae. Adding to the complexity of the family—while also contributing to the potential for evolutionary innovation—is the presence of whole genome duplications (WGD) early in most of the subfamilies (though interestingly, skipping two early-diverging genera). Resolving the timing of the early evolutionary events has been difficult, as both the diversification and the WGD events occurred within 10-20 million years following the family’s origin. Adding to the difficulty is the apparent delayed allopolyploid origin of Caesalpinioideae, probably involving progenitors of the Papilionoideae and one of the other subfamilies. This allopolyploidy likely contributed to the great diversity seen in the Caesalpinioideae, including the variation in capacity for SNF in that subfamily. A finding of allopoloyploidy along the legume backbone also means that the legume phylogeny cannot properly be represented by a standard bifurcating phylogenetic model but needs to be considered as a more complex reticulate history.