
Department of Environmental & Plant Biology
Colloquium

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*“Phylogenomics, Polytomies and the
K-Pg Boundary – Legume Evolution
in Deep Time”*

The order of magnitude larger DNA sequence datasets used in phylogenomics offer excellent scope to build enhanced phylogenies with robust resolution. However, even with data from 1000s of genes, some parts of the *Tree of Life* remain as polytomies resilient to resolution. Here I contrast two such polytomies in the early evolution of legumes. Despite the spectacular diversity, ecological prominence and enormous economic importance of legumes, the origin and early evolution of the family remain poorly understood. I present results of phylogenomic studies addressing these questions based on chloroplast exomes and thousands of nuclear gene alignments. Our results suggest rapid initial divergence of the six main lineages of legumes (i.e. the six subfamilies) around the Cretaceous-Paleogene (KPB) boundary and revise previous placements of whole genome duplications (WGDs) in early legume evolution. We show that rapid diversification, WGD and the KPB are together causing a complex phylogenomic tangle at the base of the legumes characterized by high gene tree conflict. I also characterize a second polytomy subtending the large pantropical ingoid clade of mimosoid legumes which contains 2000+ species. We found that lack of phylogenetic signal in sequences for 964 nuclear genes, rather than conflict among gene trees, is causing this putative hard polytomy, which is thus most likely the result of hyperfast diversification. We conclude that the diverse underlying causes of polytomies can be effectively revealed using a range of phylogenomic methods.