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Symposium

Integrating genes, genomes and morphology: Towards a comprehensive picture of angiosperm evolution

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Phylogenetic reconstruction within flowering plants using molecular markers over the last two decades has produced a solid framework of phylogenetic hypotheses spanning from the earliest branches, over the backbone, to relationships within orders and many families. Therefore, the time is ripe to address macroevolutionary questions.

Most important for an evolutionary synthesis is to study the evolution of phenotypic characters and to investigate co-evolutionary patterns as well as selective constraints on traits. This calls not only for an increased integration of sub-disciplines (phylogenetics, comparative morphology and anatomy, functional genetics, developmental biology, ecology) but also underscores the need to generate representative comparative data sets of phenotypic features that include sufficient numbers of taxa. The symposium will address selected characters, and model clades from within the flowering plants as examples towards a comprehensive picture of angiosperm evolution.

On the other hand, phylogeny reconstruction in flowering plants has so far heavily relied on plastid coding genes. More recently, non coding genomic regions (especially introns) added resolution and statistical confidence to angiosperm phylogenetic trees, and an analysis of nearly all coding genes in phylogenomic approaches improved backbone resolution. It thus remains important to further test phylogenetic hypotheses, in particular by using increased larger taxon and character sets, and by including the nuclear and mitochondrial genomic compartments. The symposium will therefore also address current approaches of phylogeny reconstruction in angiosperms.

With this symposium we aim at discussing current and inspiring future work of flowering plant phylogenetics and evolution. We especially want to make the point that the now existing phylogenetic framework does not mean that everything is known on flowering plant systematics but that we are rather entering a most phase of research that promises many further insights.

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