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Resolution of phylogenetic patterns within monocots

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Monocotyledons or monocots are one of two groups of angiosperms that comprise ca. 60,000 species, 92 families, and 12 orders. Exemplary monocots include agaves, grasses, sedges, bromeliads, palms, ginger, orchids, irises, lilies, yams, pondweeds, and aroids. Even the most comprehensive evolutionary phylogenetic studies leave numerous relationships unresolved and inadequately supported. Thus, various questions remain for monocots in regards to their origin, phylogeny, patterns of morphological divergence, geographic diversification, and ecological radiation. To address these questions, we will create new nuclear monocot multigene phylogenies and compare them to previously established chloroplast/mitochondrial multigene phylogenies. Since nuclear and plastid genes have different patterns of inheritance, we will analyze conflicts and sources of incongruence of gene trees before combining all the data into a consensus phylogeny. After tissue collections, DNA/RNA extractions, and synthesizing cDNA from taxa across 39 families of monocots, I will utilize conserved low copy nuclear genes generated by our lab to construct a nuclear multigene phylogeny. In previous analyses, we identified 13 challenging nodes found in a phylogeny of 125 monocots based on several chloroplast and mitochondrial plastid genes chloroplasts. Our primary experimental approach is to generate nuclear multigene phylogenies from sequence data to resolve these 13 ambiguous nodes. We have over 100 nuclear gene primers available to screen to find phylogenetic informative variation. Upon completion of all experimentation, I will construct gene tree phylogenies for each nuclear gene independently, conduct incongruence tests, and if appropriate combine all the nuclear genes into a single analysis. Ultimately, we will construct a resolved, strongly supported higher-level phylogeny for the monocots using data from all three genomic compartments (ncDNA, cpDNA, and mtDNA). This phylogeny will then be used to interpret morphological evolution and ecological/biogeographical patterns among monocot lineages.