

Public Abstract

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Monocotyledonous plants include many agriculturally and ecologically important species (e.g., grasses, ginger, palms, orchids, lilies, yams, pondweeds, seagrasses, aroids). These taxa exhibit vegetative, floral and genomic complexity and afford a prime opportunity to examine patterns of morphological evolution, genomic change, and geographic radiation. This dissertation documents three vignettes in monocot evolution, each addressing diversification and significance of both organismal (life history, biogeography, morphology) and genomic (genome size, molecular evolution) characteristics. Chapter 2 uses molecular sequence data from across plant genomes to describe evolutionary relationships among monocots and the timing of their diversification compared to other plant and animal lineages. Chapter 3 evaluates the traditional classification system of spiderworts (*Tradescantia* alliance, family Commelinaceae) using molecular sequence data, which is used to test the effects of kaleidoscopic morphological and genomic variation on evolution of the group. Finally, Chapter 4 evaluates a cutting-edge methodological approach to genome sequencing in two lineages of monocots. Each of these examples highlights the ability of monocots to serve as test cases for different types of evolutionary questions. The conclusions gleaned from this research allow for deeper understanding of monocots, which can assist in crop improvement, but also inform methodological approaches to studying evolutionary relationships among many plants and animals.