GENOME EVOLUTION IN MONOCOTS

Kate L. Hertweck

Dr. J. Chris Pires, Dissertation Advisor

ABSTRACT

Monocotyledonous plants are a well-circumscribed lineage comprising 25% of all angiosperm species, including many agriculturally and ecologically important species (e.g., grasses, gingers, palms, orchids, lilies, yams, pondweeds, seagrasses, aroids). These taxa exhibit vegetative, floral and genomic complexity. The opportunities afforded by this wealth of variation include evaluating patterns of morphological evolution, genomic change, and geographic radiation. This dissertation documents three vignettes in monocot evolution, each highlighting different taxonomic scales and relevant questions to the diversification and significance of both organismal (life history, biogeography, morphology) and genomic (genome size, molecular evolution) characteristics. Chapter 2 uses molecular sequence data from all three genomic partitions (nuclear and both organellar genomes) to infer evolutionary relationships in monocots. Chapter 3 evaluates a taxonomic classification system in the Tradescantia alliance (Commelinaceae, Commelinales), a group of closely related genera exhibiting kaleidoscopic variation in life history and genomic traits. Finally, Chapter 4 evaluates a 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.