

Advancing genome research in challenging polyploid complexes

George P. Tiley^{1,2}

¹Department of Plant and Microbial Biology, North Carolina State University, Raleigh NC, 27606, USA

²gptiley@ncsu.edu

Abstract

Collections-based and biodiversity research is increasingly important in understanding pressing issues such as plant response to climate change. Polyploidy can be a critical factor for explaining such responses, whether associated with a trait of interest, niche diversification, or speciation. However, research of polyploidy complexes can be challenging despite the increasing efficiency and scale of collecting molecular data. First, a feature of polyploid complexes is high degrees of topological conflict that introduce uncertainty in phylogenetic systematics and macroevolutionary analyses. Some of the advances on reconciling topological conflict as phylogenetic networks as opposed to phylogenetic trees will be reviewed, and the statistical limitations of current network methods will be covered. Some recent advances on network methods that explicitly consider polyploid biology will also be discussed. A second gap in the study of polyploid complexes though is general uncertainty about the ploidy level of historical specimens. While evolutionary biologists have become skilled at sequencing historical specimens and estimating large phylogenies, it necessary to link specimens with traits and metadata. Ploidy is difficult to assess from historical specimens, as it is no longer possible to make direct observations of chromosome numbers or genome sizes. Here, a new approach for estimating ploidy from sequence data will be introduced. Simulations and empirical examples will be used to demonstrate how filling in gaps in ploidy data on networks can help resolve the mechanism of polyploidy and explain the causes of topological incongruence in phylogenomic studies.