

Assembling and Reconstructing the Plastid Phylogeny of Dipsacales

Ariel Lerner and Dr. Wendy Clement
The College of New Jersey

PROJECT OVERVIEW

Dipsacales is a clade of flowering plants that includes groups such as honeysuckles (*Lonicera*), elderberries (*Sambucus*), and viburnums (*Viburnum*). Using next generation sequenced data and existing bioinformatic pipelines, we recovered the plastid genomes of 96 Dipsacales species. We used these data to reconstruct the phylogeny, or a tree-like diagram showing evolutionary relationships, of Dipsacales to ultimately compare this phylogeny to those reconstructed from other types of genetic data.

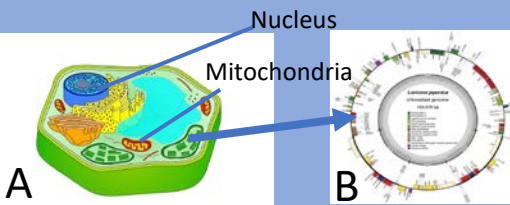


Figure 1. A. Diagram of a plant cell, with an arrow pointing from the chloroplast to a B. plastid genome (chloroplast DNA). Plants contain DNA from three different organelles: the nucleus, the mitochondria, and the chloroplast. Our goal was to assemble the genome of the chloroplast and use the DNA from the chloroplast genome to reconstruct the phylogeny of Dipsacales.

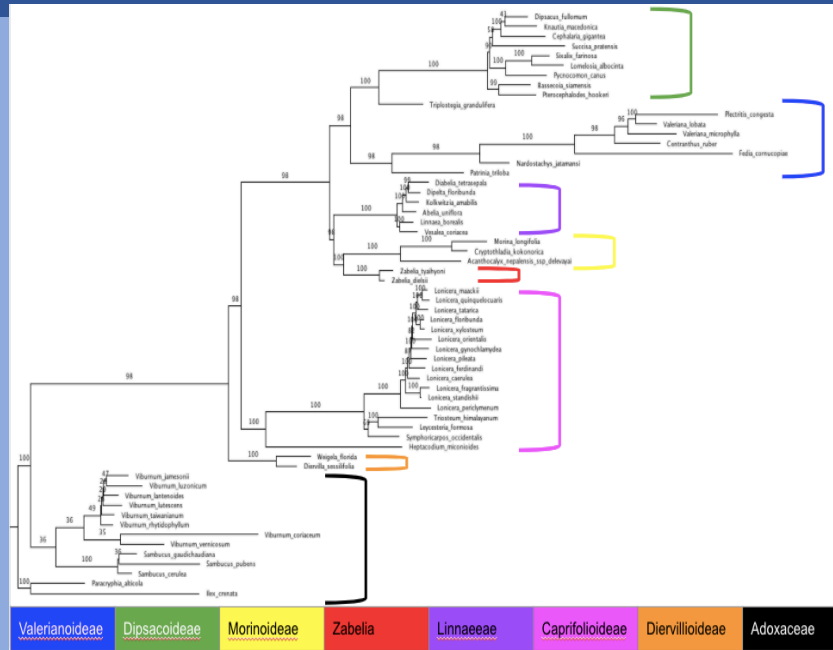


Figure 2. Dipsacales whole genome plastid phylogeny reconstructed using reference-based assembly. The alignment was 277,607 bp.

PROJECT OUTCOMES

Two bioinformatic pipeline were utilized to reconstruct Dipsacales plastid phylogenies. A reference-based assembly using closely-related available plastid reference sequences was performed mapping DNA sequence reads to the reference to obtain the genome (Figure 2). A second approach isolated and assembled just the protein coding regions of the plastid using a bioinformatic pipeline, Hybpiper (Figure 3). Both methods required the resources of the high performance computing cluster, ELSA HPC at TCNJ. Results showed very similar phylogenies, however slight differences were found regarding the placement of *Zabelia* (Table 1).

FUTURE DIRECTIONS

Using two different bioinformatic pathways, two different plastid phylogenies were reconstructed. Future directions include investigating discrepancies between the two phylogenies. We will also compare the structure of this plastid tree with Dipsacales trees reconstructed with nuclear data to ultimately propose the most likely evolutionary relationships within Dipsacales.

	Placement of <i>Zabelia</i>
Whole genome phylogeny	Sister to Morinaceae; <i>Zabelia</i> + Morinaceae sister to Linnaeae
Coding regions only	<i>Zabelia</i> + Morinaceae sister to Dipsacoideae + Valerianoideae

Table 1. Differences between the trees with respect to the position of the genus *Zabelia*.

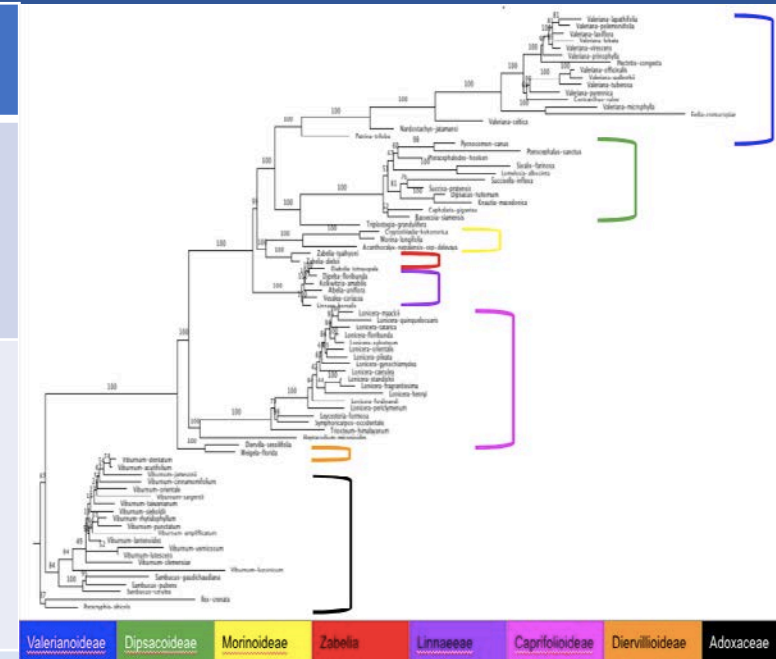


Figure 3. Dipsacales plastid phylogeny reconstructed using Hybpiper bioinformatics pipeline and exons (genes/coding regions) only. Alignment length of 98,974 bp.

Acknowledgements

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