

EXTENSIVE CHLOROPLAST GENOME REARRANGEMENT AMONGST THREE CLOSELY RELATED *HALAMPHORA* SPP. (BACILLARIOPHYCEAE), AND EVIDENCE FOR RAPID EVOLUTION AS COMPARED TO LAND PLANTS

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Diatoms are the most diverse lineage of algae, but the diversity of their chloroplast genomes, particularly within a genus, has not been well documented. Herein, we present three chloroplast genomes from the genus *Halamphora* (*H. americana*, *H. calidilacuna*, and *H. coffeaeformis*), the first pennate diatom genus to be represented by more than one species. *Halamphora* chloroplast genomes ranged in size from ~120 to 150 kb, representing a 24% size difference within the genus. Differences in genome size were due to changes in the length of the inverted repeat region, length of intergenic regions, and the variable presence of ORFs that appear to encode as-yet-undescribed proteins. All three species shared a set of 161 core features but differed in the presence of two genes, *serC* and *tyrC* of foreign and unknown origin, respectively. A comparison of these data to three previously published chloroplast genomes in the non-pennate genus *Cyclotella* (Thalassiosirales) revealed that *Halamphora* has undergone extensive chloroplast genome rearrangement compared to other genera, as well as containing variation within the genus. Finally, a comparison of *Halamphora* chloroplast genomes to those of land plants indicates diatom chloroplast genomes within this genus may be evolving at least ~4–7 times faster than those of land plants. Studies such as these provide deeper insights into diatom chloroplast evolution and important genetic resources for future analyses.