

DIATOM EVOLUTION THROUGH THE LENS OF LARGE TRANSCRIPTOME, TRAIT, AND TAXONOMIC DATA SETS

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Despite their species richness and global importance as primary producers and anchors of aquatic food webs, the primary evolutionary drivers of diatom diversification remain poorly known. We are undertaking two parallel efforts to better understand the phylogeny, diversification, and ecological history of diatoms. The first effort builds upon a growing genomic and transcriptomic dataset for diatoms. We used hundreds of molecular markers to resolve parts of the diatom tree that have presented a challenge for analyses based on fewer markers. Similarities in clade age, species richness, and primary production motivate comparisons between diatoms and flowering plants, whose genomes have been inordinately shaped by recurrent whole genome duplications (WGDs). We used a broadly sampled genomic and transcriptomic dataset to show that WGD may have played a similarly important role in the evolution of diatom genomes. A second, complementary effort compiled all publicly available DNA sequence data for 11 genes and >1100 diatom taxa. We used this densely sampled phylogeny to better understand patterns of character evolution, habitat shifts, and species diversification. Results from this project are providing new insights into the historical importance of transitions between the plankton and benthos and marine and freshwaters. They further highlight that shifts in the mode of sexual reproduction and the evolution of active motility set in motion a species radiation that produced the majority of present-day diatom diversity.