

PARALLEL SEQUENCING OF DIATOM PLASTID GENOMES USING A BAIT-CAPTURE APPROACH

Elizabeth C. Ruck¹, Teofil Nakov and Andrew J. Alverson¹

¹ Department of Biological Sciences, University of Arkansas, Fayetteville, AR 72701, USA

The sequencing of diatom plastid genomes has revealed diverse evolutionary forces shaping these genomes. Genome architectural features like genome rearrangement, reduction and expansion have been documented, and gene content analysis has shown evidence of gene loss, duplication, pseudogenization and potential gains via horizontal transfer. Next generation sequencing has accelerated the accumulation of these data, with a total of 53 complete or nearly complete diatom plastid genomes publicly available. Still, this represents a very small sample of diatom diversity. We are using a sequence capture strategy to expedite targeted high-throughput sequencing of 200 plastid genomes from species that span the phylogenetic breadth of diatoms. We are using a biotinylated RNA probe set that was custom designed from ten previously sequenced diatom plastid genomes. These probes serve as “baits” for in-solution capture of plastid genome sequences from multiplexed Illumina DNA libraries. Both pre- and post-captured libraries are being sequenced to estimate capture efficiency and evaluate the costs and benefits of this approach in comparison to genome skimming as an alternative strategy for de novo sequencing and assembly of diatom plastid genomes.