

# CHLOROPLAST GENOMES OF CLOSELY RELATED *STEPHANODISCUS* SPECIES AND POPULATIONS: TOWARDS A PHYLOGEOGRAPHY

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*Stephanodiscus niagarae* is a cosmopolitan species with a known distribution throughout North America in temperate freshwater lakes and reservoirs. It is also found in fossil deposits in North America, Africa, Asia, and Europe. Several closely related descendant species of *S. niagarae* are endemic to one or few lakes in several locations in the United States (together forming the *S. niagarae* complex). One of these species, *Stephanodiscus yellowstonensis*, from Yellowstone Lake (Yellowstone National Park [YNP]) has a well-documented record of morphological evolution from sedimentary cores that span the Holocene. Here, we use chloroplast genomes of closely related species and populations of *S. niagarae* to look at relatedness of spatially separated strains. We collected live *S. niagarae* individuals from Lewis Lake (YNP), Hebgen Lake (Montana, USA), Buffalo Bill Reservoir (Wyoming, USA), and Boysen Reservoir (Wyoming, USA). In addition, we had archival pellets of single strains of *S. yellowstonensis* from Yellowstone Lake (YNP), and of *S. niagarae* from Jackson Lake (Grand Teton National Park) and Lake Okoboji (Iowa, USA). In total, fourteen strains of *S. niagarae* and one strain of *S. yellowstonensis* were grown in continuous clonal cultures, pelleted at stationary growth phase, and total genomic DNA extracted using DNeasy plant mini kits (Qiagen). Libraries were prepared from extracted DNA, and, using a paired end 150 bp run, DNA were sequenced on Illumina's HiSeq 4000 or NextSeq 500 platforms. Chloroplast genomes were cleaned, assembled, and circularized in the software program Novoplasty. The genetic structure of the chloroplast was conserved amongst all strains, however, we found 118 polymorphic sites. Using TNT, we built a parsimony tree and found geographic signal between our locations (i.e., strains from the same lake are generally more related to each other than strains from other lakes). This is an important finding because these polymorphisms show the first genetic evidence of differences among populations of the *S. niagarae* complex where there are many known morphological differences. Further, our findings suggest our methodology may be a relatively inexpensive way to investigate the phylogeography of diatoms.