

## MOLECULAR AND MORPHOLOGICAL DATA REVEAL HIDDEN DIVERSITY IN COMMON NORTH AMERICAN *FRUSTULIA* SPECIES (AMPHIPLEURACEAE)

Andréanne Bouchard<sup>1</sup>, Paul B. Hamilton<sup>2</sup>, Julian Starr<sup>1</sup> and Ananda Savoie<sup>2</sup>

1. Dept. of Biology, University of Ottawa, Ottawa, Canada. Research and Collections, Canadian Museum of Nature, Ottawa, Canada.

2. Research and Collections, Canadian Museum of Nature, Ottawa, Canada.

*Frustulia* Rabenhorst is an old established diatom genus that is common and widespread across North America. Like many diatom genera, *Frustulia* has been the subject of considerable taxonomic confusion. Although recent studies have examined taxa from Europe and New Zealand, there exists no detailed genetic data for North American individuals. Using both molecular (i.e. *rbcL* and 18S rRNA sequences) and morphological (i.e. frustule characters and shape analysis) data, we investigated common taxa from the genus *Frustulia* in North America. European and New Zealand taxa were also included in order to study how North American species were related. We recognized nine taxa in this study including three unknowns. A new species, *F. gibsonia* sp. nov., is described. This species was found in previous studies and described as *F. cf. krammeri* based on morphology. The use of molecular characters in this study demonstrates that the group is a distinct species, not a morphotype of *F. krammeri* as was previously thought. Despite differences in phylogeny and molecular sequences, *F. gibsonia* and *F. krammeri* are quite similar morphologically, showing overlap using both traditional measurements and shape analysis. This suggests that the combination of molecular and morphological data can help in deciphering cryptic taxa. We were unable to separate *F. saxonica*, our identification of *F. crassinervia*, and *F. krammeri* based on molecular data alone, although they could be separated based on morphological characters. As evidenced by the low sequence divergence values obtained between the three taxa, they are very closely related. Future molecular research, focusing on less conserved genes, will likely be necessary to resolve the relationships of these taxonomic complexes. Alternatively, this morphological variation may be the result of phenotypic variation.