

Report by Dr. Pieter Vanormelingen of the Ph. D. thesis of Jana Veselá, entitled “Phylogenetic, morphological, and ecological context of microevolution in diatoms”

1. Overall assessment of the thesis:

The Ph. D. thesis begins with a clear introduction to diatom ecology and species diversity and delimitation. The first paper is a detailed study on the diatom communities of the Elbsandsteingebirge region based on valve morphology, including the description of a species new for science. The next chapters are dedicated to (pseudo)cryptic species delimitation using detailed morphometrics and molecular analyses, partly in combination with crossing experiments. Distributional data are also presented suggesting that the (pseudo)cryptic species identified differ in their ecology, which merits further investigation.

The thesis is well-written and obviously contains a substantial body of work on diatom ecology and species diversity, making use of a variety of different approaches (culturing, light and electron microscopy, landmark based morphometrics, molecular phylogenies, multivariate statistics...). It presents a solid contribution to our knowledge about diatom cryptic species diversity, and it is clear from her work that Drs. Veselá has gained a profound knowledge on diatom ecology and diversity. Moreover, all studies have been published or are submitted to high-rated international journals. As a result, I consider this Ph. D. thesis suitable for the defense and of a quality more than high enough to fulfill the criteria necessary for obtaining a Ph. D. degree.

2. Questions to the defendant:

Given the temporary nature of many of the headwater streams investigated in Chapter I, how important do you think habitat permanency is for determining the structure and diversity of the benthic diatom communities living in these streams, especially when compared to the importance of pH, conductivity, and nature of the substrate?

Crosses between homothallic *Navicula cryptocephala* strains in Chapter III were not successful. What do you think was the reason?

In *Frustulia rhomboides*, several varieties (*saxonica*, *crassinerva*, *rhomboides*) do not seem to correspond to the lineages outlined on the basis of LSU rDNA sequences. What is in your opinion the reason for this, are these simply different stages of the life cycle?

Why did you choose for the D1-D2 LSU rDNA region for species delimitation in *Frustulia rhomboides*? Do you think it is necessary or useful to add sequences from another (or even more than one) additional molecular marker to strengthen your conclusions?

Do you think the *Frustulia rhomboides* lineages differ in their pH preferences, given the rather wide pH range of the sites sampled?

There is an obvious congruence between valve morphology as revealed by morphometric analysis and molecular phylogenies in both the *Navicula* and *F. rhomboides* spp. studied here. Do you think it is possible to outline (pseudo)cryptic diatom species solely on the basis of morphometric analyses or can it only serve as an *a posteriori* test to see whether lineages outlined on the basis of molecular data also differ in their valve morphology?

Considering the difficulties with morphology-based species delimitation and identification, a possible solution is the use of DNA barcodes for diatom species inventories and water quality monitoring. What is in your opinion needed to develop a fully functional molecular-based monitoring of diatom communities?

Date and Signature