Supplementary Material

# Supplementary Table (excel)

# Supplementary Figures

# Supplementary Figure 1. Maximum likelihood phylogenetic trees based on 18S rRNA sequences of *Entomoneis umbratica* (MEG002). Bootstrap values below 50% were removed. Unclassified species were excluded from the BLASTn results.

# Supplementary Figure 2. Maximum likelihood phylogenetic trees based on 18S rRNA sequences of *Navicula* *avium* (MEG004). Bootstrap values below 50% were removed. Unclassified species were excluded from the BLASTn results.

**Supplementary Figure 3.** Maximum likelihood phylogenetic trees based on 18S rRNA sequences of *Pleurosigma* *inscriptura* (MEG005). Bootstrap values below 50% were removed. Unclassified species were excluded from the BLASTn results.

**Supplementary Figure 4.** Maximum likelihood phylogenetic trees based on 18S rRNA sequences of *Nitzschia* *reversa* var. *latus* (MEG012), *Nitzschia* *dissipatoides* (MEG028), and *Nitzschia* *anomalus* (MEG011). Bootstrap values below 50% were removed. Unclassified species were excluded from the BLASTn results.

**Supplementary Figure 5.** Phylogenetic tree topologies using organelle genomes at the family level.

**Supplementary Figure 6.** Phylogenetic tree topologies using organelle genomes at the order level.

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