Supplementary information captions

Evolutionary diversity eclipsed by morphological resemblance in the diatom genus *Nitzschia* Hassall (*Bacillariaceae*)

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Supplementary Table S1. Characteristics of primers used for phylogenetic studies.

Supplementary Data S2. Dataset file with accession numbers of all analysed sequences. The *New Dataset* sheet contains all accession numbers. The *Collapse…* sheets contain names of taxa included in collapsed clades on the respective phylogenetic trees for *rbc*L, *psb*C, SSU, and the 3-gene dataset.

Supplementary Data S3. Phylogeny files: ZIP archive containing sequence alignments used for molecular analyses (FASTA files), the corresponding partitioning file, and all consensus-tree (.contree) files used for phylogenetic tree visualisation. Bayesian Inference files are included only for the concatenated SSU–*rbcL–psbC* dataset. In the raw alignment and consensus-tree files, strains D.LDZ5 and D.LDZ23 retain the pre-description working label *Nitzschia* cf. archibaldii where applicable; these labels refer to *Nitzschia eclipsis* sp. nov. in this study.

Supplementary Data S4. Metadata for the 41 metabarcoding datasets screened for sequence matches to the 263-bp *rbc*L fragment of *Nitzschia eclipsis* strain D.LDZ5. The table provides the data repository, BioProject or other data-access identifier, sampled habitat, source publication, number of samples, sequencing technology and geographical origin. In total, 11,949 samples were included in the screening.

Supplementary Figure S5. LM and SEM micrographs of *Nitzschia* sp. from sample 2123 HA, Étang du Vignoble, Valenciennes, France. This material had previously been identified as N. archibaldii, but re-examination showed that it does not conform to the holotype and epitype concepts of that species; it was therefore excluded from the morphological account and epitypification. The arrow on the SEM micrograph indicates that the obliquely tapered lateral end of a girdle band is visible alongside the valve. Scale bar on LM micrographs = 10µm.

Supplementary Figure S6. Maximum Likelihood phylogenetic tree based on the *rbc*L marker. Phylogenetic tree of the *Bacillariaceae*, with *Eunotia bilunaris* UTEX FD412 used as the outgroup, inferred from plastid *rbc*L (327 sequences and 1,357 bp). The positions of the two strains of *Nitzschia eclipsis* sp. nov. are highlighted in blue. Branch support is presented in the order of maximum likelihood (ML), with values UFBoot ≥95%. Nodes with UFBoot support below 95% are not labelled. Clade 6B, following Mann et al. (2021), is indicated by the green box.

Supplementary Data S7. Alignment of the 263-bp *rbc*L fragment of *Nitzschia eclipsis* strain D.LDZ5 with environmental ASVs recovered from metabarcoding datasets. Algars_Adra_ASV5016 matches the reference fragment exactly, whereas Algars_ASV4487 and USA_ASV11090 differ by one nucleotide.

Supplementary Table S8. Comparison of *Nitzschia eclipsis* sp. nov. with *N. archibaldii* and selected morphologically related taxa within the *Lanceolatae* group.

Supplementary Figure S9. Light microscopy photomicrographs of *Nitzschia excavata* and *Nitzschia eclipsis* sp. nov. (**A–O**) Nitzschia excavata. (**P–Y**) *Nitzschia eclipsis* sp. nov. Scale bars = 10 μm.