Ripe for reassessment: a synthesis of available molecular data for the speciose diatom family Bacillariaceae

David G. Mann[1,2,*], Rosa Trobajo[1], Shinya Sato[3], Chunlian Li[4,5], Andrzej Witkowski[4], Frédéric Rimet[6], Matt P. Ashworth[7], Ruth M. Hollands[2] and Edward C. Theriot[8]

[1] *Marine and Continental Waters, Institute for Food and Agricultural Research and Technology (IRTA), Crta de Poble Nou Km 5.5, E-43540 Sant Carles de la Ràpita, Catalunya, Spain*

[2] *Royal Botanic Garden Edinburgh (RBGE), Edinburgh EH3 5LR, UK*

[3] *Fukui Prefectural University, 1-1 Gakuen-cho, Obama, Fukui 917-0003, Japan*

[4] *Institute of Marine and Environmental Sciences, University of Szczecin, and Natural Sciences Research and Educational Center, University of Szczecin, Mickiewicza 16a, PL-70-383, Szczecin, Poland*

[5] *Ecological Institute, South China Normal University, 510631, Guangzhou, China*

[6] *UMR CARRTEL, Savoie Mont-Blanc University, INRAE, 75bis avenue de Corzent, CS50511, F-74203 Thonon-les-Bains, France*

[7] *UTEX Culture Collection of Algae, Department of Molecular Biosciences, University of Texas at Austin, Austin, TX, USA*

[8] *Department of Integrative Biology, University of Texas at Austin, Austin, TX, USA*

*Corresponding author. email: dmann@rbge.org.uk

Abstract

The Bacillariaceae is a very species-rich family of raphid diatoms and includes the large and taxonomically difficult genus *Nitzschia*, whose species are often small-celled and finely structured and have few discrete morphological characters visible in the light microscope. The classification of *Nitzschia* is still mostly based on one developed in the second half of the 19th century by Grunow, who separated the genus into a series of sections largely on cell shape and symmetry, the position of the raphe, transverse extension of the fibulae, and folding of the valve. We assembled and analysed single-gene and concatenated alignments of nSSU, nLSU, *rbcL*, *psbC* and *cox1* to test Grunow's and subsequent classifications and to examine selected morphological characters for their potential to help define monophyletic groups. The maximum likelihood trees were equivocal as to monophyly of the family itself but showed good support for each of eight main clades of Bacillariaceae, three of which corresponded more or less to existing genera (*Hantzschia*, *Cylindrotheca* and *Bacillaria*). The other five main clades and some subclades comprised groups of *Nitzschia* species or assemblies of *Nitzschia* species with other genera (*Pseudo-nitzschia*, *Fragilariopsis*, *Neodenticula*, *Tryblionella*, *Psammodictyon*). Relationships between most of the eight main clades were not resolved robustly but all analyses recovered *Nitzschia* as non-monophyletic. The Grunowian classification of *Nitzschia* into sections was not supported, though in some respects (e.g. treatment of sigmoid species) it is better than subsequent reclassifications. Several of the main clades and subclades are cryptic (lacking morphological synapomorphies) and homoplasy is common in both light microscopical and ultrastructural characters (to the extent that organisms initially assigned to the same species sometimes prove to belong to a different main clade). Nevertheless, some characters, including the structure of the raphe canal and girdle, seem to be sufficiently conservative evolutionarily to give a provisional estimate of relationships if molecular data are unavailable. No new formal classifications are proposed but various options are explored and research needs identified.

Key words: diatoms; frustule morphology; girdle bands; molecular phylogenies based on nSSU, nLSU, *rbcL*, *psbC*, *cox1* markers; raphe canal; taxonomy

Abbreviations: *cox*1, mitochondrial gene encoding cytochrome *c* oxidase subunit 1; cpSSU rDNA, chloroplast small-subunit ribosomal RNA gene (chloroplast 16S rDNA); nLSU, nuclear large-subunit ribosomal RNA gene (28S rDNA); nSSU, nuclear small-subunit ribosomal RNA gene (18S rDNA); *psbC*, chloroplast gene encoding CP-43 photosystem II protein; *rbcL*, chloroplast gene encoding the large subunit of ribulose bisphosphate carboxylase–oxygenase (Rubisco)

1. Introduction

Diatoms are some of the most abundant and geochemically important organisms on earth, accounting for perhaps 20% of global photosynthetic carbon fixation (Mann, 1999) and dominating biological transformations of silicon (Conley, 1997, 2002) as a result of their use of this element to construct their unique silicified cell walls. The Bacillariaceae is a species-rich, ecologically diverse family of motile diatoms. It is ubiquitous, occurring in fresh, brackish, marine and hypersaline aquatic habitats from polar regions to the tropics (e.g. Hustedt, 1937–9; Medlin and Priddle, 1990), and inhabits sediments, periphyton and the water column; some species grow subaerially on damp rocks and soils. Several have been acquired as endosymbionts by dinoflagellates and foraminifera (e.g. Hehenberger et al., 2016; Lee et al., 2000) and some species (principally in the genus *Pseudo-nitzschia*) produce domoic acid, a toxin that causes ‘amnesic shellfish poisoning’ (Trainer et al., 2012). While most Bacillariaceae are photosynthetic, some are facultative heterotrophs (Hellebust and Lewin, 1977) and a few are obligate heterotrophs, being among the small number of diatoms that have completely lost the capacity for photosynthesis (e.g. Kamikawa et al., 2015; Onyshchenko et al., 2019; a few apochlorotic species have recently been discovered in the non-Bacillariacean genus *Tursiocola* by Frankovich et al., 2018). The biogeochemical impact of Bacillariaceae in the biosphere is considerable: for instance, a single species, *Fragilariopsis kerguelensis*, contributes most of the vast deposits of biogenic silica beneath the Southern Ocean (Zielinski and Gersonde, 1997). Historically, it is interesting that a member of the family, *Bacillaria paxillifera* (Fig. 1A), was one of the first diatoms to be given a formal name (Müller, 1786, as *Vibrio paxillifer*) and the first to be separated into a genus of its own, *Bacillaria* (by Gmelin, 1788).

Given these properties, it is perhaps surprising that the taxonomy of the Bacillariaceae is in a rather poor state, except with respect to the toxin-producing species. The main reasons for this are probably (1) the difficulty of studying Bacillariaceae species, since many are small-celled and delicately structured with few diagnostic characters that can be assessed in the light microscope (e.g. Fig. 1C); (2) the size of the group – the family contains many hundreds of species, with most currently classified in *Nitzschia*. This is a huge genus: VanLandingham (1978) could already list 690 acceptable and 250 unacceptable species names according to Mann (1986), while despite some revisions that narrow the concept of the genus, AlgaeBase currently lists 867 accepted names (Guiry, 2019); (3) the principal revisionary accounts of diatoms for the seminal *Rabenhorst Kryptogamen Flora* (Hustedt, 1927–66) never reached the Bacillariaceae.

Traditionally, a key feature of the Bacillariaceae has been the possession of a central or eccentric raphe usually raised above the rest of the valve on a ridge – referred to as the '*keel*' – and subtended internally by rib-like or more substantial bridges of silica, called *fibulae* (Fig. 1). Fibulae are also found in a few other families – the Entomoneidaceae, Auriculaceae, Rhopalodiaceae and Surirellaceae, referred to here as the EARS group – and genera (*Undatella*, *Thalassiophysa*); the EARS group were recovered as monophyletic by Ruck and Theriot (2011) and Ruck et al. (2016). Some earlier studies implied a close relationship of the EARS genera to the Bacillariaceae (e.g. Hustedt, 1930; Krammer and Lange-Bertalot, 1988). Karsten (1928) went as far as to put the surirelloid diatoms (as the 'Surirelloideae') within the Bacillariaceae (his 'Nitzschiaceae'.) However, molecular phylogenetic analyses have recovered the Bacillariaceae as separate from the EARS group, and monophyly of the keeled, fibula-bearing taxa has been statistically rejected (Ruck and Theriot, 2011), suggesting independent evolution of fibulae (see also Witkowski et al., 2015).

Within the Bacillariaceae the current classification into genera and sections is still based in many respects on one developed by Albert Grunow in the mid 19th century. In his first treatment of the Bacillariaceae, Grunow (1862) recognized five genera (*Denticula*, *Tryblionella*, *Nitzschia*, *Bacillaria* and *Homoeocladia*) and split *Nitzschia* into 10 groups (Supplementary Fig. 1), principally on the basis of valve shape (straight, bent, sigmoid, centrally constricted, etc: Fig. 1A–H) and fibula morphology (fibulae short or extended: compare Figs 1C, E with 2B). No distinction was made between apomorphic and plesiomorphic resemblance in these features. Later, in what remains the last comprehensive review of the family (Cleve and Grunow, 1880) new sections were added to those recognized previously and most of the 1862 groupings were altered (Supplementary Fig. 1). The outcome was that *Nitzschia* was split into 24 sections, using the characteristics listed in Table 1.

Note that the taxonomic distribution of many features remains unknown (Table 1), further complicating a modern understanding of the morphology. Note too that most of Grunow's sections were defined by a combination of character states, each partly shared by other sections (Table 1) rather than by putative synapomorphies, suggesting a purely phenetic classification for the most part. There were, however, a few cases (e.g. the three special features listed under 'Other' in Table 1 and some aspects of stria structure) where an individual feature appeared to be restricted to just one section and could therefore be proposed as a synapomorphy diagnostic of it. During the 160 years since Grunow established his classification, there have been several changes to it, but the overall framework remains the same (Supplementary Fig. 1). These changes have been made piecemeal and a full-scale morphological revision, while necessary to give morphological data an independent voice, will be an extensive and very time-consuming task, simply because of the large amount of comparative data that remains unknown. We therefore turn our attention to the abundance of molecular data gathered in order to attempt to frame specific questions for future research.

Many gene sequences are available for members of the Bacillariaceae, with a particular bias towards *Pseudo-nitzschia* because of the need for reliable classification and identification as a result of the toxicity of some species. Several phylogenetic studies of the Bacillariaceae have been made based on single genes and these have generally provided weak or no statistical support for most nodes (e.g., Lundholm et al., 2002a; Trobajo et al., 2009; Rimet et al., 2011; Kamikawa et al., 2015; Rovira et al., 2015; Witkowski et al., 2015; Stepanek et al., 2016; Carballeira et al., 2017). Only in a few studies have more than two genes been sequenced for the same clone (Ruck and Theriot, 2011; Witkowski et al., 2016; Ashworth et al., 2017; Kim et al., 2019; Lobban et al., 2019; Onyshchenko et al., 2019; Mucko et al., 2020, in press), but these studies and some of the single gene studies have limited taxon sampling relative to the known diversity of the Bacillariaceae. Until now, the largest single gene study had 195 (28S rDNA) and 175 (*rbcL*) non-identical Bacillariaceae sequences (Carballeira et al., 2017), and the largest three gene study had 56 sequences (though two may be identical) (Kim et al., 2019).

Here we have assembled and reanalysed existing molecular data (including 987 sequences from GenBank: Supplementary Table 1) and have also taken advantage of many new Bacillariaceae sequences (Supplementary Table 2) obtained during recent projects (including a marine benthic diatom project at Szczecin University and French and UK projects to provide barcodes for freshwater biomonitoring). The major purpose of our molecular analyses was to understand where morphology and molecules agree, at least broadly, so that attention can be focused on the most challenging and unresolved areas, and therefore the most promising areas for new insights. We also hope that, by identifying well-supported groups (either by molecular data alone or a combination of molecular and morphological data), such groups might be treated in depth in independent taxonomic revisions.

2. Materials and methods

2.1 Cultures and microscopy

Clones were isolated, grown and prepared as described in Supplementary File 1, and examined by light microscopy (LM) and scanning electron microscopy (SEM) as described by Sato et al. (2013), Rovira et al. (2015), Mann and Trobajo (2014), Witkowski et al. (2016) and Carballeira et al. (2017). Images were processed and assembled using Adobe Photoshop (Adobe CS5 Extended, version 12.0.4), with adjustments of grey levels to the whole image via the Levels and Curves tools, and sometimes also general application of Unsharp Mask or High Pass filters. To summarize girdle structure in Bacillariaceae we made photomontages rather than make line drawings. This was done by cutting, resizing and assembling fragments from several SEM photographs; images prepared in this way are clearly indicated in the figure captions. The original images used to identify clones and document their morphology (and to provide the basis for the morphological annotations in the *rbcL* tree in Fig. 4) are archived in University of Szczecin, INRAE Thonon, and the Royal Botanic Garden Edinburgh, UK. In addition, watermarked SEM images of clones isolated and grown in the Natural History Museum London, RBGE and Spain by RT, DGM, SS and Dr Laia Rovira have been made available as pdf files on the Algae World website (https://rbg-web2.rbge.org.uk/algae/research/Bacillariaceae_images.html). Voucher slides and/or material of cultures are held in the Royal Botanic Garden Edinburgh, the Thonon Culture Collection (TCC: https://www6.inrae.fr/carrtel-collection_eng/), and the University of Szczecin diatom collection; information specifying the sources of clones for newly deposited sequences is given in Supplementary File 1 (Table 1)..

2.2 Molecular phylogeny

Five markers were used: nuclear-encoded 18S rDNA (nSSU) and partial (D1/D2 or D1–D3) 28S rDNA (nLSU), choroplast-encoded *rbcL* and *psbC*, and mitochondrial *cox1* sequences

(Supplementary Tables 1, 2). Data were assembled from the following sources: (1) existing GenBank accessions (those available up to the beginning of 2018), (2) the Marine Benthic Diatom Project of Szczecin University (http://geocentrum.usz.edu.pl/en/szczecin-diatom-culture-collection-szcz/); (3) sequences obtained from the Thonon Culture Collection (TCC: Rimet et al. 2019 and see https://www6.inrae.fr/carrtel-collection_eng/) that have hitherto been available only from the online TCC database; (4) sequences obtained to support DNA-based biomonitoring of UK rivers; and (5) unpublished sequences accumulated over many years in Edinburgh by R. Trobajo, D.G. Mann, G. Simpson, L. Rovira and S. Sato, during miscellaneous studies of marine and freshwater Bacillariaceae. We only included sequences whose raw (unaligned) length was 1400 bp (SSU) or 1000 bp (*rbcL*, except KY320321, 988 bp, because of the availability of a nSSU sequence for this clone). nLSU sequences were accepted whether they included all three of the variable D1–D3 domains or only two of them, providing they were >500 bp long (except KP941049, 497 bp, because of the availability of a *cox1* sequence for the same clone). In the concatenated analyses some shorter sequences of SSU and *rbcL* were used, if the other genes' sequences met our usual criteria. All available *psbC* sequences were used: 232 sequences were over 1000 bp, 5 were over 900 bp, and one was 568 bp. Additional new sequences were obtained using the primers and protocols in Supplementary File 1. All previously unpublished sequences have been deposited in GenBank and their accession numbers are given in Supplementary Table 2.

Sequences were first aligned preliminarily using MUSCLE or Clustal and quick ML analyses were then performed using MEGA v. 6 or v. 7 (Kumar et al., 2016) to identify and assess similar sequences. To produce the most compact matrix and hence achieve faster analysis in the single-gene analyses (for which hundreds of accessions were available in the case of nSSU, *rbcL* and nLSU), sequences were removed if they were identical to others that were more complete or differed from them only in ambiguities, or apparently artefactual at the 5′ or 3′ ends. However, such 'suboptimal' sequences remained eligible for inclusion in concatenated 2- or 4-gene alignments.

For the concatenated gene analyses, sequences of different genes (*rbcL*+nSSU, *rbcL*+nLSU, *rbcL*+nSSU+nLSU+*psbC*) were almost always admitted *only* if they were obtained from the same clone, to avoid the possibility of creating chimaeric data by combining sequences from different taxa as a result of inaccurate or inconsistent identification (it became evident during our analyses that morphology-based identifications are often problematic in the Bacillariaceae). A very few exceptions to the rule were allowed, particularly in *Pseudo-nitzschia* and *Fragilariopsis*, where the species-level taxonomy is rather well understood and the sampling of diversity has been particularly intense, but where sequences for different genes are not always available for the same clone. In the 4-gene set (*rbcL*+nSSU+nLSU+*psbC*), clone data were included if data for three out of the four genes were available; those more often missing were the shorter regions, i.e. nLSU and *psbC*.

Combining existing and new sequence data, the datasets finally comprised 298 (nSSU), 279 (nLSU), 309 (*rbcL*), 119 (*psbC*), 111 (*cox1*), 188 (*rbcL*+nSSU), 163 (*rbcL*+nLSU) and 120 (*rbcL*+nSSU+nLSU+*psbC*) Bacillariaceae sequences. Outgroups added were (1) *Craspedostauros, Achnanthes* and *Staurotropis* (the CAS group), *Undatella*, and three *Amphora* species (*A. laevissima*, *A. obtusa* var. *crassa* and *A. vixvisibilis*, referred to here as '*Psammamphora*' because the dorsal positions of the chloroplasts and biarcuate raphe are reminiscent of species classified in sections *Psammamphora* or *Amblyamphora* by Cleve 1895), which are closely related to Bacillariaceae according to some recent analyses (Stepanek and Kociolek, 2014; Witkowski et al., 2016; Ashworth et al., 2017); (2) *Diploneis* and *Pleurosigma*, representing the large sister group of {Bacillariaceae+outgroup 1} in the analysis of raphid diatoms by Ashworth et al. (2017); and (3) the Eunotiales, which may be an adjacent branch to the Bacillariaceae (Theriot et al., 2015) or the sister group of all other raphid diatoms (e.g. Theriot et al., 2010; Stepanek and Kociolek, 2014; Ashworth et al., 2017). The last is consistent with the informal analysis of morphology by Round et al. (1990), dividing raphid diatoms into Eunotiophycidae and Bacillariophycidae on the basis of raphe structure. There were fewer choices of outgroup in the *cox1* analysis, because of poorer taxon sampling; for this gene, we selected two *Eunotia* sequences.

After selection, sequences of protein-coding genes (*rbcL*¸ *psbC* and *cox1*) were aligned using MUSCLE or Clustal implemented in MEGA v. 6 or v. 7 (Kumar et al., 2016). For SSU rDNA, SSU sequences were aligned by the SSUalign program (Nawrocki *et al.* 2009), with the covariance model based on the 10 diatoms included with the program download and supplemented with secondary structure models from 23 additional diatoms from the CRW website (Cannone et al., 2002). This model is available from E.C. Theriot. We employed SSUAlign's default settings for removal of problematically aligned regions (95%

Bayesian Posterior Probability of correct alignment). For nLSU, secondary structure was taken into account manually during alignment (see Supplementary file 1. The most problematic loop regions were subsequently eliminated from the alignments before analysis. The final alignments are given in Supplementary Files 2–9.

Maximum likelihood phylogenetic analysis was performed as detailed in Supplementary File 1. The names of terminals were corrected after analysis using TAXNAMECONVERT (Schmidt, 2004) and thereafter manually; trees were prepared for presentation and annotated using iTOL (Letunic and Bork, 2016; https://itol.embl.de/).

3. Results and Discussion

Phylogenetic trees of the Bacillariaceae are presented in Figs 3 and 4 and Supplementary Figs 2–7. We selected the four-gene tree (Fig. 3) and the *rbcL* tree (Fig. 4) for presentation in the main text. The four-gene tree shows very good support for eight major clades (see below); the *rbcL* tree has a much better representation of taxa and is used to explore the distribution of selected morphological characters used in traditional classifications or surveyed by SEM.

In both the four-gene tree and the *rbcL* tree (Figs 3, 4), and also in the single- and two-gene trees given in Supplementary Figs 2–7, the main clades are colour-coded to aid comparison. In addition, in the *rbcL* tree we have indicated to which Grunowian groups the taxa belong. This has been done (1) in order to help evaluate the traditional classifications of Bacillariaceae (especially the sections within *Nitzschia*) and (2) because the Grunowian groups act as proxies for the sets of traditionally used morphological characteristics evident in LM (Table 1).

3.1. Overall tree topologies

The Bacillariaceae are not monophyletic in any of the trees except *cox1*, which has the least satisfactory sampling of all the datasets (compare Supplementary Fig. 7 with Figs 3 and 4, and with Supplementary Figs 2–6). In the nSSU tree (Supplementary Fig. 4), only four sequences interfere with monophyly, namely a single sequence of *Craspedostauros alatus* (GenBank KX981860: this appears within clade 8C-I, which otherwise comprises *Fragilariopsis* sequences) and the three *Staurotropis* sequences (which branch off the Bacillariaceae close to clade 1). In the four-gene tree (Fig. 3) and *rbcL*–nSSU (Supplementary Fig. 2), the whole CAS (*Craspedostauros–Achnanthes–Staurotropis*—) group lies within the Bacillariaceae, with other non-Bacillariaceae (namely '*Psammamphora*', the three naviculoid taxa and Eunotiales) appearing as outgroups. With single-gene *rbcL* and *psbC* (Fig. 4 and Supplementary Fig. 6) the outgroup is composed almost wholly of Eunotiales, other non-Bacillariaceae being scattered among clades 1–8, though never within any of them. Thus, (1) the taxa that 'trespass' into the Bacillariaceae are not the same in the different trees, and so, not surprisingly, (2) there is no support for any node that makes the Bacillariaceae non-monophyletic.

The genus *Undatella*, which has never been included in the Bacillariaceae but possesses fibulae (Paddock and Sims, 1980), is placed within the least inclusive clade containing Bacillariaceae species in the *rbcL*, *rbcL*–nSSU and nSSU trees (Fig. 4, Supplementary Figs 2, 4); it appears to be a close relative of the Bacillariaceae and could arguably be included within the family.

The four-gene tree (Fig. 3) shows good support for **eight major clades** of Bacillariaceae (numbered 1–8 in the figures). Support values are >85% except for clade 5 (78% bootstrap) and clade 3, which comprises only a single representative of a clade sampled more extensively in the single-gene nSSU and *rbcL* analyses. There is also support (>85%: Supplementary Table 3), for 12 subclades (4A, 4B-I, 4B-II, 5A, 5B, 6A, 6B, 8A-I, 8A-II, 8B, 8C-I, 8C-II), either solely in the 4-gene tree or (for some clades represented in the 4-gene tree by only one terminal) in a combination of the 4-gene tree and one or more of the single-gene and other concatenated trees. The relationship between the eight major clades is unclear, with moderate support (>70%) only for a few nodes linking them and then only for those that separate from each other 'high' in the tree (i.e. those that probably diverged from each other most recently): there is 78% support for a sister relationship between clades 5 and 6 and 88% for one between clades 7 and 8. Clades 4–8 form a monophyletic group with 72% support. Deeper relationships are essentially unresolved. The *rbcL*–nLSU tree has a very similar topology to the four-gene tree, with good support (>70%) for all the numbered clades and subclades.

The single-gene *rbcL* (Fig. 4), nSSU, nLSU and *psbC* trees (Supplementary Figs 4–6), and the *rbcL*–nSSU and *rbcL*–nLSU trees (Supplementary Figs 2, 3) include clades that correspond to the eight major clades present in the four-gene tree (Fig. 3). However, perhaps not surprisingly, since they are based on a wider sampling of taxa, they also contain some extra well-supported clades not represented in the four-gene tree. These are clades W, X and Y in *rbcL* and *rbcL*–nSSU (Fig. 4 and Supplementary Fig. 2); B and F in nSSU (Supplementary Fig. 4), and apochlorotics-B (a clade of obligate heterotrophs) in nLSU (Supplementary Fig. 5). There are also some unsupported clades (‘groups’: Z in *rbcL* and *rbcL*–nSSU; E in nSSU) and grades (e.g. A, C and D in nSSU; V in *rbcL*). Some taxa that are included within the major clades in the four-gene tree are separated from them in individual gene trees; for example, *Tryblionella* cf. *compressa* and *Nitzschia* cf. *aequorea* are included in clade 8B in the four-gene tree (Fig. 3) but form a separate grade (‘V’) in *rbcL* (Fig. 4). *Cox1* (Supplementary Fig. 7) has been sampled less than the other genes and its dataset lacks representatives of three major clades (clades 1, 3 and 5).

In addition to all the groupings mentioned, there are a few taxa that are not clearly linked to any others in any tree. These include *Cymbellonitzschia banzuensis* (in nSSU, *rbcL* and *rbcL*–nSSU), *Nitzschia alba* (nLSU: information on this species is inevitably limited by the absence of photosynthesis genes), and the toxin-producing *N. bizertensis* (nSSU, nLSU). Dinotom sequences (*rbcL* only: Fig. 4) are scattered through clade 6B and clade W; the phylogeny suggests that at least six or seven different Bacillariaceae may have been involved in endosymbiotic events with dinoflagellates (see also Yamada et al., 2019, supplementary figure S1).

Some of the groupings present in our trees have been noted previously. Clade 8C (*Pseudo-nitzschia* and *Fragilariopsis*) was detected by Lundholm et al. (2002a, as “clade A”) in LSU phylogenies. It is also seen in the SSU phylogeny of Rimet et al. (2011), where a link between clade 8C and species belonging to clades 8B and 8A-I was also demonstrated.

3.2. Apparently misplaced taxa

In all trees there are sequences that seem misplaced, given the identifications made by their authors. We give three examples, which probably have different explanations, discussed later and in Supplementary File 10. The first is the *cox1* sequence KJ671739 of clone A2ni, which was identified as from “*Pseudo-nitzschia* sp.”. Whereas *Pseudo-nitzschia* sequences generally form a well-supported homogeneous monophyletic group (clade 8C), either alone or with

Fragilariopsis (in the nLSU tree: Supplementary Fig. 5), in the *cox1* tree (Supplementary Fig. 7) KJ671739 is placed anomalously, outside the *Pseudo-nitzschia–Fragilariopsis* clade, although GenBank BLAST of KJ671739 does indeed return *Pseudo-nitzschia* species (*P. lundholmiae*, and *P. hasleana*) as the nearest matches, though with low percent identity (c. 85%).

The second example is several sequences from a single study (Huang et al., 2017: strains Xmm11S4, Xmm20S5, Xmm16S2 and Xmm28S1), supposedly representing *N. dubiiformis*, *N. palea*, *N. capitellata* and *N. epithemioides*. Each of these species is also represented in our SSU dataset by other sequences (from other clones), none of which group with the Xmm strains. We consider that all for these Xmm clones were misidentified, since none of the photographs provided by Huang et al. show the diagnostic characteristics of the four species named.

The third example of apparently misplaced sequences is given by two of our own strains, BC0799 and TCC886. TCC886 is referred to in our trees (nSSU, *rbcL*, *rbcL*–nSSU: Fig. 4, Supplementary Figs 2, 4) as "*Nitzschia* cf. *palea*" but it was originally identified by us with LM, and also by Luc Ector (personal communication), as *N. palea*. It agrees with descriptions of *N. palea* (e.g. Krammer and Lange-Bertalot, 1988; Cantonati et al., 2017) in shape, dimensions, and stria and fibula density (Fig. 5J; compare *N. palea* in Fig. 5C–I). However, whereas other *N. palea* sequences (except the Xmm strain already mentioned) belong to one shallowly branching subclade of clade 6B, whatever the gene analysed (e.g. Figs 3, 4), TCC886 is positioned far away from clade 6B, on its own (SSU) or in an unsupported grouping ('Z') also including *N. lorenziana* (*rbcL*, *rbcL*–nSSU). Clone BC0799 (Fig. 5A, B, K) was likewise identified by us originally (by LM) as *N. palea* and, like TCC886, falls outside the main *N. palea* clade, lying within clade 6B in a very well supported subclade (100% support in both *rbcL* and *rbcL*–nLSU) containing other delicate '*Lanceolatae'* species. Although the fine striation of BC0799, which is almost unresolvable in LM (c. 47 in 10 µm) is beyond the limit given for *N. palea* in floras (Krammer and Lange-Bertalot, 1988; Cantonati et al., 2017), it is not greater than the highest densities recorded by Trobajo et al. (2009) for clones assigned to the *N. palea* complex on the basis of their gene sequences. The overall shape, fibulae and stria pattern of clone BC0799 conform to those of *N. palea* (compare Fig. 5A, B with Fig. 5C–I). The ultrastructure of BC0799 and TCC886 also agrees well with *N. palea*, with uniseriate striae, two longitudinal rows of poroids within the raphe canal (Fig. 5K–N), and an interruption of the striae at the junction between the valve face and the distal mantle (not shown).

3.3. How well do the traditional classifications of the Bacillariaceae agree with the molecular phylogenies?

The following points emerge from a comparison of the principal clades of the molecular phylogenies (see the 4-gene phylogeny in Fig. 3) with the Grunowian and other historical classifications (Fig. 4 and also Table 1, Supplementary Fig. 1):

- Clade 1 consists of *Bacillaria* sequences. However, two further sets of species identified as *Bacillaria* [the three 'Bacillaria II' sequences in nSSU (Supplementary Fig. 4), and 'cf. Bacillaria' in nSSU, *rbcL* (Fig. 4) and *rbcL*–nSSU (Supplementary Fig. 2)] lie outside clade 1, implying that *Bacillaria* is polyphyletic (but see General discussion).
- The genus *Nitzschia* is non-monophyletic. *Nitzschia* species comprise all of clades 2, 4B-II, 6, 8A, almost all of 8B, and X, and there is also a scatter of species elsewhere (Figs 3, 4, Supplementary Figs 2–7).
- Clade 2 contains the type species of *Nitzschia*, *N. sigmoidea*, and is therefore by definition 'typical' *Nitzschia*. It corresponds quite well to the group referred to earlier (by Mann, 1986) as 'subgenus *Nitzschia'*, which was characterized by the presence of flaps of silica (conopea) externally, extending out on either side of the raphe (Fig. 6A; see also Lobban et al., 2019). However, the *rbcL* tree (Fig. 4) indicates that clade 2 also includes some species (*N. alicae*, *N.* aff. *sublinearis*, *N. heufleriana*) that lack conopea and so have not previously been thought to belong to 'subgenus *Nitzschia*' (see section 3.4).
- Clades 3 and 7 correspond to the genera *Hantzschia* and *Cylindrotheca*, respectively. Three subclades, 4B-I, 8C-I and 8C-II, also correspond to genera that are currently accepted, namely *Psammodictyon*, *Fragilariopsis* and *Pseudo-nitzschia* (Figs 3 and 4). *Fragilariopsis* was recovered within *Pseudo-nitzschia* in some previous analyses based on nLSU or ITS rDNA (e.g. Lundholm et al., 2002a; Lim et al., 2018) and in our nLSU tree too (Supplementary Fig. 5), but its position there was without support and the two genera are separated in all our trees apart from nLSU.
- Only a few clades correspond to Grunowian sections. One of them that does is clade 5B (Figs 3, 4), which corresponds to Grunow's *Nitzschia* sect. *Apiculatae* (e.g. Fig. 2E), Interestingly, this section was abandoned and subsumed within an undifferentiated

section *Tryblionella* by Hustedt (e.g. 1930), which was in turn promoted to a separate genus by Round et al. (1990), who emphasized the wide and folded valves and frequently interrupted striae (Fig. 2C–E) as characteristics of the genus. Our analysis contained three further isolates that fall within the definition of *Tryblionella* by Round et al. (1990). These are *T. debilis* (*rbcL* only, Fig. 4; a valve is shown in Fig. 2C), *T. compressa* (nLSU only, Supplementary Fig. 5), and *T.* cf. *compressa* (all analyses except *cox1*: for a valve, see Fig. 2D). The relationships of *Tryblionella debilis* are unclear: if it is indeed related to *N. tubicola*, as *rbcL* suggests, *T. debilis* would belong to clade 5, like *T. apiculata, T. hungarica* and *T. gaoana*, but *Tryblionella* would nevertheless be non-monophyletic. The position is clearer with respect to *Tryblionella compressa* and *T.* cf. *compressa*, since they clearly belong to clade 8B, far from the other *Tryblionella* species in clade 5 (Figs 3, 4), despite sharing folded valves (as required for both *Tryblionella* and *Apiculatae* according to Grunow: Table 1). The modern and older definitions of *Tryblionella* therefore need to be revised.

- Most of Grunow's sections *Dubiae* and *Bilobatae* probably belong in clade 4B (Figs 3, 4), but one species, *N. umbonata*, is apparently quite unrelated (Fig. 4, where it appears in group Z), despite having an almost identically shaped valve and raphe to *N.* cf. *dubia*.
- The sigmoid *Nitzschia* species (e.g. Fig. 1G) do not constitute a monophyletic group (see, for example, the positions of taxa belonging to Grunow's *Sigmoideae*, *Sigmata* and *Obtusae* in Fig. 4) and there is therefore a conflict with the amalgamation of all into an expanded *Sigmoideae* that was made by Hustedt (1956). The sigmoid species fall into clades 2 (which contains Grunow's *Sigmoideae* species), 6A (containing Grunow's *Sigmata*) and 6B (containing Grunow's *Obtusae* but also representatives of other Grunowian sections).
- Grunow's sections *Lanceolatae*, *Lineares* and *Nitzschiella* are polyphyletic (Fig. 4). The artificiality of the *Lanceolatae* was already evident from the single-gene nSSU study by Rimet et al. (2011) but is even clearer with expanded datasets.
- The single *Denticula* species included (*D. kuetzingii*) is embedded in clade 8B, sister to *N. amphibia* (a member of Grunow's sect. *Lanceolatae*), again undermining the validity of the current concept of *Nitzschia* (Fig. 3).

3.4. Can the major molecular clades and subclades be characterized morphologically?

We have mapped some morphological features onto the *rbcL* tree (Fig. 4) in order to see whether any of them characterize the major clades and could perhaps serve for identifying taxa where molecular data cannot be obtained (e.g. in fossils or rare species). The features comprise some that are not used in traditional classifications (because they cannot be assessed in LM), such as the structure of the striae and raphe canal. In addition, of course, the Grunowian sections to which particular sequences are assigned in Fig. 4 summarize the distribution of the LM characters listed in Table 1. Wherever possible, we used information derived from the clone that was sequenced. However, it is important to have in mind that there is often little or no extra information about a clone in GenBank beyond a name and a source location and author(s); in such cases we usually used morphological information published for the species to which the sequences were assigned. Our surveys were aided by the catalogues of diatom images published by Gaul et al. (1993) and Henderson and Reimer (2003), a survey of publications since 2003, and our own data.

Inspection of the characters plotted in the *rbcL* tree (Fig. 4), either implicitly (via the characters summarized in the Grunowian classification) or explicitly, reveals the following:

- None of the eight major clades, except possibly clade 1, can be defined by even a single morphological synapomorphy. The possible exception may be the special colony type discovered in *Bacillaria paxillifera* in the 18th century and generally considered to be the defining characteristic of the genus *Bacillaria* (though not of the section *Bacillaria* within *Nitzschia* as defined by Grunow in Cleve and Grunow, 1880), but even this is not certain because of the lack of documentation for some of the clones sequenced.
- Most morphological characters show some degree of homoplasy when mapped on our molecular trees, even those that are invariable within at least one of the major clades. For example, constant hantzschioid symmetry (i.e. no nitzschioid frustules are formed) is present throughout clade 3 (corresponding more or less to the genus *Hantzschia*) but, though rare outside, it does occur in at least two other taxa in the molecular trees (*N. varelae* in clade 6B and *Cymbellonitzschia*: Fig. 4 and see also Carballeira et al., 2017, and Stepanek et al., 2016). Constant hantzschioid symmetry is also present in three species that can be assigned to clade 2 on the basis of their morphology (presence of

conopea: Mann and Trobajo, 2014). Again, since the three Grunowian groups possessing sigmoid frustules do not comprise a single clade (see above), either sigmoid shape or non-sigmoid shape or both must be homoplasious in the Bacillariaceae.

- One ultrastructural character that has until now (e.g. Mann, 1986; Mann and Trobajo, 2014; Lobban et al., 2019) appeared to be a reliable guide to relationships is the presence of external silica flaps (conopea), adjacent to the raphe. This had previously appeared to be a synapomorphy for clade 2 (which, as already noted, includes the type species of *Nitzschia*, *N. sigmoidea*: Fig. 6A) but is now revealed to have been lost in at least three species (*N. heufleriana*, *N. alicae* and *N.* aff. *sublinearis*: for SEM of the clones that we studied, see Fig. 1I and Supplementary Fig. 8; also Hlúbiková et al., 2009). Hence, the presence of conopea seems to be a sufficient basis for assigning particular Bacillariaceae to clade 2 but it is not essential for group membership.
- The presence (Fig. 2F) or absence (Fig. 2A) of central raphe endings, generally detected in LM by the presence or absence of a wider space between the central fibulae or by a very small thickening of the valve between the raphe slits (a 'central nodule'), has long been important in the taxonomy of Bacillariaceae. The first use of the character seems to have been by Grunow (in Cleve and Grunow, 1880: Table 1) and the character was also emphasized by Hustedt (e.g. 1929, 1949). Since almost all raphid diatoms outside the Bacillariaceae possess central raphe endings, their absence is presumably apomorphic in the family. The distribution of this character state (Fig. 4) indicates many independent losses of central raphe endings and sister species sometimes differ in this respect (e.g. in clade 6B, *N. capitellata* has central endings but *N. palea* does not). In contrast, central raphe endings are consistently absent, so far, in clades 1 and 2.
- The striae are similar in most Bacillariaceae, comprising single (uniseriate) lines of simple round or oval poroids, and this appears to be the ancestral condition (Fig. 4). However, clade 4B-I contains species in which the areolae are chambered ('loculate': Fig. 2F) and clades 5B and 8C have independently evolved bi- to multiseriate striae (Figs 2E, 6B; see also the single-gene SSU analysis by Rimet et al., 2011).
- Some ultrastructural characters appear to be at least as helpful as some of the LM characters used in traditional classifications, despite evidence of homoplasy. One set of underused valve characters comes from the structure of the raphe canal walls, for

example a doubling of the striae within the raphe canal (Fig. 6D, E, G; see also Trobajo et al., 2006, 2013), which in our dataset is almost restricted to clade 8A-I (Fig. 4); the exception is one species of clade 8B (*N. amphibia*: Fig. 6D). Another, though more homoplasious character is the number of longitudinal rows of areolae in the canal, which can be zero (e.g. in *Pseudo-nitzschia* and *Fragilariopsis*: Fig. 6B); consistently only one in most species of clades 8B and 8A-II (Fig. 6C) but occurring also elsewhere; one to two (e.g. in *N. palea*, Fig. 6F); strictly two, as in many of clade 8A-II and some clade 6B (Fig. 5K); through to three or more rows, e.g. in the type species of *Nitzschia*, *N. sigmoidea* (in clade 2: Fig. 6A), and *N. sigma* (in clade 6A; Fig. 6H). A difference in the number of longitudinal rows of poroids within the raphe canal appears to distinguish clade 8A-I, with two or more rows (Fig. 6E, G), from 8A-II and 8B, both with only one row (Fig. 6C, D), thus reinforcing the morphological separation between these subclades evident from the doubling of the striae within the raphe canal. The absence of poroids in the raphe canals of *Fragilariopsis* and *Pseudo-nitzschia* (noted also by Lundholm et al., 2002a) correlates with the planktonic habit of these genera, in which the raphe has lost much of its usual functional significance (raphe-associated motility requires a solid substratum to work: Edgar and Pickett-Heaps, 1983), except just after cell division in *Pseudo-nitzschia*, when the cells slide over each other after cell division to create stepped colonies. The same simplification of raphe canal structure (loss of poroids and narrowing of the canal) occurs also in some other marine planktonic species currently classified in *Nitzschia*, including *N. bicapitata*, *N. braarudii* and *N. sicula* (Hasle, 1964; see also Lundholm et al., 2002a), and is perhaps adaptive.

- Grunow's classification depended in part on fibula morphology – whether the fibulae are clearly visible or not, and if visible, whether they are extended across the valve (Fig. 2B) or not (Fig. 1J. Unfortunately, most of the species with highly extended fibulae (Grunow's sections *Perrya*, *Epithemioideae*, *Grunowia*, *Scalares*, *Insignes*, and the genus *Denticula*: Table 1), have yet to be characterized by molecular data: exceptions are *N. epithemioides* (nSSU: the species occupies a somewhat isolated position [in Group D] in Supplementary Fig. 4) and *Denticula kuetzingii* (embedded in clade 8B: Figs 3, 4). In Fig. 4 we have plotted five character states for the fibulae, based on their shape and structure, how much they extend inwards into the cell lumen (shallow vs deep) and whether they extend along the transapical ribs of the valve (the ‘interstriae’ of Ross et al., 1979). The character states are: (1) narrow, shallow, well separated, rib like fibulae (in clade 7, *Cylindrotheca*: see Reimann and Lewin, 1964; Round et al., 1990); (2) wider but shallow, solid fibulae that are not extended across the valve and whose bases are usually connected by ridges running parallel to the raphe (Figs 1J, 6B, 7A); (3) deep fibulae that are extended along one or more of the transapical ribs of the valve face but do not reach the midline of the valve (Fig. 7B); (4) deep fibulae that are extended across most or all of the valve face (Fig. 2B); and (5) shallow fibulae that are hollow and striated (because they are penetrated by poroids like those of the valve face: Fig. 7C). The distribution of these states in Fig. 4 suggests that, despite evidence of homoplasy, fibula morphology is a rather conservative character. For example, clade 4B species have type 3 fibulae, though this type is also found in other clades. In our dataset, the only species with type 5 fibulae are *Simonsenia* species and *Tryblionella debilis*. Fibula morphology thus separates *T. debilis* from the two other, unrelated groups of *Tryblionella* (the *T. apiculata* group in clade 5B and the *T. compressa* group in clade 8B), both of which have rather small solid fibulae. SEM observations of *T. gracilis* (Mann, 1978, fig. 721, as “*Nitzschia tryblionella*”) indicate that this species has somewhat similar fibulae to *T. debilis* and can be predicted to be related to it. There are also similarities between *T. debilis* fibulae and the hollow fibulae that Sims and Paddock (1982) discovered in *T. circumsuta* (classified in a different section to *T. debilis* by Grunow in Cleve and Grunow, 1880; Table 1), which they referred to as ‘fenestral fibulae’.

- Details of ornamentation support some molecular groupings that are surprising from gross morphology. For example, clade 4 includes species that have different shapes and symmetries and were consequently classified by Grunow in three different sections (*Panduriformes*, *Lineares* and *Dubiae*): this grouping was also evident in the studies by Rimet et al. (2011) and Lobban et al. (2019). Despite this, the clade 4 members studied are alike in having a dense covering of round or vermiform warts on the girdle bands and valve margin (Fig. 7D–F), which we have not found elsewhere apart from *Tryblionella apiculata* (Fig. 2E) and *T. hungarica*. The sister relationship between *Nitzschia amphibia* and *Denticula kuetzingii* is also reflected in details of ornamentation, namely the presence in both of widely spaced ‘blisters’ on the girdle bands (Fig. 7G, H); these taxa also resemble each other in possessing cribra in their poroids (e.g. Figs 6D, 7G, H).

- The girdle is rarely studied in detail in any group of diatoms and there is no documentation of its structure in most Bacillariaceae. However, our observations suggest that it may characterize particular clades. For example, all clade 8A-1 clones that we have examined (including *N. fonticola*, *N. acidoclinata*, *N. perminuta*, *N. hantzschiana*, *N. soratensis*, *N. costei*) have a complex cingulum structure in which there is a wide band 1 with a single row of small round poroids, two narrow bands (bands 2 and 3) lacking poroids, and finally a wide band 4 bearing a single row of elongate poroids (Fig. 8F, G). This structure contrasts with the examples of clade 8B that have been studied (in *Denticula kuetzingii*, *N. amphibia*, *N. inconspicua* and *Tryblionella* cf. *compressa*), where wide and narrow bands alternate (Fig. 8D, E, H, I): bands 1 and 3 are wide and bands 2 and 4 narrow. We term this a “serial repeat” girdle. Furthermore, in contrast to species of clade 8A-1 and 8B, and also *Psammodictyon constrictum* (Fig. 8J) and *Nitzschia sigma* (Fig. 8L), in all of which there are abrupt changes in band width and structure across the girdle, the girdle bands of several species in clades 1, 2, 3, 4B-IIa, and 5A change ±gradually in width and complexity from the valve outwards, from a wide band with two or more longitudinal rows of poroids next to the valve, to narrow bands with fewer rows of much smaller and more closely spaced poroids (or no poroids at all) distally. Examples are *Bacillaria paxillifera*, *N. sigmoidea*, *Hantzschia amphioxys* sensu lato and *N. linearis* (Fig. 8A–C, L).
- The principal difficulty in studying girdle structure is that the bands furthest from the valve are usually the thinnest and most delicate and the most easily lost during specimen preparation. However, even if this means that the whole of the girdle cannot be reconstructed, some useful information can often be gained from the morphology of the first band (i.e. the one closest to the valve) or bands. For example, whereas clade 8A and 8B *Nitzschia* species have a single row of poroids in band 1 or none (Figs 7D, E, 8D, E, H, I, Supplementary Fig. 9A), some (but not all) superficially similar species in clade 6B have two rows of poroids (Supplementary Fig. 9B, C). Clade 2 species also have two or more rows (Fig. 8A and see also Mann and Trobajo, 2014).

- As might be expected from the recovery of *Pseudo-nitzschia*, *Fragilariopsis* and *Psammodictyon* as well-supported monophyletic groups in at least some trees, the particular morphological characters that traditionally define them seem to be synapomorphies. These are the stepped colonies of most *Pseudo-nitzschia* species, the ribbon-like colonies of *Fragilariopsis*, and the chambered areolae (reflected in the decussate striae: Fig. 2F) of *Psammodictyon.*
- We have not made a phylogenetic analysis of 'metric' characters, i.e. the continuously varying classical features traditionally used to separate species, such as valve outline and size, and the linear densities of striae and fibulae. However, inspection of the clades suggests that, for example, clade 8A-II species and a subgroup of clade 6B (marked by an asterisk in Figs 3 and 4) are in general more finely striated (>> 30 striae in 10 μm) and delicate than 8A-I and 8B; clade 5B species, on the other hand, are coarsely structured. The evolution of size and 'delicacy' may be worth further analysis.

4. Overall discussion

4.1. Problems of GenBank sequences

The sequences in GenBank are a precious source of data, even if they are not identified beyond family or genus, and any sequences of Bacillariaceae can potentially help to detect how the group has evolved molecularly. However, taxon identifications in GenBank are not peer-reviewed but rely on the expertise of depositors and, even if identifications are correct when the sequences are submitted, they may become incorrect later, as a result of changes to the classification. Hence interpretation of molecular phylogenies based on GenBank sequences needs to be cautious, especially in a family like the Bacillariaceae, where the taxonomy is often contentious.

An example where incorrect identifications could easily have led to misleading conclusions about non-monophyly is given by some of the '*Bacillaria*' sequences in GenBank. Our nSSU, *rbcL*–nSSU, and *rbcL* trees suggest rejection of *Bacillaria* as a monophyletic group, since in each case there are one or more '*Bacillaria*' sequences outside clade 1. The clade 1 sequences in the nSSU tree comprise five isolates, all identified as *Bacillaria paxillifera* (the type species) or *Bacillaria* sp., which group with 78% support (Supplementary Fig. 4); voucher material or published photographs are available for some of these five (e.g. BAC901CAT in our collections; EW234 in An et al., 2017) and confirm the generic identifications. Three other clones (BA14c, RVSN23 and Xmm24S4) were also identified by their authors as *B. paxillifera* or *Bacillaria* cf. *paxillifera* but form a separate, though rather poorly supported (66% bootstrap) clade in the nSSU tree ('Bacillaria II' in Supplementary Fig. 4). This clade is apparently quite closely related to the clade 1 clones but does not form a monophyletic group with them, since the node linking the two *Bacillaria* clades (which has no bootstrap support) also subtends clade 2 *Nitzschia* species and some further taxa, including three non-Bacillariaceae sequences (two *Undatella* species and '*Navicula pulchripora*'). However, none of the three 'Bacillaria II' clones can be confirmed as belonging to *Bacillaria* as this genus is currently defined. We had the opportunity to check the identity of clone BA14c (generously shared with us by Dr F. Pniewski) and found that, while it does indeed possess a more-or-less central raphe like typical *Bacillaria* species, it does not form the characteristic motile colonies of the genus and it differs from *B. paxillifera* in fibula structure. The identities of the other two nSSU sequences of 'Bacillaria II' are also doubtful and are discussed, together with the Xmm clones of the four species mentioned earlier (section 3.2: *N. dubiiformis*, *N. palea*, *N. capitellata* and *N. epithemioides*) in Supplementary file 10.

Such examples, and the '*Pseudo-nitzschia*' clone A2ni mentioned in section 2.2, show the need for careful evaluation of the identifications assigned to GenBank sequences and in some cases the accuracy of the sequence itself (for example, whether a protein-coding sequence is implausible because of indels or 'wrong' amino-acids or extra stop codons). We refer to these two checks as 'curation' of the sequences, following e.g. del Campo et al. (2018) and Rimet et al. (2019). Curation is especially important for nSSU, which was the first DNA marker to be used for microalgal classification (e.g. Medlin et al., 1988). From this 'head start', and because a few small hypervariable regions within the gene (e.g. the V4 and V9 regions) often discriminate between closely related species (e.g. Zimmermann et al., 2011), nSSU has become a favoured "barcode" marker for metabarcoding (e.g. Piredda et al., 2018) and also still provides the largest single set of diatom sequences for phylogenetic analysis. However, the demonstrated utility of nSSU has also meant that it is often used to document clones isolated by laboratories that do not specialize in identifying diatoms and other protists (in contrast to *rbcL*, *psbC*, and nLSU sequences, which have mostly been generated by laboratories with considerable experience in diatom taxonomy), resulting in many errors of identification. Hence nSSU sequences often need to be checked, including examination of voucher material, if this still exists, or photographs. The bonus of doing this is that, at the same time, data can be gathered for formal analysis of morphology, to determine which, if any, morphological features are shared by the members of monophyletic molecular groups.

4.2. Options for a revision of the Bacillariaceae

Although *Nitzschia* is very clearly paraphyletic (consistent with previous findings, e.g. by Lundholm et al., 2002a; Rimet et al., 2011; Stepanek et al., 2016; Lobban et al., 2019; Mucko et al., 2020, in press), we consider that it would be premature to suggest formal changes to the genera, subgenera and sections of the Bacillariaceae until :

1. there has been further opportunity to check (curate) the sequences already available, to minimize misidentifications. Curation of *rbcL* sequences is already undertaken annually to incorporate new GenBank accessions into the Diat.barcode database (Rimet et al., 2019), though this exercise is arguably more rigorous for freshwater diatoms, given the primary use of Diat.barcode to support to river biomonitoring through metabarcoding. No formal mechanisms currently exist, as far as we know, for curating nSSU, nLSU and *psbC* sequences.
2. there has been a more comprehensive sampling of the diversity present within the Bacillariaceae. Our *rbcL* and nSSU trees each contain c. 300 unique sequences, but some of these represent multiple samplings of the same morphospecies and the total number of species sequenced for any gene is still far from the 867 “accepted” species names in *Nitzschia* according to AlgaeBase (Guiry, 2019). Sampling of the family is therefore still sparse. Furthermore, the full morphological diversity of *Nitzschia* has not yet been sampled either molecularly or morphologically: many characters remain poorly studied across a range of taxa and six of the 24 morphology-based sections created by Grunow (*Pseudotryblionella*, *Circumsutae*, *Insignes*, *Scalares*, *Perrya* and *Pseudoamphiprora*) are unrepresented in any of our trees. All six are marine or brackish groups and some are very rare: *Perrya* and *Pseudoamphiprora* species have probably never been seen alive.

3. several existing, valid genus names in the Bacillariaceae (some created many years ago but often neglected and rarely used) have been typified, because some of these names may be available for some of the potential splits of the family identified below. Examples are *Zotheca* (Pantocsek, 1902) and *Grunowia* (Rabenhorst, 1864). No type has been designated for *Zotheca* but among the species included by Pantocsek is one – *Z. punctata* – that is probably related to our *T.* cf. *compressa* and *Tryblionella compressa*; the genus name might therefore be available for clade 8B. For *Grunowia*, a type has been designated and this is *G. sinuata* (basionym *Denticula sinuata*), currently treated as *Nitzschia sinuata*. The girdle structure of *N. sinuata* (Mann, 1978, fig. 790) corresponds to that present in clade 8A-I, suggesting *Grunowia* might be available for this group, but so far there are no sequences for any gene in *N. sinuata*. Other potentially useful names are *Pritchardia* Rabenhorst (1864), *Perrya* Kitton (1874), and several recently described splits for which there are no molecular data (Supplementary Fig. 1). Finally, the name *Nitzschiella,* as well as being the name Grunow gave to one of his sections, is also available at generic level (Rabenhorst, 1864) and, depending on how it is lectotypified, could be available for either clade 4A (if typified with *N. longissima*) or clade 6 or 6B (if typified with *N. acicularis*). We recommend making it available for clade 6 or 6B, since the species related to *N. acicularis* (e.g. *N. palea*, *N. paleacea, N. capitellata*) are quintessential *Nitzschia* species for many people (lightly silicified and delicate valves, with very few morphological features to characterize them in LM) and the name *Nitzschiella* (=‘little *Nitzschia*’) seems appropriate.
4. it has been decided whether *Craspedostauros*, *Achnanthes* and *Staurotropis* (hereafter the ‘CAS genera’) belong in the Bacillariaceae or not. The molecular data are currently equivocal because of the lack of support for the basal nodes of the trees and we cannot detect any morphological character that unambiguously supports evolution of the CAS genera from fibulate Bacillariaceae. The pore occlusions of CAS genera are cribra and volae (Round et al., 1990, Cox, 1999; Ashworth et al., 2017), rather than the fine sieve-like structures (hymenes: Supplementary Fig. 9D–F) present in Bacillariaceae, and no CAS species have fibulae. The possession of two chloroplasts positioned fore and aft in most CAS cells is shared with Bacillariaceae, but it does not

> discriminate between the possibilities of CAS being part of the ingroup or instead a closely related outgroup. One intriguing similarity between the Bacillariaceae and the CAS genus *Achnanthes* is that the silica deposition vesicle, containing the nascent valve, is moved bodily across the cell during valve formation (Pickett-Heaps et al., 1990), so that the sternum or raphe-sternum lies on one side of the valve rather than centrally. However, this does not happen in all CAS genera (the raphe is central in *Craspedostauros* and *Staurotropis*). Overall, there are as yet no strong arguments against the monophyly of the fibulate Bacillariaceae from molecular or morphological data, and one argument for it (possession of fibulae!). We therefore consider that it is unproven, and on balance unlikely, that the CAS genera belong within the Bacillariaceae, but this need to be tested further by deeper sampling of the genome (for instance using whole chloroplast genomes) and formal analysis of CAS and Bacillariaceae morphology.

The programme of work outlined above is unlikely to be completed quickly. However, although we do not make any formal proposals for a new classification here, we can identify some of the constraints that should apply during any future taxonomic revision. One is stability of names. In their analysis of Surirellales and Rhopalodiales, in which they showed that several existing genera were not monophyletic, Ruck et al. (2016) noted that “non-monophyly at the genus level requires decisions and trade-offs that balance sinking some generic names into others, or creating (sometimes many) new names” and they set a “goal of retaining as many old names as possible.” We agree with this approach. In the Bacillariaceae, however, minimizing name changes will be particularly problematic, because *Nitzschia* species are distributed among several major (=speciose) clades. In Table 2 we summarize a few of the ways in which the Bacillariaceae could be revised. The options given (A–D) all assume that the topology of the 4-gene tree of Bacillariaceae, except for the position of the CAS genera, will be confirmed by further sampling of taxa and genes.

- Option A: This is the most extreme option and would combine all Bacillariaceae into one genus and attempt to conserve the name *Nitzschia* against the earlier *Bacillaria*. If this was done, the majority of names in the Bacillariaceae would remain as they are now because, compared to *Nitzschia* (with its 867 accepted species names: Guiry, 2019), the other genera of Bacillariaceae are all relatively small (even *Pseudo-nitzschia* and *Hantzschia*, with c. 60 and c. 100 species respectively: op. cit.). The advantages of option A would be (1) that there would have to be a relatively small number of new names to accommodate other Bacillariaceae in *Nitzschia* (and in fact many *Pseudo-nitzschia* species already have names in *Nitzschia*) and (2) a simple morphological definition of the genus – a combination of fibulate raphe system, fore-and-aft chloroplasts, and hymenate pore occlusions would characterize the vast majority of species (Fig. 1, 9D–F). However, option A would create an even larger *Nitzschia* than the monster it already is and would lead eventually, given the likely increase of species numbers through discovery and revision (cf. Mann and Vanormelingen, 2013), to a genus containing several thousand species. This would make *Nitzschia* one of the largest genera of photosynthetic eukaryotes (even now, only 22 genera of angiosperms contain more species than *Nitzschia*: Frodin, 2004). Further disadvantages would be the loss of several accepted genera – *Bacillaria*, *Pseudo-nitzschia*, *Fragilariopsis*, *Psammodictyon*, *Simonsenia*, *Cylindrotheca* and *Hantzschia* – which form well-supported monophyletic groups with morphological autapomorphies and, in several cases, somewhat similar ecology. Altering the status of *Pseudo-nitzschia* in particular would be very disruptive because of its importance in causing harmful algal blooms and hence an enormous body of research literature ‘tied’ to the name.

- Option B represents another way to avoid extensive reassignment of existing *Nitzschia* species to other genera. It is predicated on *Bacillaria* being a basal branch off the Bacillariaceae phylogeny, as several of our trees indicate. This would again require the abandonment of most genera of the Bacillariaceae.
- Options C and D achieve a conciliation with the molecular data by erecting new genera (or resurrecting and redefining old names) for some of the clades or subclades. Option C would probably be the worst of the four we identify in Table 2, since it would neither avoid the extensive renaming of *Nitzschia* species, nor maintain the current concepts of *Pseudo-nitzschia* and *Psammodictyon*.
- Option D would maintain currently recognized genera, including *Pseudo-nitzschia* and *Fragilariopsis*, but would require drastic changes in *Nitzschia* itself. It would also require major redefinition of *Tryblionella* (restricting this to the *Apiculatae* of Grunow) and of

Denticula, which could perhaps be used for clade 8B. It should be remembered too that the number of generic groupings listed for option D is a minimum, since the better sampled single-gene trees (SSU and *rbcL*) suggest the existence of several further near-basal branches, e.g. 'group Z' in the *rbcL* tree (comprising *N. umbonata*, *N. lorenziana* and *N.* cf. *palea* TCC886: Fig. 4 and Supplementary Fig. 2), and '*Bacillaria* sp.' SH349.These groups, like *Cymbellonitzschia*, may not contain many species, although very recently Mucko et al. (2020, in press) have described a new species (*Nitzschia inordinata*) that is related to '*Bacillaria*' SH349. The two species have a similar valve and raphe structure (our unpublished data for SH349) but *N. inordinata* has sigmoid frustules (SH349 is straight: An et al. 2017).

Kociolek and Williams (2015) suggested that diatomists have been overcautious in erecting new genera, noting that 64000 fish taxa are grouped into 12000 genera, whereas roughly the same number of diatom taxa are grouped into only 1200 genera. This comparison is arguably not a good basis for guiding taxonomic decisions in diatoms, because in fish there are many easily recognizable morphological characteristics available for classification and identification (see also below, 'Cryptic clades'). Nevertheless, we do favour splitting *Nitzschia* (e.g. option D), despite the large number of new nomenclatural combinations it will require, because it will allow long-established genera, such as *Pseudo-nitzschia*, *Fragilariopsis*, *Cylindrotheca* and *Hantzschia*, to be retained. In addition, although the new genera required (to accommodate each of clades 4A, 4B-II, 5A, 6 and 8A or 8A-I and 8A-II, and other groupings for which there is as yet limited or no robust support) may not possess any morphological synapomorphies, they may in time be found to possess unique features of primary or secondary metabolism, once it becomes routine to determine the metabolome of isolates or to estimate metabolic potential from genomes.

4.3. A strategy for a future revision

Obtaining representatives of the unsampled morphological groups. The obvious next step towards revising the Bacillariaceae is to isolate and sequence members of unsampled morphological groups. As mentioned previously, these include Grunow's sections *Circumsutae*, *Pseudotryblionella*, *Pseudo-amphiprora*, *Perrya*, *Scalares* and *Insignes*, which are predominantly marine or brackish epipelic diatoms. Other sections that are rather poorly sampled include *Tryblionella* and *Grunowia* as defined by Grunow, and there is a general problem, that tropical diversity has been sampled much less than temperate diversity.

Sampling hidden diversity. Choosing clones for sequencing based only on morphology will likely miss significant aspects of biodiversity in the Bacillariaceae. This is illustrated by the example given in section 3.2, concerning morphological similarities in LM and SEM (Fig. 5) between *Nitzschia palea sensu stricto* (clade 6B), *N.* cf. *palea* BC0799 (clade 6B, but outside *N. palea sensu stricto*) and *N.* cf. *palea* clone TCC886 (group Z in *rbcL* and *rbcL*–SSU), or between the different lineages of "*N. inconspicua*", which is a paraphyletic 'species' (Rovira et al., 2015, confirmed by the present paper: Figs 3, 4). Or again, it is unlikely that it could ever have been suspected from morphology *Nitzschia umbonata* branches from a deep node of the Bacillariaceae (Fig. 4): *N. umbonata* has been an unquestioned member of the *Dubiae* group from 1880 onwards (Cleve and Grunow, 1880, as *N. thermalis;* Krammer and Lange-Bertalot, 1988), but in the *rbcL* tree other *Dubiae* belong far from *N. umbonata*, in clade 4B. In this respect, metabarcoding (increasingly used for biomonitoring and biodiversity surveys) may be helpful, by identifying unexpected diversity and discovering localities for targeted isolation and sequencing.

Markers to be sequenced. The lack of robust support for any of the basal nodes within the Bacillariaceae, even in the four-gene analysis, suggests that a wider sampling of the genome may be needed before the deeper relationships can be established. Other chloroplast genes (*psaA*, *psaB*, *psbA*, and *atpB*) have phylogenetic information profiles much more closely resembling that of *rbcL* and *psbC*, suggesting that the plastome should be explored further as a source of the necessary data (Theriot et al., 2015). *Within* each of the main clades (i.e. in each of the genera and putative genera in option D of Table 2) the present range of genes may be sufficient to solve most taxonomic problems. Indeed, the *rbcL*+nLSU combination seems to approach the four-gene set in terms of resolution and support and could be an economic way to characterize and place new isolates. The use of nSSU needs comment: while providing some information on species-level discrimination (hence its value as a barcode marker for broad characterizations of eukaryote diversity), nSSU has very low *phylogenetic* signal over the entire length of the sequence (especially when compared to *psbC* and *rbcL* sequences) across the entire diatom tree, especially for closely related diatoms; its main attractive property as a phylogenetic (rather than barcode) marker is that phylogenetic signal rises slowly and steadily to deeper reaches in the tree

(Theriot et al., 2015). Conversely, *psbC* and *rbcL* have a great amount of phylogenetic signal across the diatom tree, especially towards the tips of the tree (Theriot et al., 2015).

Morphological characterization. In itself, a well-supported molecular phylogeny is not particularly informative, unless the focus of the study is how genes evolve. In most cases, what makes a phylogeny interesting is what it implies about how the properties of the organisms have evolved – their morphology, ecology, metabolism, etc – but, as we have already noted, for many of the sequences in Bacillariaceae in GenBank, there is little information about the diatom from which they were obtained, apart from a species or genus name. It is important, therefore, that new sequences for phylogeny reconstruction are accompanied by ancillary data on organisms' properties, including as full a documentation as possible of morphology. For the Bacillariaceae it would be helpful to expand the list of characters that diatomists routinely survey. In particular, our data (e.g. Figs 4, 6–8) suggest that details of the raphe canal and the structure of the girdle deserve more attention.

To that end, we advocate reconsideration of all morphological features of these diatoms from a phylogenetic perspective. That is, we advocate that those attempting phylogenetics of these diatoms cautiously abandon traditional views of characters. For example, shape is not a single character, but is a compilation of curvatures along the length of the frustule. Many features should be re-examined from the simple perspective that similarity is sufficient to propose homology, to be tested against congruence among characters (Patterson, 1988). Where this approach has been taken in the Bacillariaceae (in admittedly a very limited attempt), the results have been surprisingly congruent (Lobban et al., 2019). It has also produced reasonably congruent results in the EARS group (Ruck and Kociolek, 2005; Ruck and Theriot, 2011; Ruck et al., 2016). Among *Aulacoseira* species, a combination of molecular data, qualitative morphological data, and quantitative morphological data often complemented, rather than conflicted with each other (Edgar and Theriot, 2004). The utility of morphometric data in Bacillariaceae phylogeny has not yet been explored.

4.4. Cryptic clades

Having drawn attention earlier to what we believe are promising new sources of morphological data (section 3.4), we note that, for several of the major clades (2, 4, 5, 6 and 8) and subclades

(4B, 6B, 8A and 8B) within the Bacillariaceae, there seem to be no morphological characters that are common to *all* the known members of the group and absent in all other groups. In some of these clades, however, particular morphological characters are present in *most* of the species included and are found nowhere else (i.e. they are most likely to be derived characters), but they have apparently been lost or modified secondarily in a few. Examples are clades 2 (the presence of conopea characterizes most members but *N. sublinearis*, *N. alicae* and *N. heufleriana* have apparently lost them) and subclade 8C-II (almost all 8C-II species form stepped colonies but *Pseudo-nitzschia americana* does not: Lundholm et al., 2002b). In other clades or subclades (4, 4B, 5, 6, 6B, 8A, 8B), however, the prevalent valve morphology and life-form do not separate the clade from other clades and there is no evidence that any morphological synapomorphy has ever been present: the clade is ‘cryptic’.

Cryptic clades have also been reported in groups that are much more character-rich than diatoms (e.g. in Leguminosae and Rhamnaceae within the angiosperms: Wojciechowski et al., 1993; Richardson et al., 2000), though diligent study sometimes reveals that some initially ‘cryptic’ clades do in fact possess morphological or anatomical apomorphies. For example, Pennington and Gemeinholzer (2000) discovered new fruit-wall characters that separated some, though not all, of the clades of *Andira* species (Leguminosae) that had previously seemed to be cryptic. Such discoveries are less likely in diatoms and other unicellular organisms because of the much more limited list of morphological characters that are available. Indeed, in the Bacillariaceae, the only potentially *rich* source of characters that has not been fully tapped is the girdle: our observations suggest that girdle characters may help define and characterize some clades and subclades (for example, clade 8A-I), but there is as yet too little information to be sure. If future studies confirm that many Bacillariaceae clades are indeed cryptic, it will imply that any ‘key innovations’ they possess (a key innovation being “a trait … that provides access to novel resources and that, as a result, facilitates an increase in the total diversification (species richness) of the parent clade”: Rabosky, 2017) are physiological or biochemical, not morphological. An example of such a clade may be the heterotrophic *Nitzschia* species, which are morphologically diverse but may have a single origin (Onyshchenko et al., 2019).

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Appendix. Supplementary material

Supplementary Table 1. GenBank accessions used to construct the 4-, 2- and single-gene trees.

Supplementary Table 2. New sequences obtained for the present study.

Supplementary Table 3. Bootstrap support values for the main clades and subclades of Bacillariaceae in the concatenated and single-gene trees.

Supplementary Fig. 1. Changes in the generic and sectional classification of the Bacillariaceae. The classification of Bacillariaceae has developed in a complex way over more than 200 years. We show only the principal changes and have structured the diagram to show the classification as it existed at four dates: (1) the first formal classification of the Bacillariaceae by Grunow (1862, as the 'Nitzschieae'); (2) the revised system that Grunow developed for his monograph of the family in 1880 (in Cleve and Grunow, 1880); (3) the classification as it existed by Hustedt's death in 1967; and (4) an estimate of the current state (incorporating the infrageneric groupings of Krammer and Lange-Bertalot, 1988, generic changes made by Round et al., 1990, and new genera proposed by various authors since the introduction of scanning electron microscopy). Genera are shown in capitals; sections within *Nitzschia* are shown in lower case type. The date of erection of each genus is given at the first time of mention and entirely fossil genera have been omitted. The order in which the *Nitzschia* sections are listed corresponds closely to the order in Grunow's 1880 monograph (in Cleve and Grunow, 1880), but some adjustments have been made to make the diagram less cluttered.

Supplementary Fig. 2. Maximum likelihood phylogenetic tree of Bacillariaceae from a concatenated *rbcL*–SSU dataset, with bootstrap supports >70% indicated as grey spots of varying diameter.

Supplementary Fig. 3. Maximum likelihood phylogenetic tree of Bacillariaceae from a concatenated *rbcL*–LSU dataset.

Supplementary Fig. 4. Maximum likelihood phylogenetic tree of Bacillariaceae from a single-gene SSU dataset.

Supplementary Fig. 5. Maximum likelihood phylogenetic tree of Bacillariaceae from a single-gene partial LSU dataset. Apochlorotic species shown white on black.

Supplementary Fig. 6. Maximum likelihood phylogenetic tree of Bacillariaceae from a single-gene *psbC* dataset.

Supplementary Fig. 7. Maximum likelihood phylogenetic tree of Bacillariaceae from a single-gene *cox1* dataset. Apochlorotic species shown white on black.

Supplementary Fig. 8. Non-conopeate species belonging to clade 2 according to the *rbcL* dataset (Fig. 4), SEM. A, B. *Nitzschia heufleriana*, clone BC0307: fractured valve (A), seen with the proximal mantle uppermost (right), and exterior of valve face (B). C. *Nitzschia alicae*, clone BC0330: exterior of valve face. D. *Nitzschia* aff. *sublinearis*, clone BC0850: exterior of valve face. Scale bars = 1 µm.

Supplementary Fig. 9. Girdle band and poroid structure in Bacillariaceae, specimens tilted 25°, SEM (except D, TEM). A. *Nitzschia* cf. *aequorea*, clone NIT1004CAT (clade 8): band 1 (valvocopula) with a single row of poroids (arrow). B. *Nitzschia* cf. *lembiformis*, clone R2 (clade 6B): band 1 with two rows of poroids (arrow). C. *Nitzschia* sp., clone BC0317 (clade 6B): band 1 with two rows of poroids (arrow). D. *Fragilariopsis* sp.: hymenes with pores in a hexagonal array. E. *Nitzschia heufleriana*: hymenes with pores in a hexagonal array. F. *Nitzschia draveillensis*: hymenes with pores in a regular scatter (sensu Mann 1981). Scale bars = 1 µm (A, B), 500 nm (C) or 100 nm (E, F).

Supplementary File 1. Methods for isolation, culturing, DNA extraction and sequencing, and table of metadata for clones sequenced for the present paper.

Supplementary File 2. Alignment of sequences in 4-gene dataset.

Supplementary File 3. Alignment of sequences in *rbcL*–SSU dataset.

Supplementary File 4. Alignment of sequences in *rbcL*–LSU dataset.

Supplementary File 5. Alignment of sequences in *rbcL* dataset.

Supplementary File 6. Alignment of sequences in SSU dataset.

Supplementary File 7. Alignment of sequences in LSU dataset.

Supplementary File 8. Alignment of sequences in *psbC* dataset.

Supplementary File 9. Alignment of sequences in *cox1* dataset.

Supplementary File 10. Analysis and discussion of some apparently misidentified species.

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Table 1. The characters used by Grunow (in Cleve and Grunow, 1880) to distinguish 24 sections of *Nitzschia*. Each section had a unique combination of character states, though very few individual character states were restricted to a single section and there was no attempt to distinguish between plesiomorphic and apomorphic states. A key to the character states is given below. In many cases (indicated by ("?") Grunow did not comment about the character state for a particular section; this was probably because the character state was implicit (e.g. frustules that are not sigmoid, nor curved, nor asymmetrical are straight), or because the character did not help to distinguish that section from otherwise similar groups. The colours have no significance except to help make the pattern of variation more obvious.

Key to character states:

Keel: +++ = strongly eccentric; ++ = eccentric; + = slightly eccentric; 0 = central; 0* = central and sharply angled (vaulted) at the raphe.

Longitudinal fold: **yes** = present (strongly or weakly developed); **no** = absent (explicitly stated by Grunow); ? = not specified.

Symmetry: **sigmoid**, **asymmetrical**, straight, or curved (the last only in *Nitzschiella*: information comes from Grunow's species descriptions rather than in the group description). In the case of sections with 'straight' cells, Grunow did not specify that they were straight, but this can be inferred from the absence of other indications.

Central constriction of the outline: ++ = strongly developed; + = slightly developed or with only a central nick along one margin; absent; ? = not specified.

Fibulae: ++++ = some fibulae extended across the whole width of the valve; +++ = fibulae strongly extended transapically, but not reaching the distal margin; +++* = fibulae appearing as dashed or dotted transapical lines; ++ = fibulae somewhat extended transapically; + = fibulae clearly visible; i = fibulae indistinctly visible; i/+ = fibulae indistinctly visible or clearly visible.

Central nodule: **yes** = present; **no** = absent; [no] = absence noted for one of the two species included but no information given for the other; ? = not specified.

Striae: **decussate** (the areolae forming diagonal as well as transapical rows); **continuous** (striae continuous across the valve); **interrupted** (striae interrupted or less noticeable along a longitudinal fold); fine (striae particularly difficult to resolve or invisible); **speckled** = valve surface with irregularly scattered dots ("unregelmässig punktirter Oberfläche": Grunow in Cleve and Grunow, 1880, p. 77) as well as fine striae.

Other: **X** = keel (raphe) accompanied by parallel lines, one on either side; **Y** = raphe deflected towards the distal side at the centre; **Z** = valves with long narrow extensions

	Keel position	Longitudinal fold	Shape/Symmetry	Central constriction	Fibula morphology	Central nodule	Striae	Other
Tryblionella	+++	**yes**	straight	?	i	?	?	
Panduriformes	+++	**yes**	straight	++	i/+	?	**decussate**	
Apiculatae	+++	**yes**	straight	absent/+	i/+	?	**interrupted**	
Pseudo-tryblionella	+++	**yes**	straight	?	+	?	**continuous**	
Circumsutae	+++	**yes**	straight	?	+	**yes**	**speckled**	
Dubiae	++	**no**	straight	+/++	?	?	?	
Bilobatae	+	**no**	straight	+/++	?	?	?	
Pseudo-amphiprora	**0***	**no**	straight	++	+	**yes**	?	
Perrya	**0***	?	straight	absent	**++/+++***	[no]	?	
Epithemioideae	+++	?	straight	?	**++++**	?	?	
Grunowia	+++	?	straight	?	**+++**	?	?	
Scalares	++	?	straight	?	**+++**	?	?	
Insignes	+	?	sigmoid/straight	?	**+++**	?	?	
Bacillaria	**0**	?	straight	?	+	?	?	
Vivaces	++	?	**asymmetrical**	absent	+	**no**	?	
Spathulatae	**0**	?	sigmoid/straight	?	?	**no**	**fine**	**X**
Dissipatae	+	?	straight	?	?	**no**	**fine**	
Sigmoideae	**0**	**no**	**sigmoid**	?	+	**no**	?	
Sigmata	++	**no**	**sigmoid**	?	+	**no**	?	
Obtusae	+++	?	**sigmoid**	?	+	**yes**	?	**Y**
Spectabiles	+++	**no**	**asymmetrical**	?	++	?	?	
Lineares	++	**no**	straight	absent/+	+	?	?	
Lanceolatae	+++	**no**	straight	?	+	?	?	
Nitzschiella	+++	?	straight/curved	?	?	?	?	**Z**

Table 2. Some possible ways (options A–D) to revise the Bacillariaceae to create monophyletic genera, based on the main clades in the 4-gene and *rbcL* molecular phylogenies (Figs 3 and 4). The single and two-gene trees suggest the existence of several further clades that would need to be classified as separate genera in options C and D. The genera considered here are those whose relationship seems well established from the molecular data (i.e. either there is strong support in one or more molecular tree). Excluded from the Table are the genera that have not yet been sequenced (e.g. *Gomphonitzschia*, *Gomphotheca*, *Alveus*, *Giffenia*). These comprise few species and so will have little impact on nomenclature, whether they are maintained or sunk into larger groupings. Also excluded are a few genera (e.g. *Simonsenia*, *Cymbellonitzschia*) for which molecular data exist but whose positions are unclear and which may lie outside the eight main clades.

Bold type indicates a genus that would retain more or less the same circumscription in that particular revision (A–D) as it currently has (cf. Round et al. 1990); non-bold type indicates a genus that would differ very substantially from the present concept, in both definition and content.

Molecular clades (Figs 3 and 4)	**A**	**B**	**C**	**D**
clade 1	*Nitzschia*[1]	***Bacillaria***	***Bacillaria***	***Bacillaria***
clade 2		*Nitzschia*	*Nitzschia*	*Nitzschia*
clade 3			***Hantzschia***	***Hantzschia***
clade 4A			NEW[2]	NEW?[2]
clade 4B-I			*Psammodictyon*	***Psammodictyon***
clade 4B-II				NEW
clade 5A			*Tryblionella*[3]	NEW
clade 5B				*Tryblionella*[3]
clade 6A			*Nitzschiella?*[2]	NEW
clade 6B				*Nitzschiella?*[2]
clade 7			***Cylindrotheca***	***Cylindrotheca***
clade 8A-I			NEW	NEW
clade 8A-II				NEW
clade 8B			*Denticula*[3]	*Denticula*[3]
clade 8C-I			*Pseudo-nitzschia*	***Fragilariopsis***
clade 8C-II				***Pseudo-nitzschia***

[1] Given the impact on names, it seems likely that the International Botanical Congress would accept conservation of *Nitzschia* against the earlier *Bacillaria*, if there was a consensus among diatomists that a single genus was the best option.

[2] *Nitzschiella* has not been typified. It was described by Rabenhorst (1864), who included in it species belonging to clades 4A, 6B, and 7. If it is typified with *N. acicularis*, the name could be available for clade 6 or subclade 6B; if typified with *N. longissima* it could be available for clade 4A. However, either possibility will require the type material of each species to be studied in detail to confirm that it is consistent with the current usage of the name.

[3] Any plausible use of the names *Denticula* and *Tryblionella* in a revised classification will require a major change in the circumscription of the genus.

Figure captions

Fig. 1. Bacillariaceae. A. *Bacillaria paxillifera*, SEM: the valve (in internal valve view) is straight and has an almost central raphe system. B. *Nitzschia dubia*, clone TA37: straight valve with constricted centre (white arrow), where the central raphe endings are located. C. *Nitzschia pusilla*, clone BC0333, LM. The only features visible are the linear-lanceolate outline and the line of fibulae along one side of the valve. D, E. *Nitzschia pusilla*, clone BC0333, external and internal views, SEM. The raphe is strongly eccentric and lies on a distinct raised 'keel' (arrow in D), subtended internally by fibulae (E). SEM reveals the delicate uniseriate striae of tiny round poroids. F–H. Living cells of *Tryblionella apiculata* (F), *Nitzschia flexa* (G) and *Cylindrotheca closterium* with two chloroplasts, one towards each end of the cell ('fore and aft' arrangement), with the nucleus lying in between. I. *Nitzschia heufleriana*, clone BC0307: fractured specimen tilted 55° illustrating aspects of valve structure in Bacillariaceae, SEM. Beneath the raphe slit (white arrow) is a cylindrical raphe canal (rc) subtended internally by fibulae (e.g. f). The valve face (vf) and the deep proximal mantle (pm) lie at an acute angle to each other, forming a vault with the raphe canal at its apex; the raphe and raphe canal form the 'keel' of the valve. On the far side from the raphe and proximal mantle there is a much shallower distal mantle (dm). The raphe canal wall (rcw) bears a single row of poroids (e.g. black arrows) linking the raphe canal to the exterior. J. *Nitzschia pusilla*, clone BC0333: fractured valve, seen from the inside, SEM. The raphe canal is separated from the valve face (vf) by a line of fibulae (e.g. arrows). Scale bars 5 μm (A, B, F–H) or 1 μm (C–E, I, G).

Fig. 2. Bacillariaceae valve morphology (including features used by Grunow in his classification of 1880), SEM. A. *Nitzschia* cf. *perminuta*: the raphe lacks a central nodule, running uninterrupted from one pole to the other; note also that the valve face is flat. B. *Nitzschia disputata*: fibulae extended transapically across the valve face (contrast Fig. 1E, I). C. *Tryblionella debilis*, clone BC0502: the valve face of the wide valve is undulate transapically and the striae are interrupted by a plain axial area (white arrow). Note also that there is a marginal ridge (black arrow) on the side opposite the raphe. D. *Tryblionella* cf. *compressa*, clone NIT1007CAT: valve face undulate as in *T. debilis* but without a plain area; again, a marginal ridge is present (black arrow). E. *Tryblionella apiculata*, clone s0863: centre of valve, distal aspect,

showing the folded valve face, including a plain axial area (white arrow) interrupting the multiseriate striae, and a very shallow marginal ridge (black arrow). F. *Psammodictyon constrictum*: detail of valve centre, proximal aspect, showing central raphe endings, folded (undulate) valve face, and chambered (loculate) areolae in the distal part of the valve face, creating transapical and diagonally orientated (decussate) striae. Scale bars = 2 µm.

Fig. 3. Maximum-likelihood four-gene (SSU, LSU, *rbcL* and *psbC*) phylogeny of Bacillariaceae, with bootstrap supports >70% indicated as grey spots of varying diameter: the widest diameter indicates 100%. A. Eight main, well supported clades of Bacillariaceae are evident, numbered 1 to 8. An asterisk within clade 6B marks a subclade of species referred to in the text (section 3.4, last paragraph), with particularly delicate, fine structure. B. The existing genera of Bacillariaceae (colour shading) are shown on the tree. *Nitzschia* (pale blue) is paraphyletic with respect to all other genera except *Bacillaria*, while one group of nonfibulate diatoms (the CAS genera *Craspedostauros*, *Achnanthes* and *Staurotropis*) are apparently nested within the Bacillariaceae. However, there is no support for any of the basal nodes.

Fig. 4. Maximum-likelihood *rbcL* phylogeny of Bacillariaceae, with bootstrap supports >70% indicated as grey spots of varying diameter: the widest diameter indicates 100%. The eight main clades of the 4-gene tree are coloured as in Fig. 3 and the asterisk in clade 6B marks the same subclade of finely structured species as is identified in Fig. 3. In addition, the Grunowian section or genus is given for each terminal taxon (which therefore also indicates the distributions of the characters listed in Table 1) and the distributions of selected characters are plotted in concentric circles around the tree: the legends for each concentric ring are given, in centrifugal order (A–E). Genera that postdate Grunow's classification are indicated by square brackets. Original images supporting morphological data for many of our own clones (Supplementary Table 2) are available at https://rbg-web2.rbge.org.uk/algae/research/Bacillariaceae_images.html .

Fig. 5. *Nitzschia palea* and *palea*-like species. A–I, valves in valve view, LM, all to the same scale. A, B. *Nitzschia* cf. *palea*, clone BC0799. C, D. *Nitzschia palea*, clone BC0605: note the difference in the appearance and density of the fibulae in these two specimens. E–I. *Nitzschia palea*, clones BC0786, BC0375, BC0670, BC0373 and BC0234, respectively. J. *Nitzschia* cf. *palea*, clone TCC886. K–N. Valve exterior near

the centre, SEM. K. *Nitzschia* cf. *palea*, clone BC0799, with two longitudinal rows of poroids in the raphe canal. L. *Nitzschia palea*, clone India, also with two longitudinal rows of poroids in the raphe canal. M. *Nitzschia palea*, clone Belgium 2, mostly with one poroid in the raphe canal opposite each valve face stria, but occasionally with two (arrows). N. *Nitzschia* cf. *palea*, clone TCC886, with one or two poroids in the raphe canal opposite each valve face stria. Scale bars = 5 µm (A–J) or 500 nm (K–N).

Fig. 6. Raphe canal structure and porosity in Bacillariaceae. A, B, broken valves, C–H, intact valves in external view, tilted 25° (except A). A. *Nitzschia sigmoidea*, clone BC0787: the raphe canal bears several longitudinal rows of poroids (black and white arrowheads) and is accompanied on either side by a plain silica flap, the 'conopeum' (arrow; contrast *N. heufleriana*, Fig. 1G). B. *Pseudo-nitzschia multiseries*, with multiseriate striae and a nonporous raphe canal (arrow). C. *Nitzschia inconspicua*, with a single longitudinal row of poroids in the raphe canal, one for each uniseriate transapical stria. D. *Nitzschia amphibia*, clone BC0503, with a single longitudinal row of poroids in the raphe canal, but with two poroids opposite each valve face stria. Note also the cribra in the poroids. E. *Nitzschia* cf. *perminuta*, with two longitudinal rows of poroids, the one further from the raphe with a single poroid opposite each valve face stria (white arrow), the one nearer the raphe with two (black arrow); i.e. at this position each stria is biseriate. F. *Nitzschia palea*, clone Brazil, mostly with a single poroid in the raphe canal opposite each valve face stria, but sometimes with two (arrows). G. *Nitzschia* cf. *romana*, clone BC0650, with biseriate transapical striae within in the raphe canal, the poroids here being arranged in three ill-defined longitudinal rows. H. *Nitzschia* cf. *sigma*, clone NIT1013ABR, with c. 4–5 raphe canal poroids opposite each valve face stria. Scale bars = 500 nm, except A, 5 µm.

Fig. 7. Fibulae and external ornamentation, SEM; specimens tilted 25°. A–C. The fibula morphologies plotted in Fig. 4. A. *Nitzschia* cf. *microcephala*, clone L56, with short shallow fibulae (linked by a slight longitudinal ridge). B. *Nitzschia linearis*, clone BC0083: fibulae extended along the transapical ribs of the valve face (see also Fig. 2B). C. *Tryblionella debilis*, clone BC0502, specimen fractured through one of the broad fibulae: the valve striae continue onto and across the fibulae. D–H. External ornamentation in clade 4B. D. *Nitzschia linearis*, clone BC0273 (clade 4B-Iia): distal mantle with small round warts and band 1 with vermiform markings. E. *Psammodictyon constrictum* (clade 4B-I): centre of epitheca showing all bands

covered with small round warts. F. *Nitzschia* sp., clone s0819 (clade 4B-IIa), with small round warts on the girdle bands. G. *Nitzschia amphibia*, clone BC0486: sparse warts (e.g. arrows) on bands 1 and 3 (cf. Fig. 4D). H. *Denticula kuetzingii*, sparse warts on bands 1 and 3. Scale bars = 1 µm.

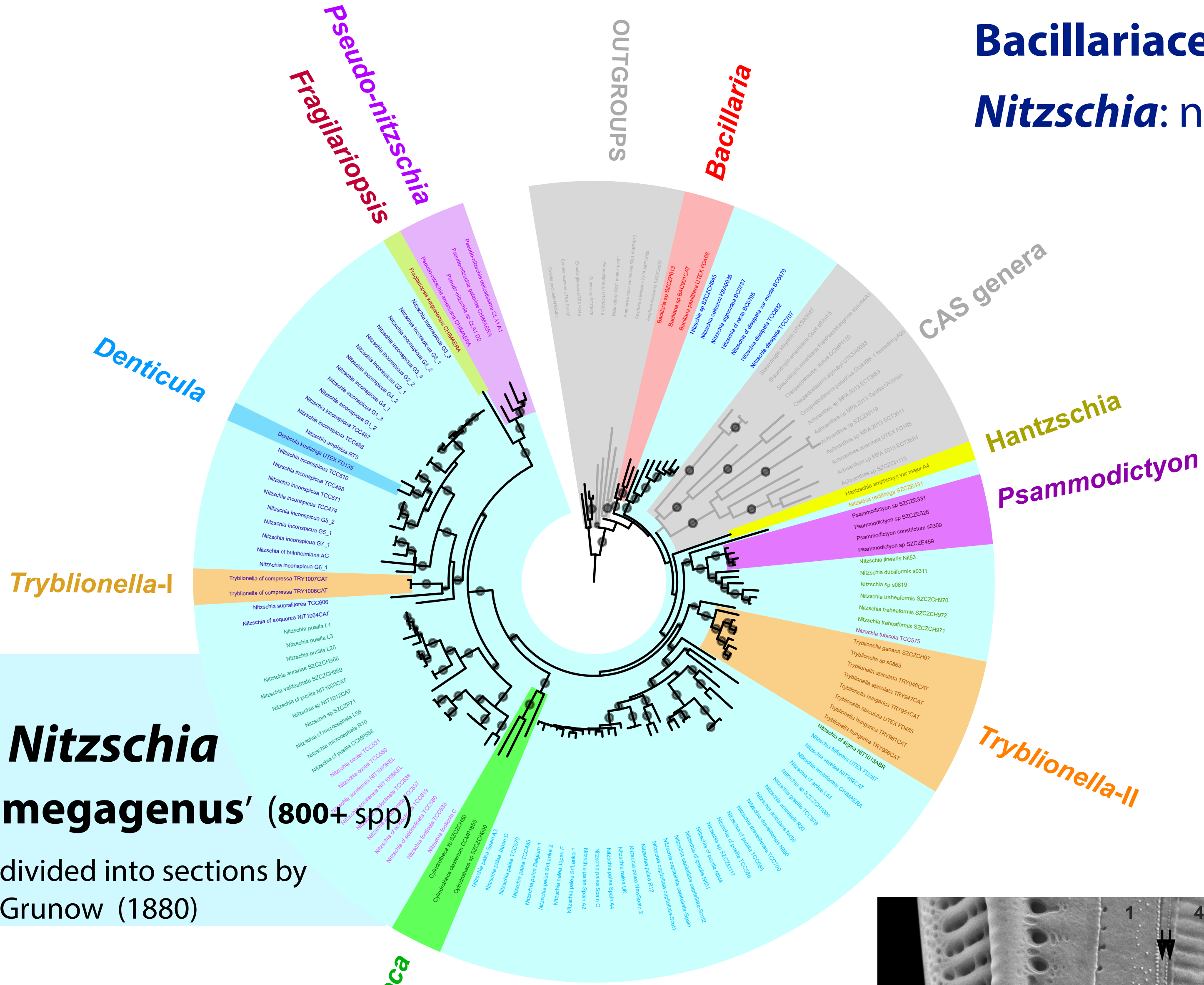
Fig. 8. Girdle structure of selected Bacillariaceae; each image is a photomontage (hence no scale bars are given), created by cropping SEM photos to isolate the epitheca, adjusting dimensions to compensate for tilt in the original photograph, and reorientating to promote comparability; the original photographs are available from the corresponding author on request but are included in the sets at https://rbg-web2.rbge.org.uk/algae/research/Bacillariaceae_images.html. A. *Nitzschia sigmoidea*, clone BC0787, with five graded, porose bands. B. *Nitzschia linearis*, clone BC0083, with five or six graded bands (the more advalvar have a single row of poroids, often hidden by the adjacent band). C. *Bacillaria paxillifera,* clone BAC901CAT, with five ±graded porose bands. D. *Nitzschia amphibia*, Bristol 138 material, with a 'serial repeat' girdle: bands 1 and 3 are wide (band 1 with a single line of poroids), 2 and 4 (arrows) very narrow. E. *Denticula kuetzingii*, also with a 'serial repeat girdle: bands 1 (nonporous) and 3 wide, 2 and 4 (arrows) very narrow. F. *Nitzschia soratensis*, with a complex girdle: bands 1 and 4 are wide, each with a single row of round poroids; bands 2 and 3 (arrows), nonporous and narrow. G. *Nitzschia* cf. *fonticola*, clone NIT337TM: girdle as in *N. soratensis*, except that band 4 bears strongly elongate poroids. H. *Nitzschia inconspicua*, clone L62, with serial repeat girdle (cf. D, E). I. *Nitzschia* cf. *microcephala*, clone L56, with serial repeat girdle in which band 3 is scarcely wider than band 2. J. *Psammodictyon constrictum*: complex girdle with several ranks of poroids on band 1, which is much wider than the others, and a line of smaller elongate poroids on band 5. K. *Nitzschia sigma*, complex girdle, with a wide band 1 with a single row of poroids, graded nonporous bands 2–4 (4 arrowed), and a wide band 5 with a single row of elongate poroids. L. *Hantzschia amphioxys* agg. (modified from Mann, 1978, fig. 640), with a graded girdle of mostly porous bands (band 7 arrowed).

rbcL, *psbC*, nLSU, nSSU, *cox1*

Diatoms:

Bacillariaceae: 8 major clades

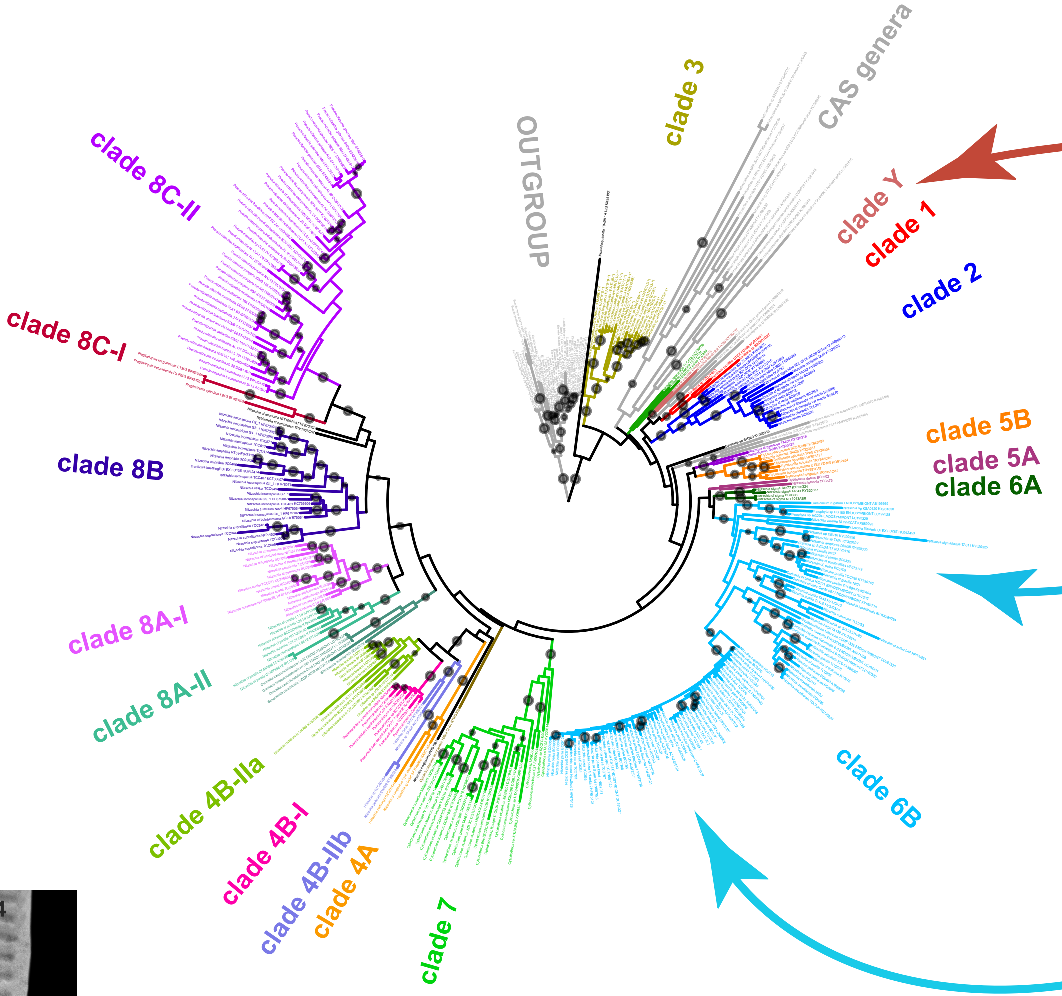
Nitzschia: non-monophyletic

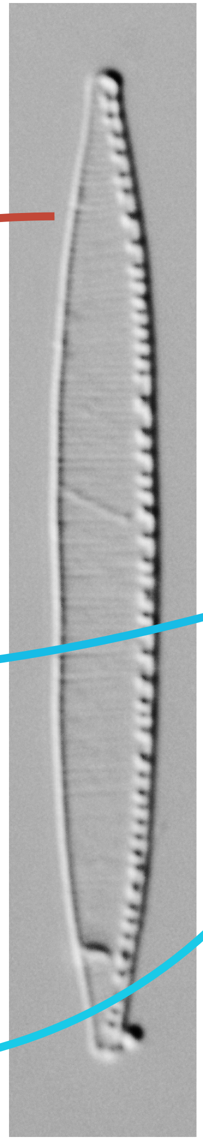


Nitzschia

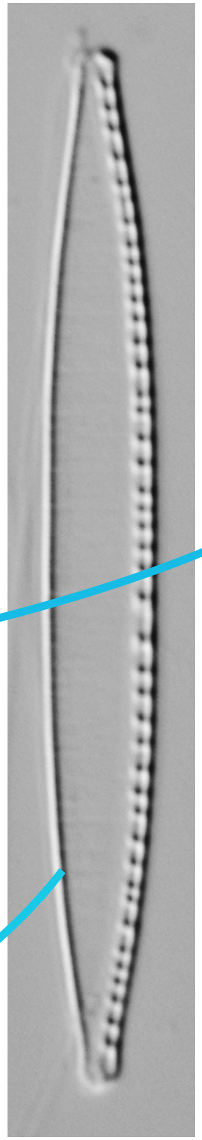
'megagenus' **(800+ spp)**

divided into sections by
Grunow (1880)

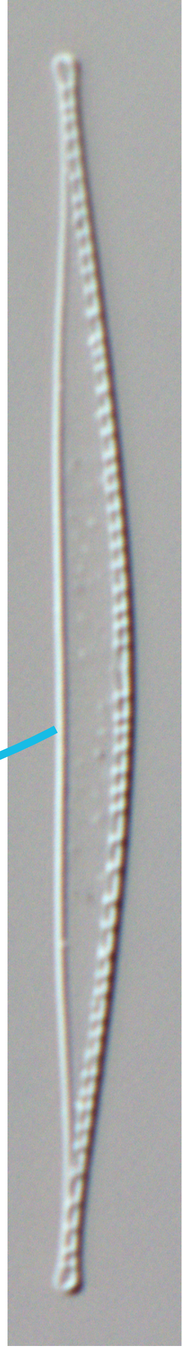




Nitzschia cf. *palea*
clade Y



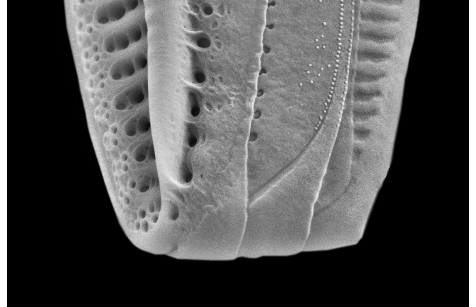
Nitzschia palea
clade 6B



Nitzschia varelae
clade 6B

several clades are 'cryptic'

no morphological synapomorphies

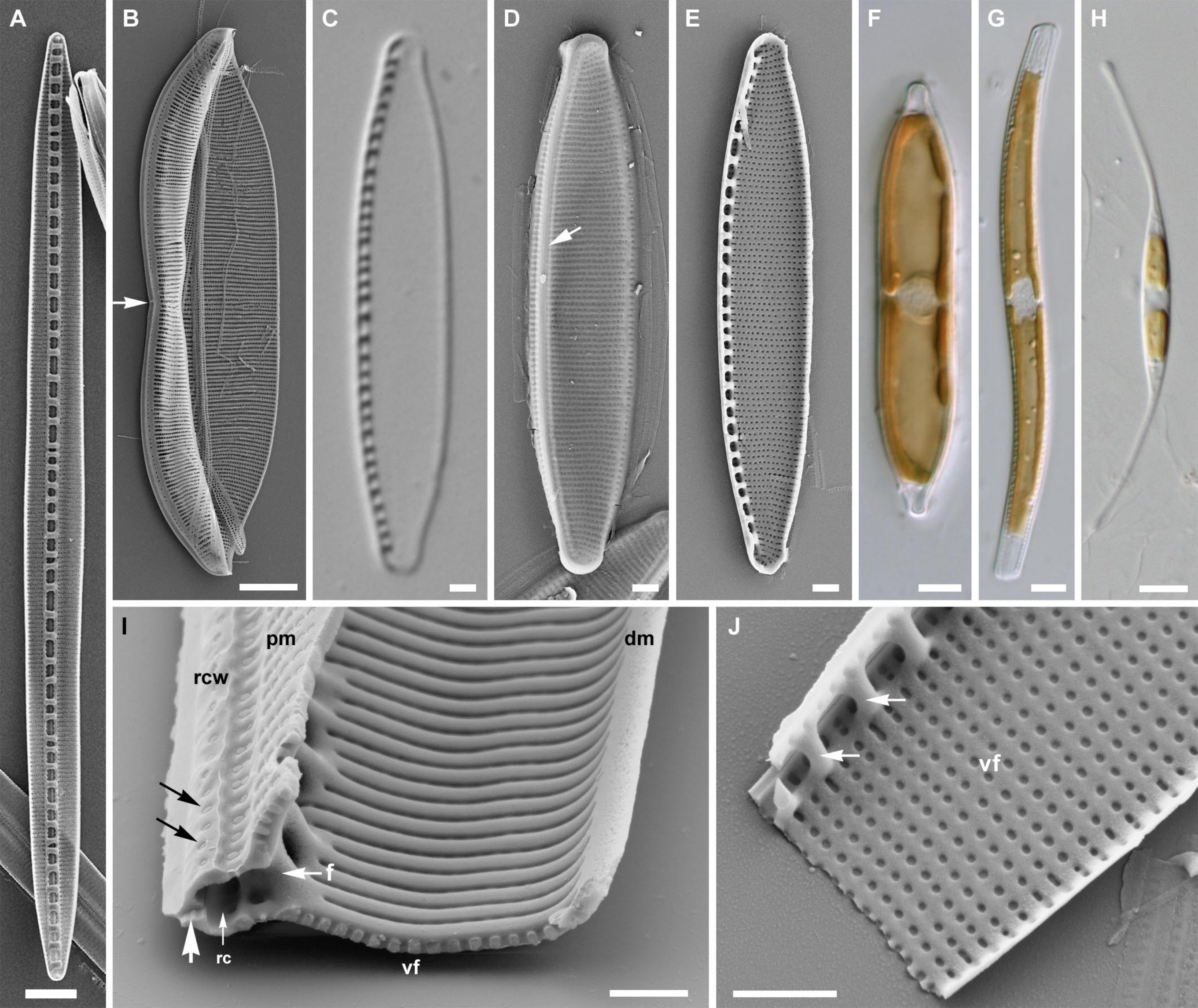


some new SEM characters useful,

e.g. girdle structure

Highlights

- First multigene phylogeny of Bacillariaceae
- Major conflicts with existing morphology-based classification
- Non-monophyly of the most speciose diatom genus, *Nitzschia*
- Several major clades are ‘cryptic’
- Options discussed for achieving a comprehensive new classification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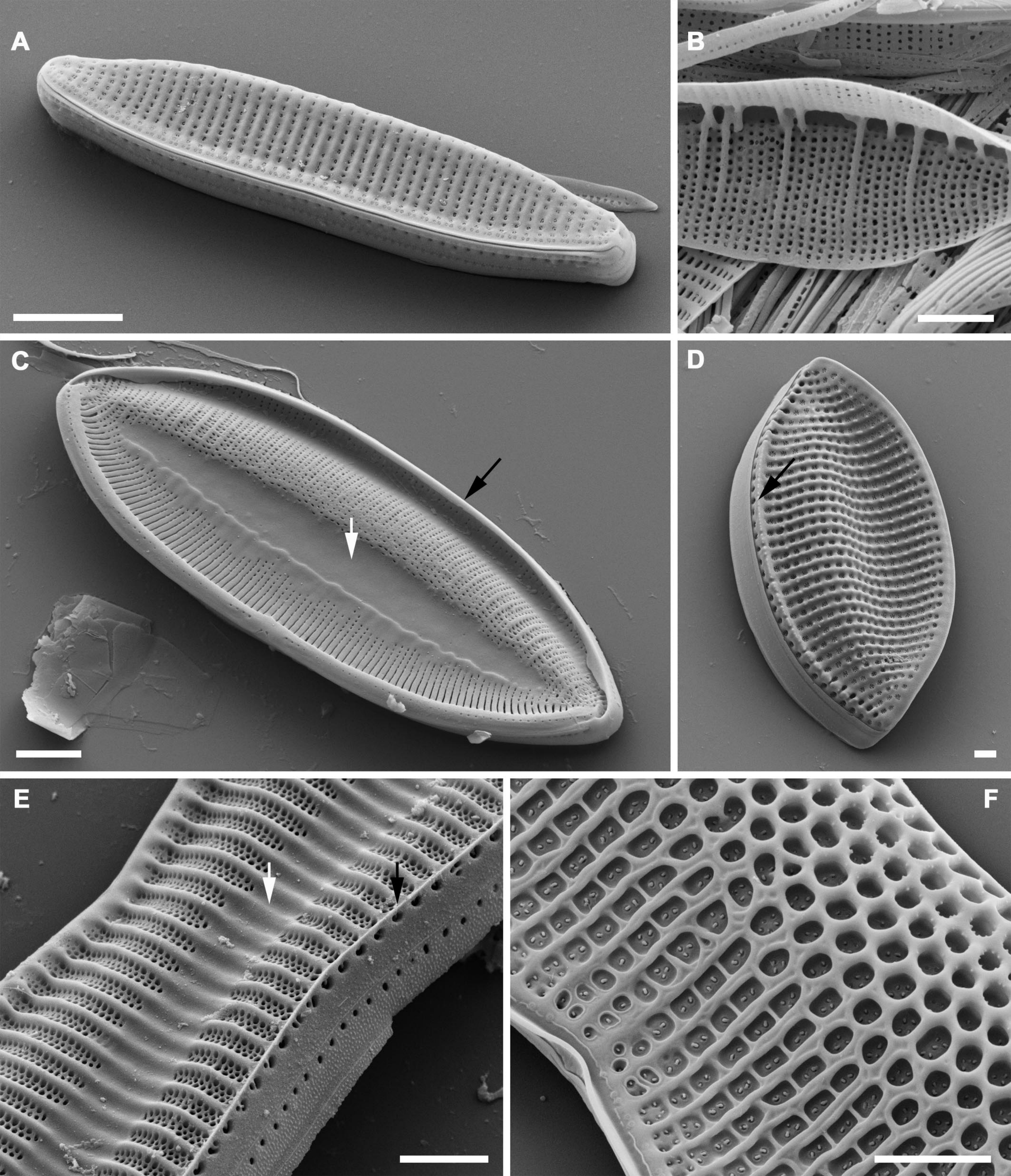
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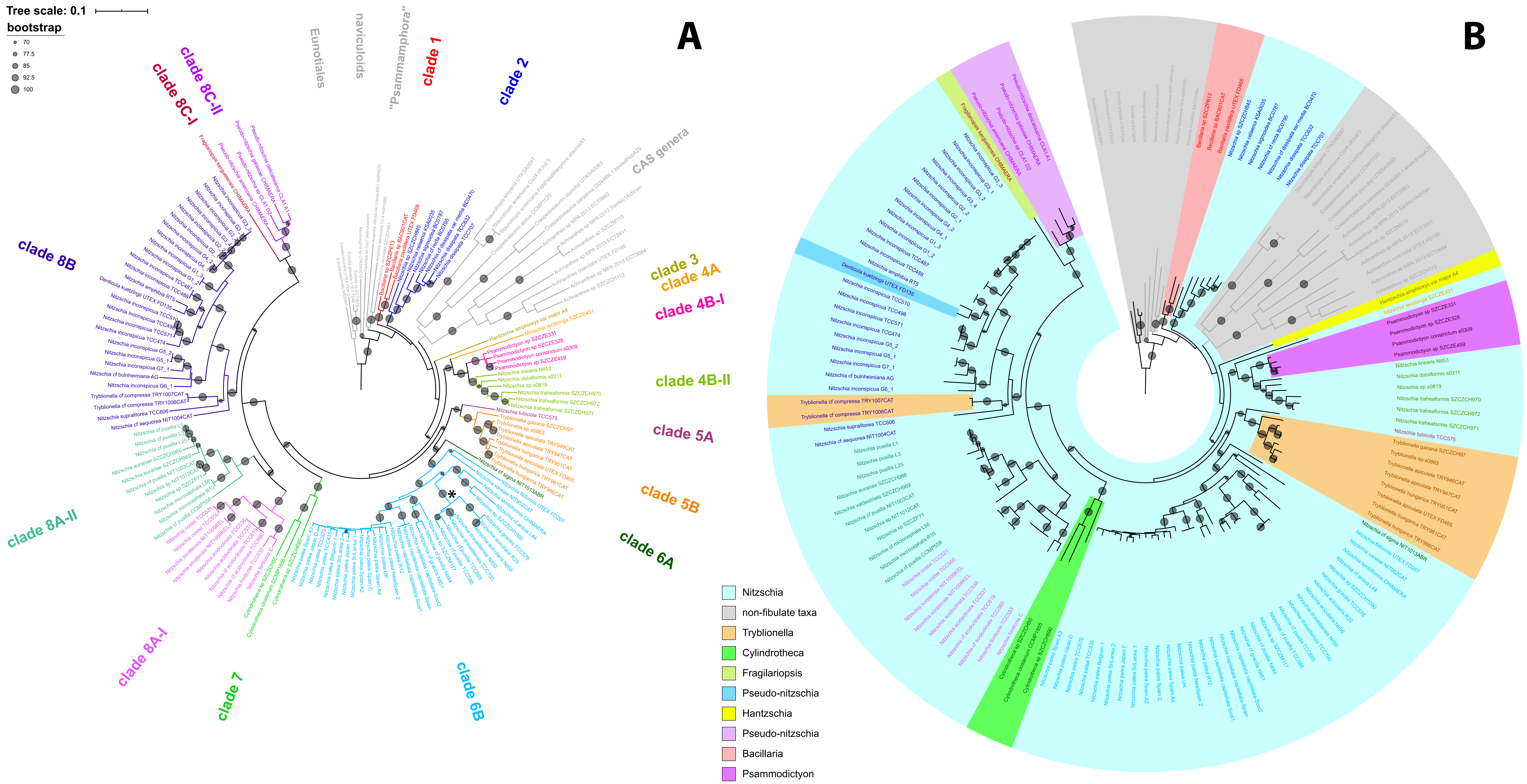
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Eunotiales
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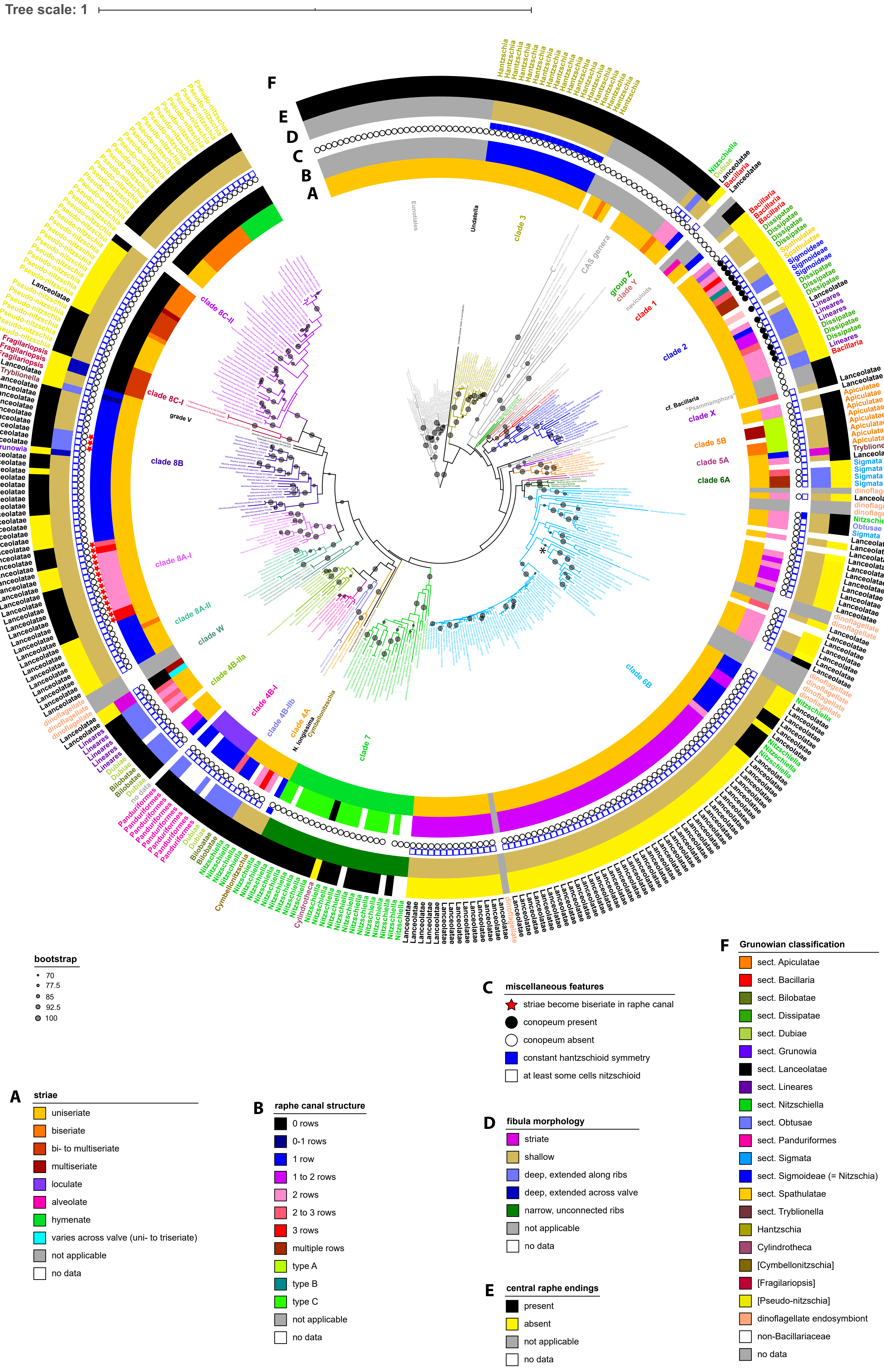
CAS genera
clade 3
clade 4A
clade 4B-I
clade 4B-II
clade 5A
clade 5B
clade 6A
clade 6B
clade 7
clade 8A-I
clade 8A-II
clade 8B
clade 8C-I
clade 8C-II
*
🟦 Nitzschia
⬜ non-fibulate taxa
🟧 Tryblionella
🟩 Cylindrotheca
🟩 Fragilariopsis
🟦 Pseudo-nitzschia
🟨 Hantzschia
🟪 Pseudo-nitzschia
🟥 Bacillaria
🟪 Psammodictyon

Tree scale: 1
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cf. Bacillaria
"Psammamphora"
clade X
clade 5B
clade 5A
clade 6A
clade 6B
clade 7
Cymbellonitzschia
N. longissima
clade 4A
clade 4B-IIb
clade 4B-I
clade 4B-IIa
clade W
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clade 8B
grade V
clade 8C-I
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Hantzschia
Pseudo-nitzschia
Fragilariopsis
Tryblionella
Lanceolatae
Grunowia
Bacillaria
Dissipatae
Spathulatae
Sigmoideae
Lineares
Apiculatae
Sigmata
dinoflagellate
Nitzschiella
Obtusae
Lanceolatae?
Dubiae
Bilobatae
no data
Panduriformes
Cylindrotheca
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77.5
85
92.5
100
A
striae
uniseriate
biseriate
bi- to multiseriate
multiseriate
loculate
alveolate
hymenate
varies across valve (uni- to triseriate)
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raphe canal structure
0 rows
0-1 rows
1 row
1 to 2 rows
2 rows
2 to 3 rows
3 rows
multiple rows
type A
type B
type C
not applicable
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C
miscellaneous features
striae become biseriate in raphe canal
conopeum present
conopeum absent
constant hantzschioid symmetry
at least some cells nitzschioid
D
fibula morphology
striate
shallow
deep, extended along ribs
deep, extended across valve
narrow, unconnected ribs
not applicable
no data
E
central raphe endings
present
absent
not applicable
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F
Grunowian classification
sect. Apiculatae
sect. Bacillaria
sect. Bilobatae
sect. Dissipatae
sect. Dubiae
sect. Grunowia
sect. Lanceolatae
sect. Lineares
sect. Nitzschiella
sect. Obtusae
sect. Panduriformes
sect. Sigmata
sect. Sigmoideae (= Nitzschia)
sect. Spathulatae
sect. Tryblionella
Hantzschia
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non-Bacillariaceae
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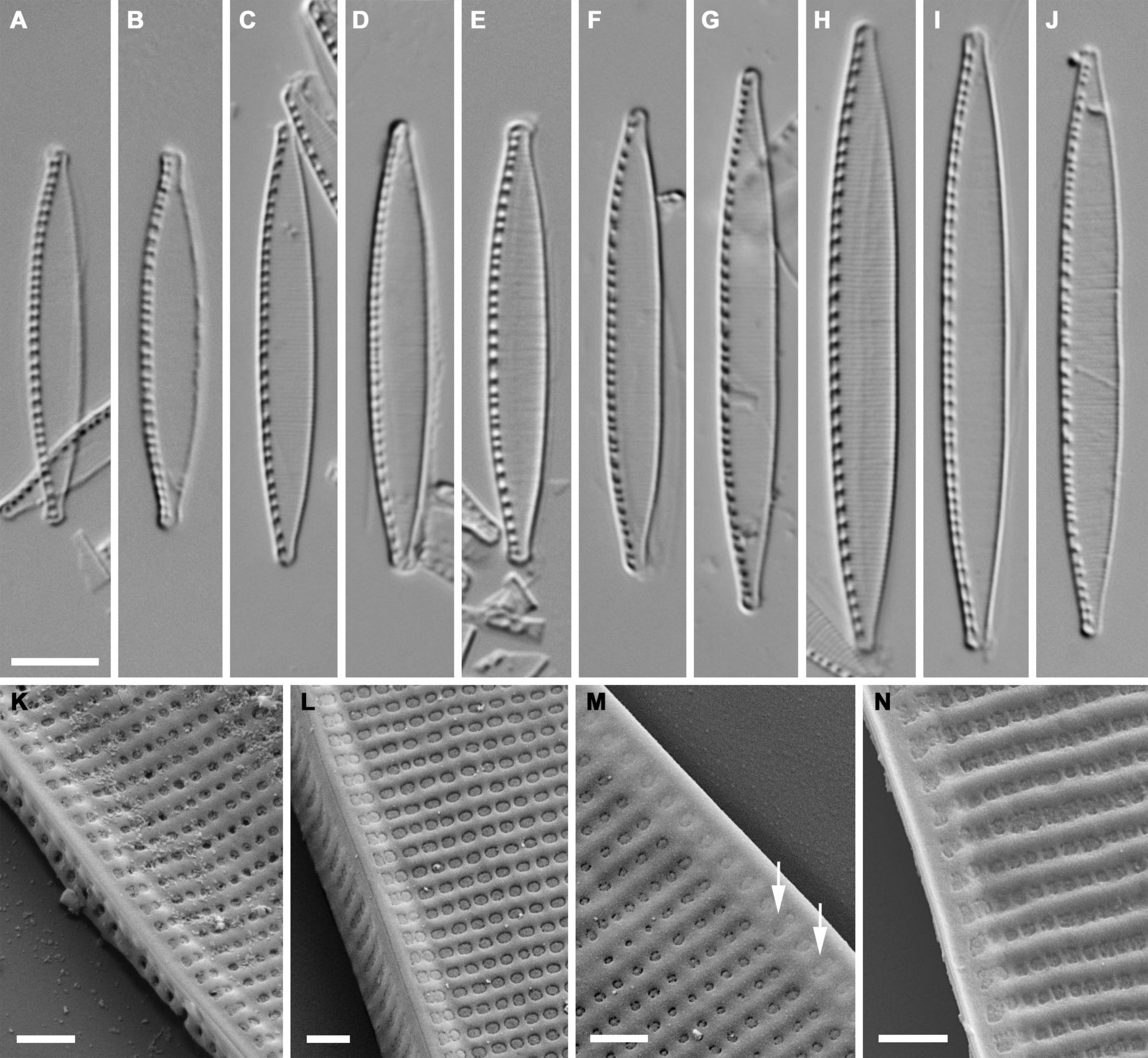
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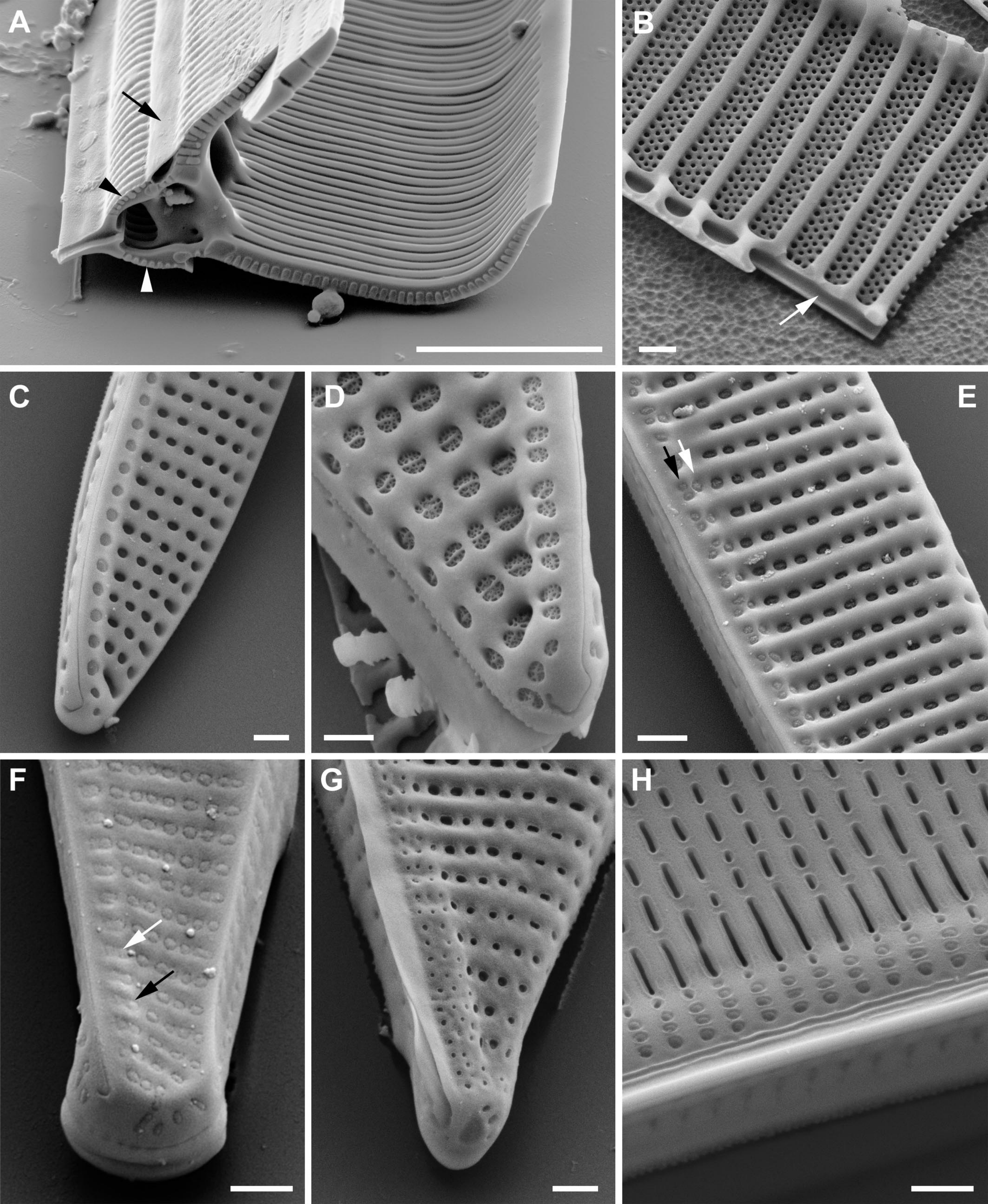
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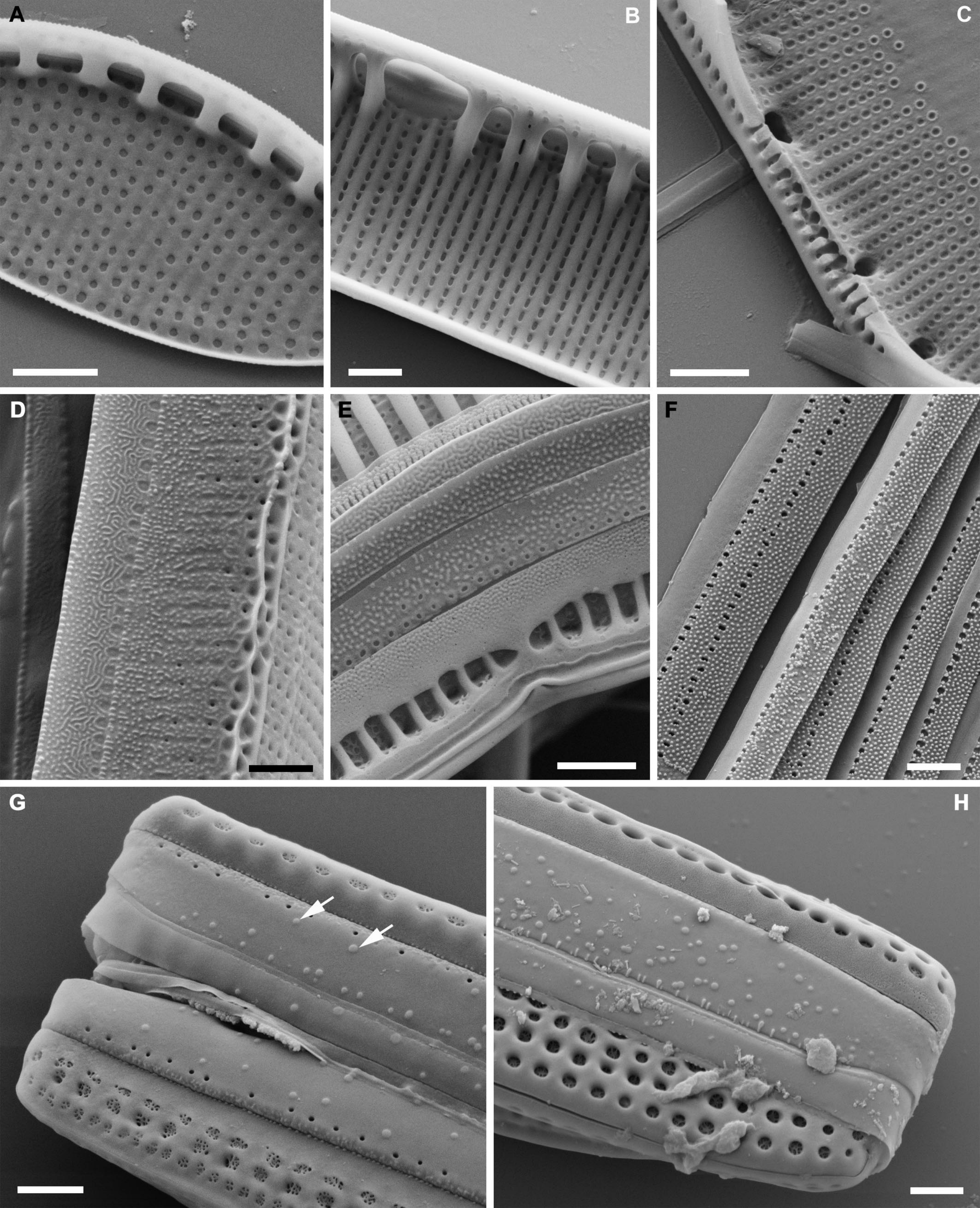
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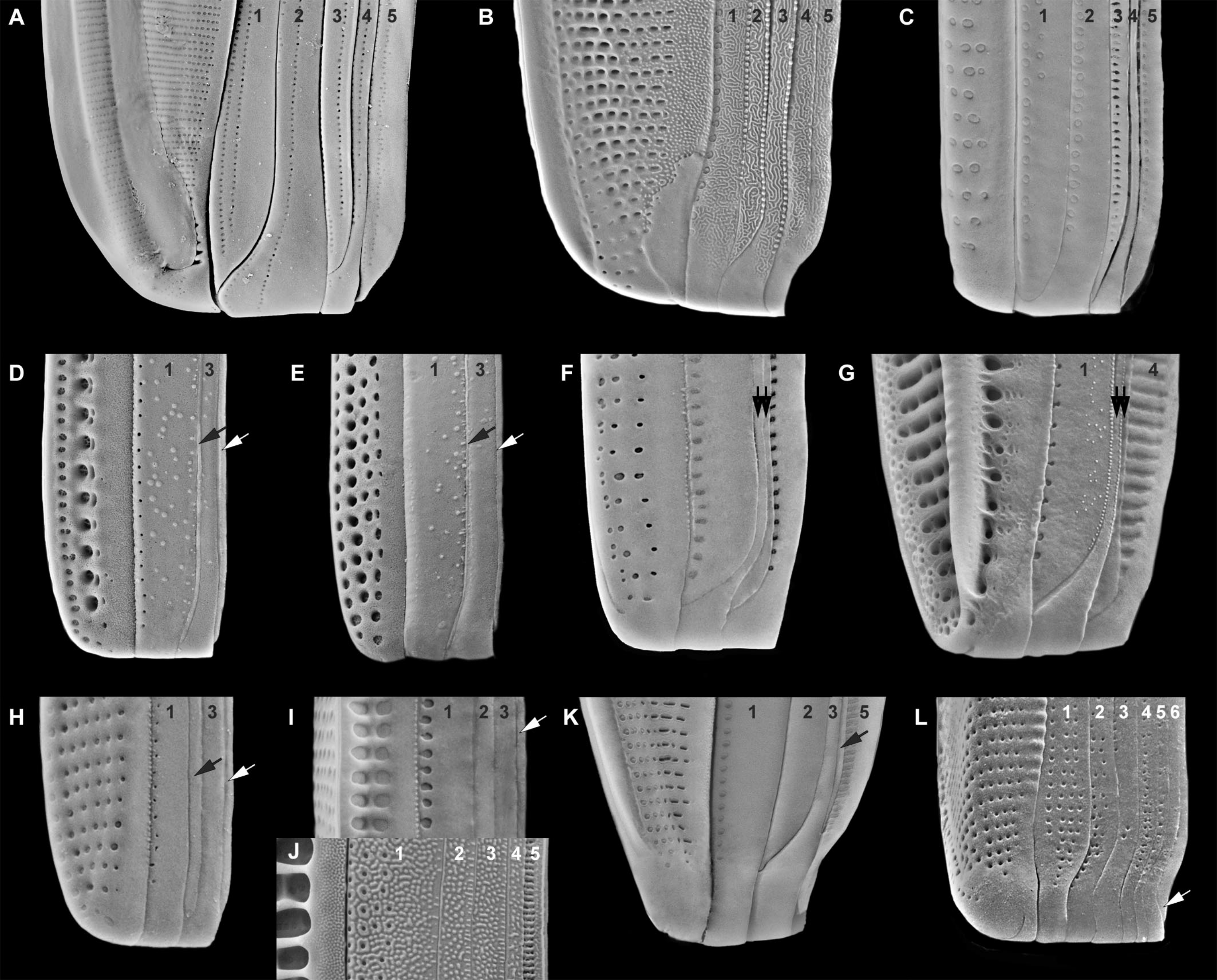
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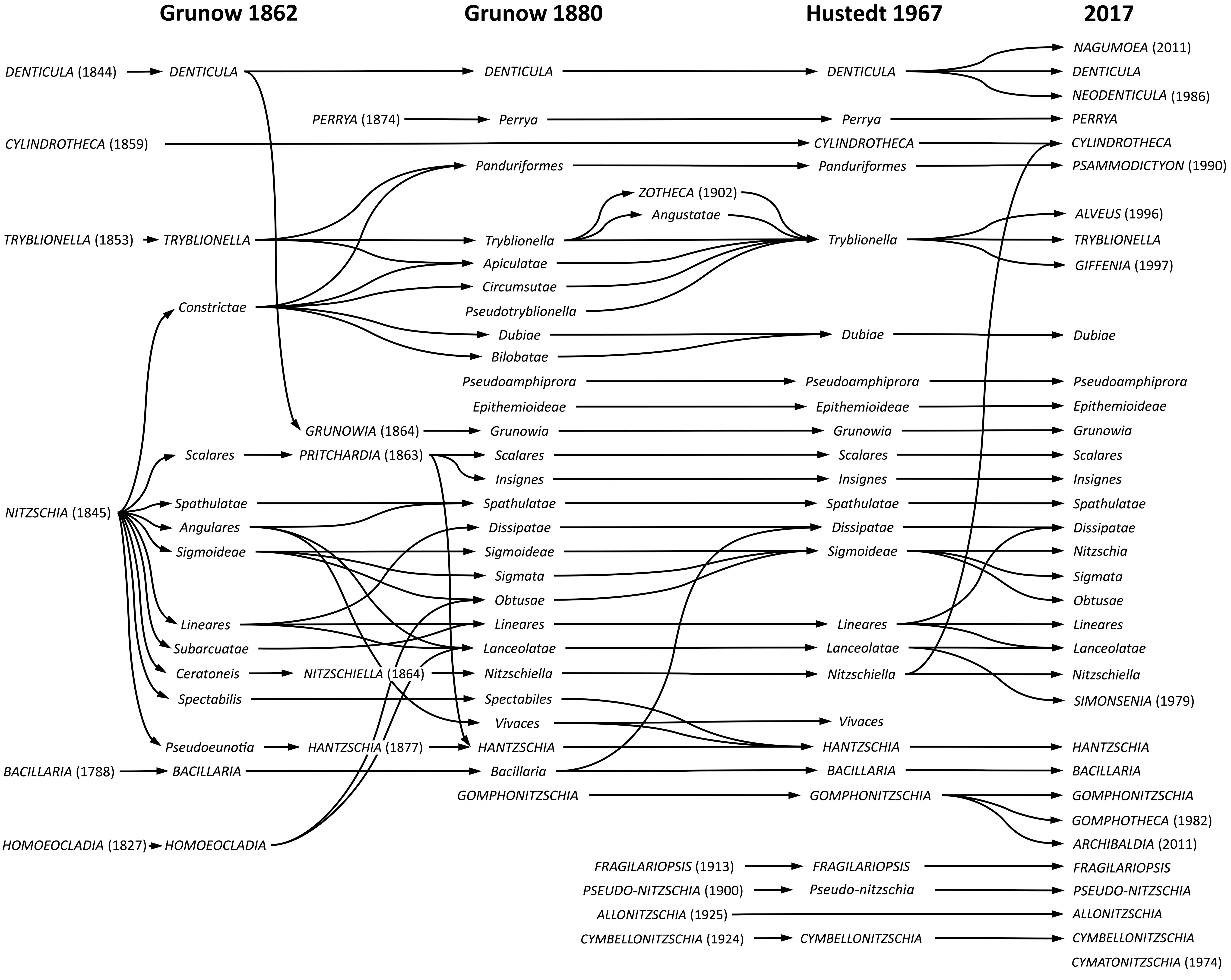
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Obtusae
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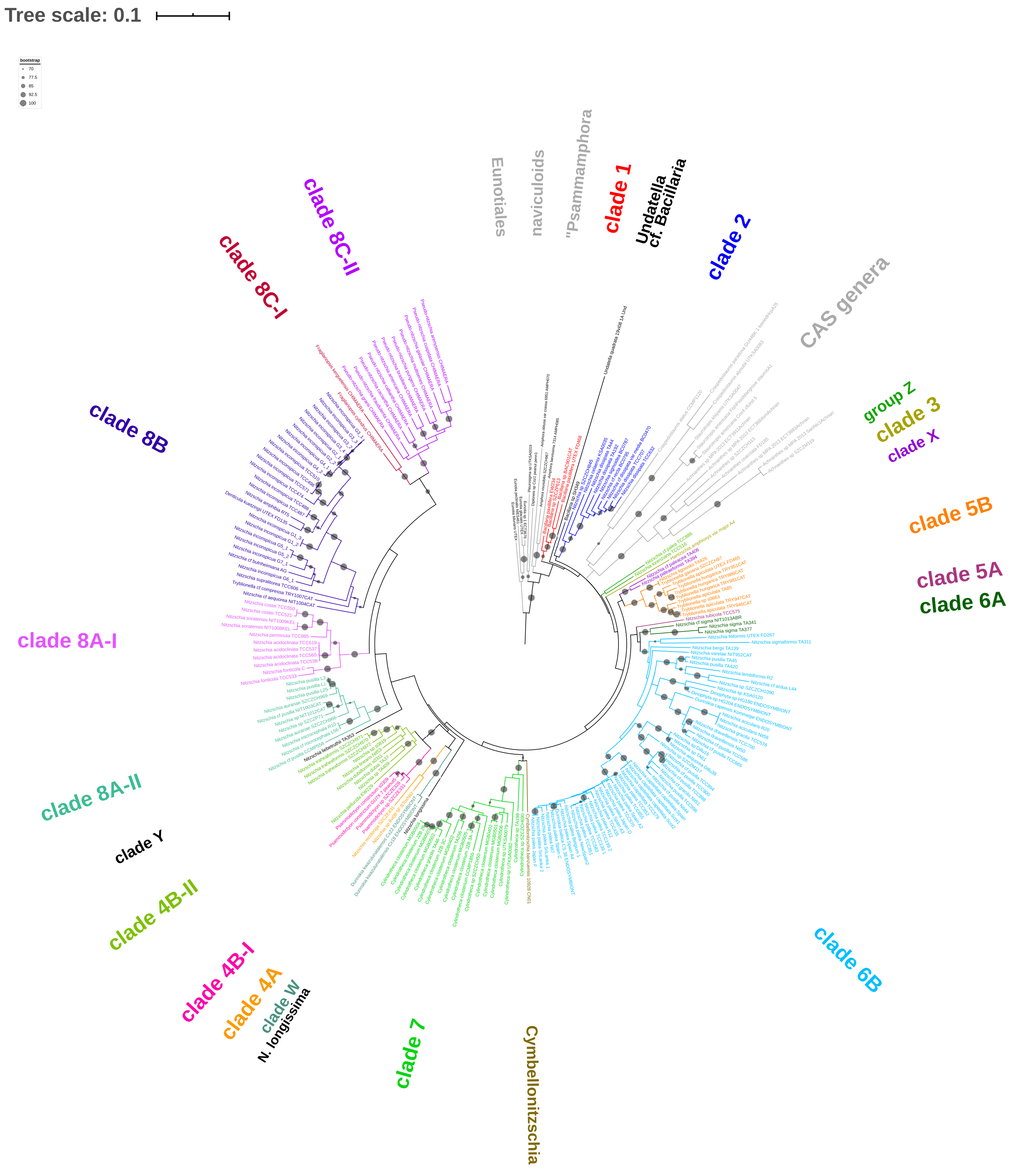
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cf. Bacillaria
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group Z
clade 3
clade X
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clade 5A
clade 6A
clade 6B
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clade 7
N. longissima
clade W
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clade 4B-I
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Undatella quadrata 19v08 1A Und


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Eunotia formica AT 111Gel09
Eunotia sp AT 73Gel02
Nitzschia sigmoidea BC0787
Nitzschia dissipata TCC707
Nitzschia cf dissipata var media BC0866
Nitzschia cf dissipata var media BC0649
Nitzschia cf recta BC0795
Nitzschia cf recta BC0769
Bacillaria sp BAC901CAT
Hantzschia cf amphioxys HANT015-11
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Nitzschia cf promare CCMP1116
Nitzschia cf traheaformis SZCZCH971
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Pseudo-nitzschia calliantha ICMB 109
Pseudo-nitzschia mannii AL 101
Pseudo-nitzschia pungens ICMB 143
Pseudo-nitzschia multistriata CM2
Pseudo-nitzschia brasiliana ICMB 176
Pseudo-nitzschia americana FBJun06 6
Pseudo-nitzschia linea ICMB 156
Pseudo-nitzschia arctica RCC2002
Pseudo-nitzschia pseudodelicatissima AL 15
Pseudo-nitzschia sp CLA1 D2
Pseudo-nitzschia fryxelliana NWFSC 241
Pseudo-nitzschia dolorosa AL 59
Pseudo-nitzschia galaxiae ICMB 174
Pseudo-nitzschia galaxiae ICMB 177
Pseudo-nitzschia delicatissima AR1
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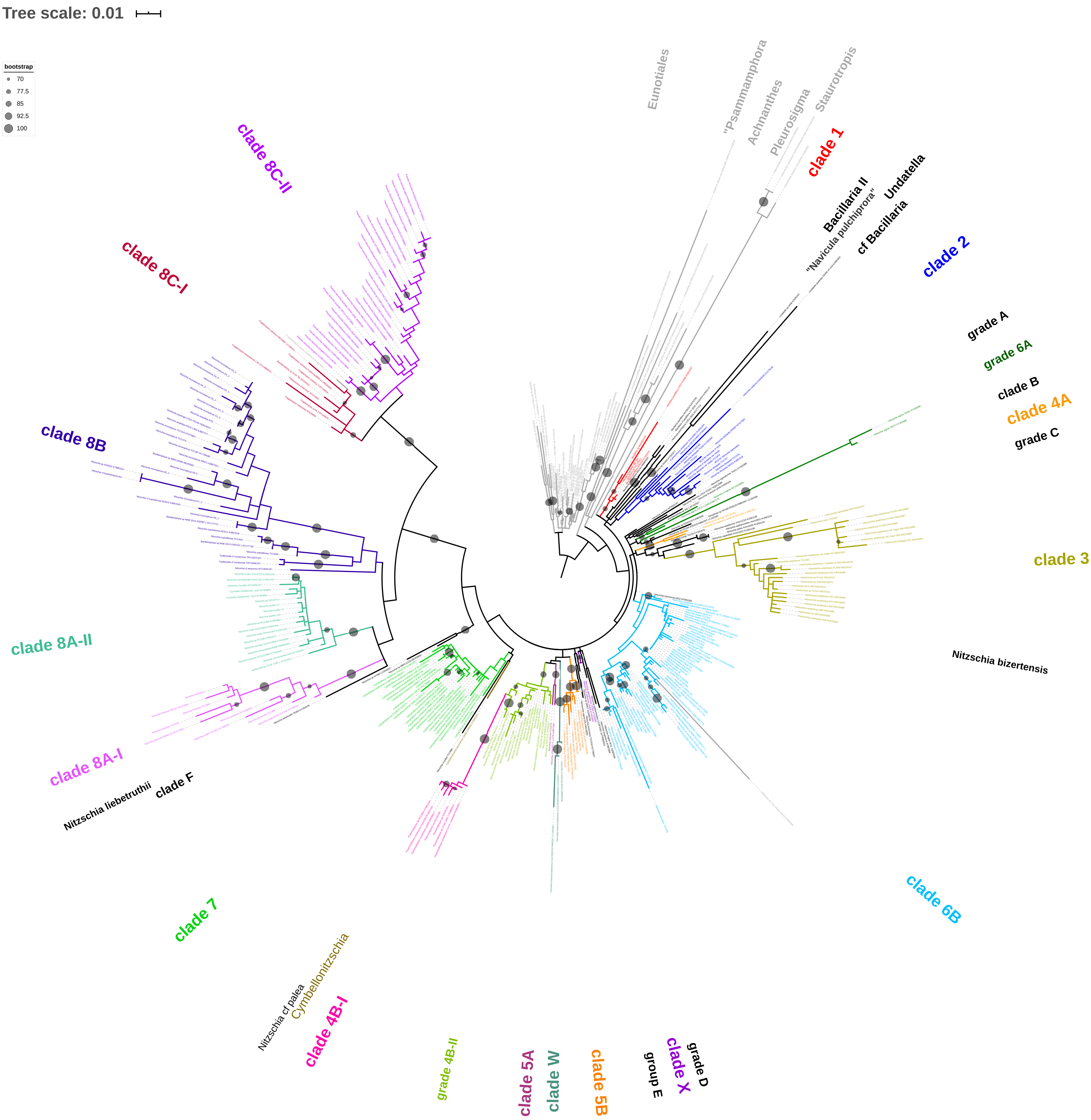
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clade 1
Bacillaria II
"Navicula pulchiprora"
Undatella
cf Bacillaria
clade 2
grade A
grade 6A
clade B
clade 4A
grade C
clade 3
Nitzschia bizertensis
clade 6B
grade D
clade X
group E
clade 5B
clade W
clade 5A
grade 4B-II
clade 4B-I
Cymbellonitzschia
Nitzschia cf palea
clade 7
Nitzschia liebetruthii
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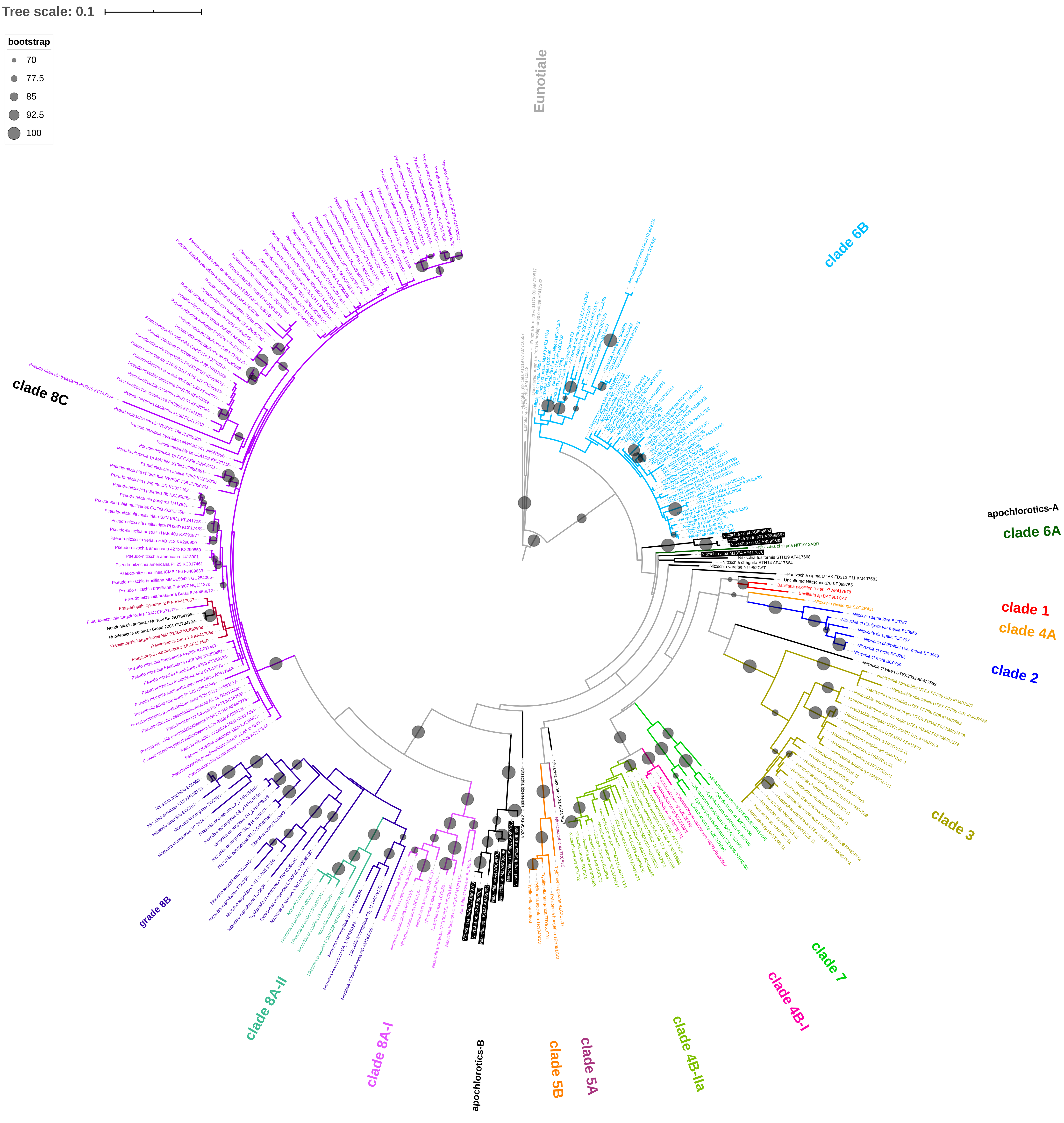
clade 8A-I
clade 8A-II
clade 8B
clade 8C-I
clade 8C-II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clade 2
clade 3
clade 7
clade 4B-I
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clade 5B
apochlorotics-B
clade 8A-I
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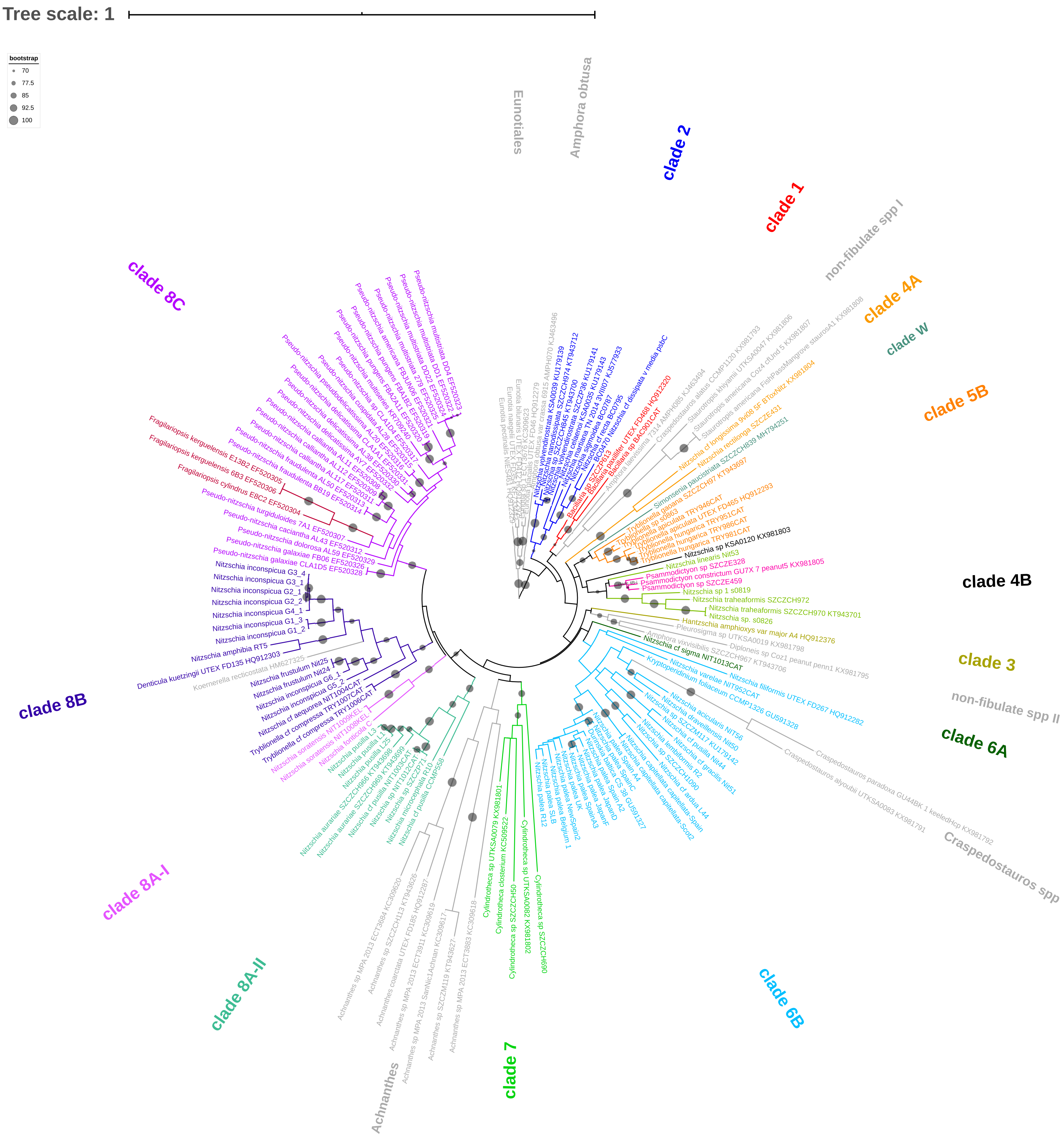
grade 8B
clade 8C



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clade 1
non-fibulate spp I
clade 4A
clade W
clade 5B
clade 4B
clade 3
non-fibulate spp II
clade 6A
Craspedostauros spp
clade 6B
clade 7
Achnanthes
clade 8A-II
clade 8A-I
clade 8B
clade 8C
Eunotia pectinalis NIES461 HQ912229
Eunotia naegelii UTEX FD412 HQ912230
Eunotia bilunaris UTEX FD411 HQ912243
Eunotia sp ECT3676 KC309623
Amphora obtusa var crassa 6915 AMPH070 KJ463496
Nitzschia volvendirostrata KSA0039 KU179139
Nitzschia nanodissipata SZCZCH974 KT943712
Nitzschia sp SZCZCH845 KT943700
Nitzschia volvendirostrata SZCZP36 KU179141
Nitzschia celaeno KSA0035 KU179143
Nitzschia mariana TN 2014 3VII07 KJ577933
Nitzschia sigmoidea BC0787
Nitzschia cf recta BC0795
BC0470 Nitzschia cf dissipata v media psbC
Bacillaria sp SZCZP613
Bacillaria paxillifer UTEX FD468 HQ912320
Bacillaria sp BAC901CAT
Amphora laevissima 7314 AMPH085 KJ463494
Craspedostauros alatus CCMP1120 KX981793
Staurotropis khiyamii UTKSA0047 KX981806
Staurotropis americana Coz4 cfUnd 5 KX981807
Staurotropis americana FishPassMangrove staurosA1 KX981808
Nitzschia cf longissima 9vi08 5F BToxNitz KX981804
Nitzschia rectilonga SZCZE431
Simonsenia paucistriata SZCZCH839 MH794251
Tryblionella gaoana SZCZCH97 KT943697
Tryblionella sp s0863
Tryblionella apiculata TRY946CAT
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Nitzschia sp KSA0120 KX981803
Nitzschia linearis Nit53
Psammodictyon sp SZCZE328
Psammodictyon constrictum GU7X 7 peanut5 KX981805
Psammodictyon sp SZCZE459
Nitzschia sp 1 s0819
Nitzschia traheaformis SZCZCH972
Nitzschia traheaformis SZCZCH970 KT943701
Nitzschia sp. s0826
Hantzschia amphioxys var major A4 HQ912376
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Diploneis sp Coz1 peanut penn1 KX981795
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Nitzschia cf sigma NIT1013CAT
Nitzschia filiformis UTEX FD267 HQ912282
Nitzschia varelae NIT952CAT
Kryptoperidinium foliaceum CCMP1326 GU591328
Craspedostauros paradoxa GU44BK 1 keeledHep KX981792
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Nitzschia acicularis NIT56
Nitzschia draveillensis Nit50
Nitzschia sp SZCZM117 KU179142
Nitzschia cf pusilla Nit44
Nitzschia cf gracilis Nit51
Nitzschia lembiformis R2
Nitzschia sp SZCZCH1090
Nitzschia cf ardua L44
Nitzschia capitellata capitellata Spain
Nitzschia capitellata capitellata Scot2
Durinskia baltica CS 38 GU591327
Nitzschia palea Spain A4
Nitzschia palea SpainC
Nitzschia palea Spain A2
Nitzschia palea JapanD
Nitzschia palea JapanF
Nitzschia palea SpainA3
Nitzschia palea UK
Nitzschia palea NewSpain2
Nitzschia palea Belgium 1
Nitzschia palea SLB
Nitzschia palea R12
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Cylindrotheca sp UTKSA0079 KX981801
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Nitzschia microcephala R10
Nitzschia sp SZCZP11
Nitzschia sp NIT1012CAT
Nitzschia cf pusilla NIT1003CAT
Nitzschia auraiae SZCZCH969 KT943699
Nitzschia auraiae SZCZCH966 KT943698
Nitzschia pusilla L25
Nitzschia pusilla L3
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Nitzschia soratensis NIT1008KEL
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Nitzschia inconspicua G6_1
Nitzschia frustulum Nit24
Nitzschia frustulum Nit25
Koernerella recticostata HM627325
Denticula kuetzingii UTEX FD135 HQ912303
Nitzschia amphibia RT5
Nitzschia inconspicua G1_2
Nitzschia inconspicua G1_3
Nitzschia inconspicua G4_1
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Nitzschia inconspicua G2_1
Nitzschia inconspicua G3_1
Nitzschia inconspicua G3_4
Pseudo-nitzschia galaxiae CLA1D5 EF520328
Pseudo-nitzschia galaxiae FB06 EF520326
Pseudo-nitzschia dolorosa AL59 EF520329
Pseudo-nitzschia caciantha AL43 EF520312
Pseudo-nitzschia turgiduloides 7A1 EF520307
Fragilariopsis cylindrus E8C2 EF520304
Fragilariopsis kerguelensis 6B3 EF520306
Fragilariopsis kerguelensis E13B2 EF520305
Pseudo-nitzschia fraudulenta BB19 EF520314
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Pseudo-nitzschia calliantha AL112 EF520309
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Pseudo-nitzschia delicatissima AY7 EF520331
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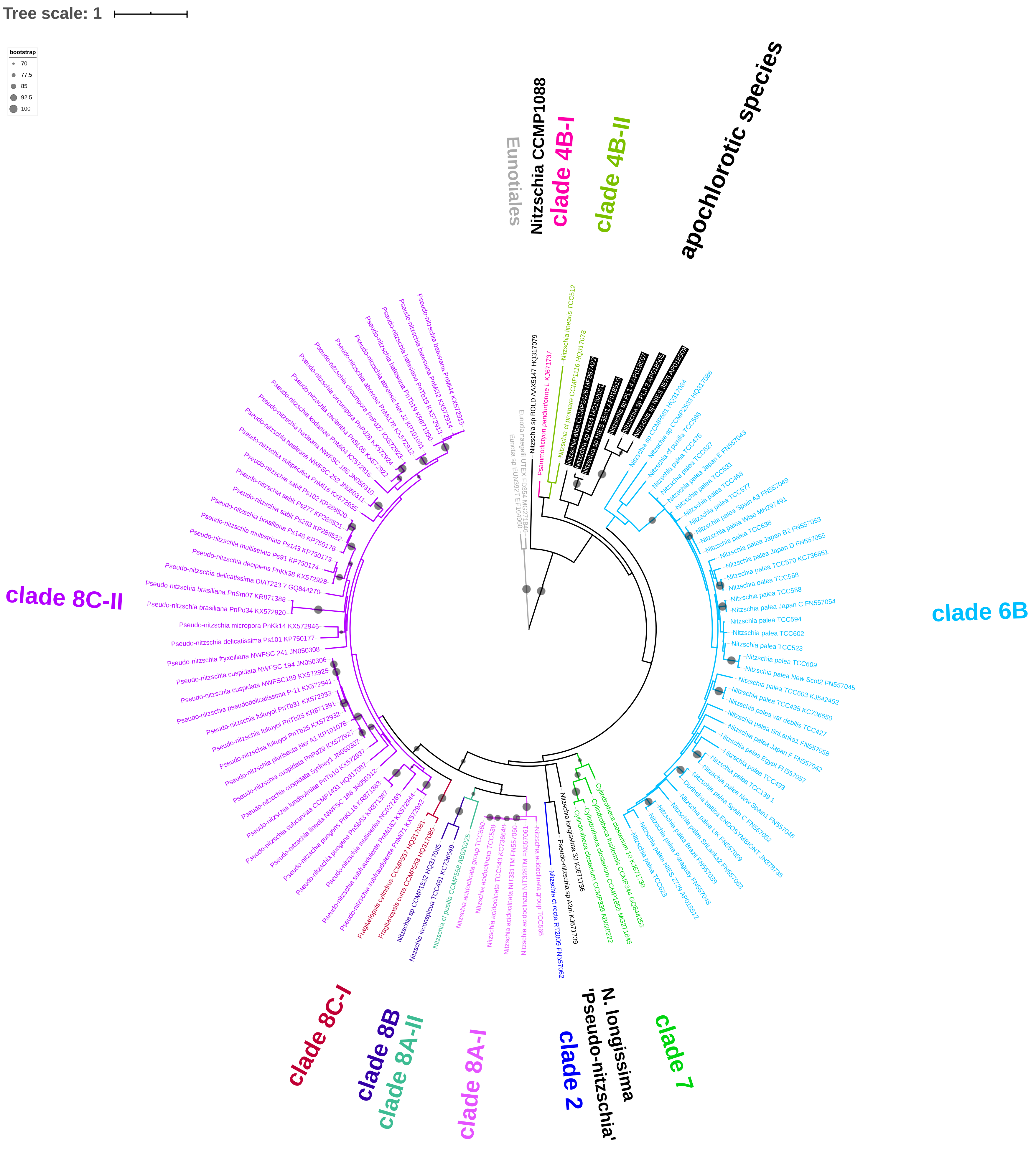

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92.5
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clade 4B-II
apochlorotic species
clade 6B
clade 7
N. longissima
'Pseudo-nitzschia'
clade 2
clade 8A-I
clade 8A-II
clade 8B
clade 8C-I
clade 8C-II
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Eunotia sp EUN392T EF164960
Nitzschia sp BOLD AAX5147 HQ317079
Psammodictyon panduriforme L KJ671737
Nitzschia linearis TCC512
Nitzschia cf promare CCMP1116 HQ317078
Nitzschia alba CCMP2426 MF997422
Nitzschia sp Nitz4 MG182051
Nitzschia sp NIES 3581 AP018510
Nitzschia sp PL1 4 AP018507
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Nitzschia sp CCMP2533 HQ317086
Nitzschia sp CCMP581 HQ317084
Nitzschia cf pusilla TCC586
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Nitzschia palea TCC568
Nitzschia palea TCC588
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Nitzschia palea TCC594
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Nitzschia palea TCC609
Nitzschia palea New Scot2 FN557045
Nitzschia palea TCC603 KJ542452
Nitzschia palea TCC435 KC736650
Nitzschia palea var debilis TCC427
Nitzschia palea SriLanka1 FN557058
Nitzschia palea Japan F FN557042
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Nitzschia palea Brazil FN557039
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Nitzschia palea NIES 2729 AP018512
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Cylindrotheca fusiformis CCMP344 GQ844253
Cylindrotheca closterium CCMP1855 MG271845
Cylindrotheca closterium CCMP339 AB020222
Nitzschia longissima 33 KJ671736
Pseudo-nitzschia sp A2ni KJ671739
Nitzschia cf recta RT2009 FN557062
Nitzschia acidoclinata group TCC566
Nitzschia acidoclinata NIT328TM FN557061
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Nitzschia acidoclinata TCC543 KC736648
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Nitzschia cf pusilla CCMP558 AB020225
Nitzschia inconspicua TCC481 KC736649
Nitzschia sp CCMP1532 HQ317085
Fragilariopsis curta CCMP553 HQ317080
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Pseudo-nitzschia subfraudulenta PnMi71 KX572942
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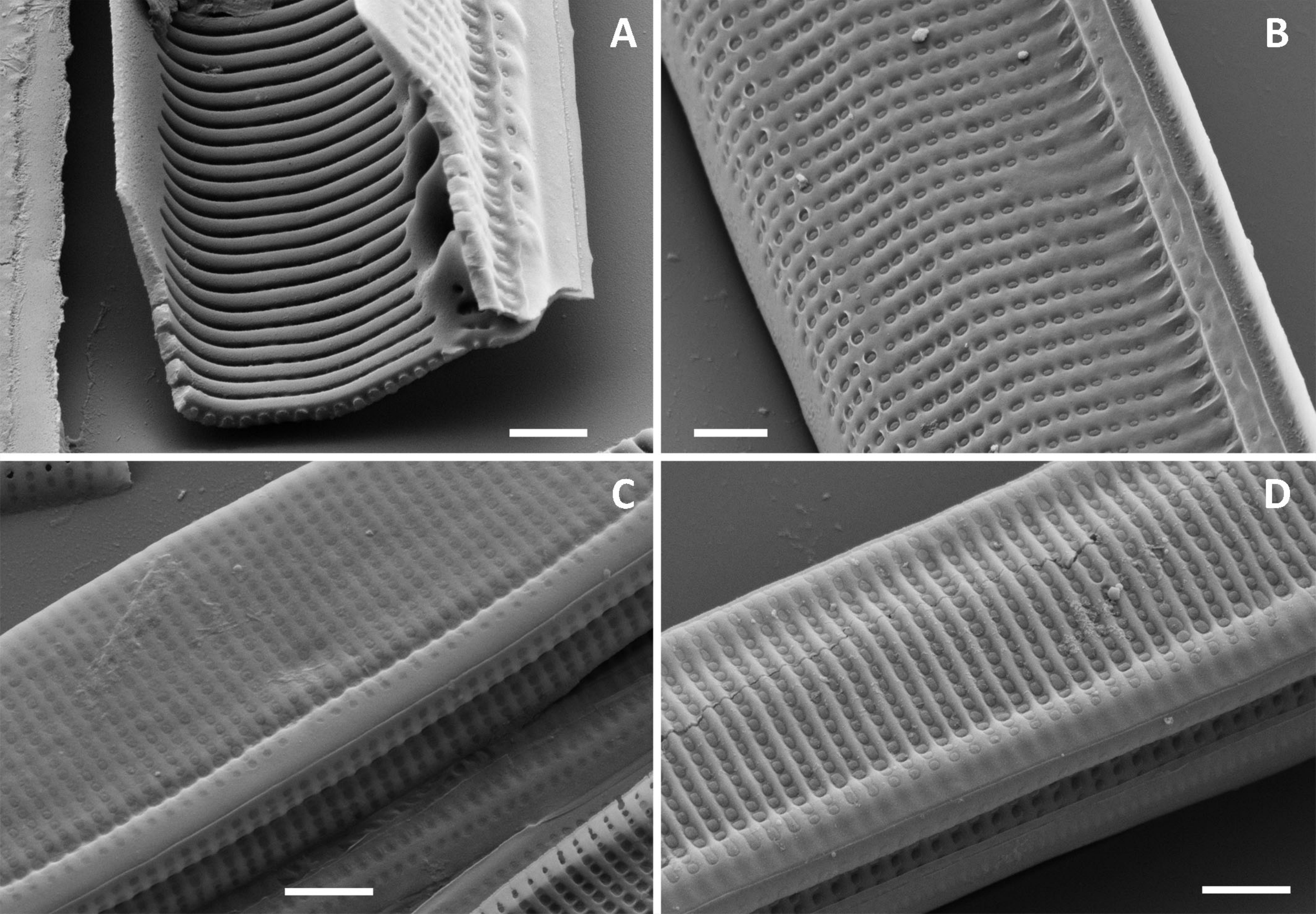
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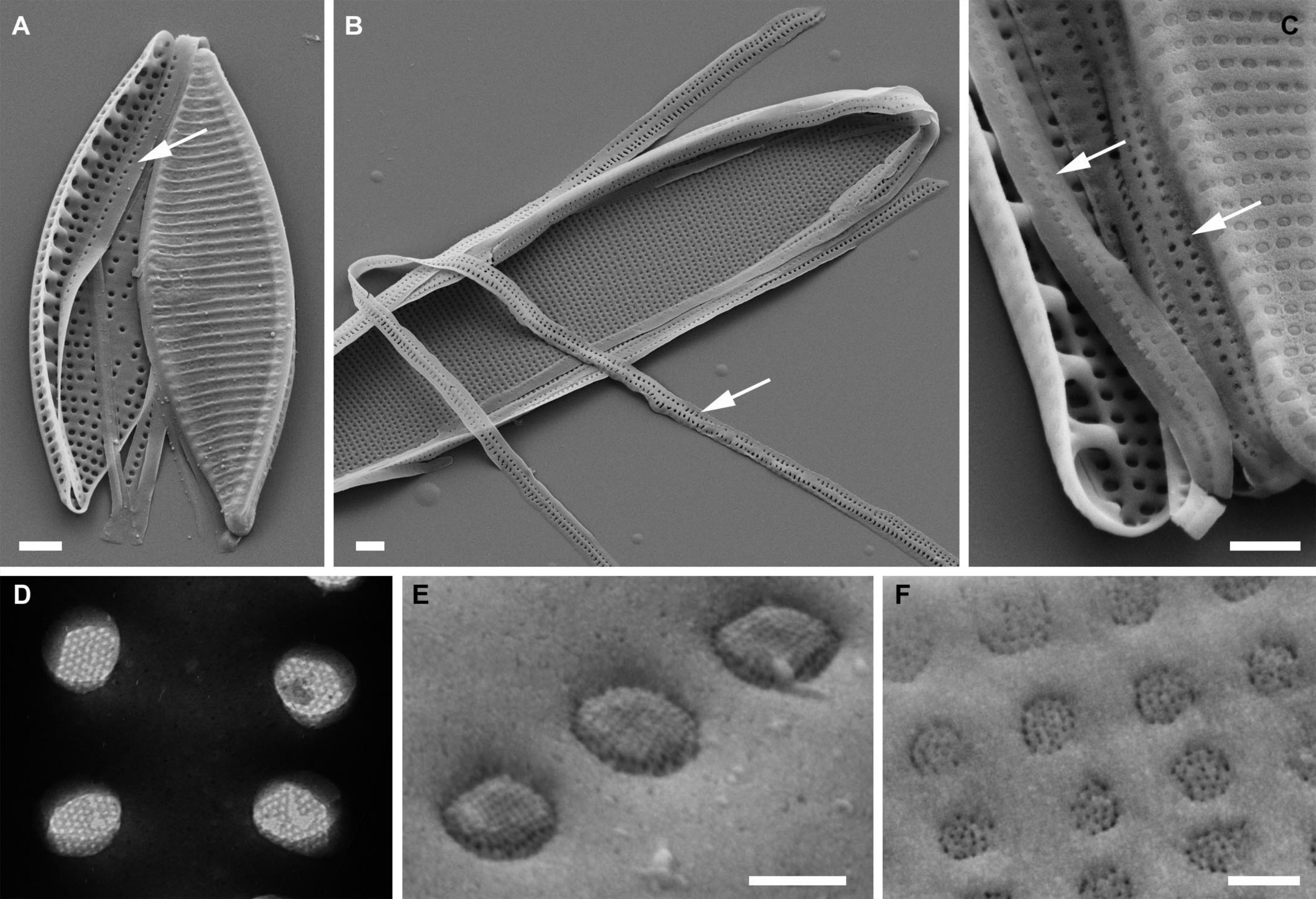
D


A
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E
F

Supplementary Table 1. GenBank sequences used in the six analyses (four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL*, SSU, LSU, *psbC* and *cox1*).

GenBank #	**Taxon and clone**	**Gene**	**Use of sequence**
AB020222	Cylindrotheca closterium CCMP339	*cox1*	*cox1*
AB020225	Nitzschia pusilla CCMP558	*cox1*	*cox1*
AB085830	Eunotia formica var. sumatrana A 0045	SSU	SSU
AB085831	Eunotia monodon var. asiatica A 0046	SSU	SSU
AB085832	Eunotia pectinalis A 0047	SSU	SSU
AB183591	Bacillariophyta sp. MBIC10099	SSU	SSU
AB183668	Nitzschia sp. MBIC11128	SSU	SSU
AB195669	Galeidinium rugatum ENDOSYMBIONT	*rbcL*	*rbcL*
AB218885	Nitzschia navis-varingica BCEA 03-4-2	LSU	LSU
AB218886	Nitzschia navis-varingica BLEC 03-1-2	LSU	LSU
AB271108	Durinskia capensis ENDOSYMBIONT	*rbcL*	*rbcL*
AB430616	Nitzschia dubiiformis s0311	SSU	four-gene, SSU+*rbcL*, SSU
AB430617	Psammodictyon constrictum s0309	SSU	four-gene, SSU+*rbcL*, SSU
AB430656	Nitzschia dubiiformis s0311	LSU	four-gene, LSU+*rbcL*, LSU
AB430657	Psammodictyon constrictum s0309	LSU	four-gene, LSU+*rbcL*, LSU
AB430696	Nitzschia dubiiformis s0311	*rbcL*	four-gene, LSU+*rbcL*, SSU+*rbcL*, *rbcL*
AB430697	Psammodictyon constrictum s0309	*rbcL*	four-gene, LSU+*rbcL*, SSU+*rbcL*, *rbcL*
AB899686	Nitzschia sp. IriSm01	LSU	LSU
AB899687	Nitzschia sp. IriIs01	LSU	LSU
AB899692	Nitzschia sp. IriSs06	LSU	LSU
AB899693	Nitzschia sp. I4	LSU	LSU
AB899696	Nitzschia sp. M1	LSU	LSU
AB899698	Nitzschia sp. O2	LSU	LSU
AB899699	Nitzschia sp. IriSm02	LSU	LSU
AB899700	Nitzschia sp. IriSL01	LSU	LSU
AB899702	Nitzschia sp. A4	LSU	LSU
AB899705	Nitzschia sp. D2	LSU	LSU
AF289049	Cylindrotheca closterium	LSU	LSU
AF374482	Thalassiosira antarctica	SSU	SSU
AF416759	Pseudo-nitzschia pseudodelicatissima SZN-B34	LSU	LSU
AF416760	Pseudo-nitzschia pseudodelicatissima SZN-B35	LSU	LSU
AF417639	Pseudo-nitzschia inflatula No7	LSU	LSU

AF417640	Pseudo-nitzschia pseudodelicatissima P-11	LSU	LSU
AF417643	Pseudo-nitzschia cf. subpacifica P-28	LSU	LSU
AF417646	Pseudo-nitzschia subfraudulenta rensubfrau	LSU	LSU
AF417649	Pseudo-nitzschia micropora VPB-B3	LSU	LSU
AF417657	Fragilariopsis cylindrus 2-E-F	LSU	LSU
AF417659	Fragilariopsis curta 1-A	LSU	LSU
AF417660	Fragilariopsis vanheurckii 3-18	LSU	LSU
AF417661	Nitzschia communis M1762	LSU	LSU
AF417664	Nitzschia cf. agnita STH14	LSU	LSU
AF417665	Cylindrotheca fusiformis UTEX2083	LSU	LSU
AF417666	Cylindrotheca closterium K-520	LSU	LSU
AF417667	Nitzschia lecointei 5-21	LSU	LSU
AF417668	Nitzschia fusiformis STH19	LSU	LSU
AF417669	Nitzschia cf. vitrea UTEX2033	LSU	LSU
AF417670	Nitzschia alba M1354	LSU	LSU
AF417672	Nitzschia pellucida 99NG1-16	LSU	LSU
AF417673	Nitzschia laevis M1285	LSU	LSU
AF417674	Nitzschia navis-varingica VHL987	LSU	LSU
AF417676	Nitzschia cf. promare CCMP1116	LSU	LSU+*rbcL*, LSU
AF417677	Hantzschia amphioxys UTEX657	LSU	LSU
AF417678	Bacillaria paxillifer Tenerife7	LSU	LSU
AF440767	Pseudo-nitzschia delicatissima NWFSC 002	LSU	LSU
AF440773	Pseudo-nitzschia pseudodelicatissima NWFSC 040	LSU	LSU
AF440777	Pseudo-nitzschia cf. heimii NWFSC 059	LSU	LSU
AF469672	Pseudo-nitzschia brasiliana Brasil 8	LSU	LSU
AF525665	Fragilariopsis sublineata	SSU	SSU
AJ535145	Eunotia sp. M16	SSU	SSU
AJ535146	Eunotia cf. pectinalis f minor L474	SSU	SSU
AJ535163	Undatella sp. p446	SSU	SSU
AJ535164	Nitzschia frustulum p345	SSU	SSU
AJ866995	Eunotia bilunaris EBIL1	SSU	SSU
AJ867003	Nitzschia palea NPAL6	SSU	SSU
AJ867013	Nitzschia linearis NLIN3	SSU	SSU
AJ867018	Nitzschia dissipata NDIS1	SSU	SSU
AJ867019	Nitzschia supralitorea NZSU1	SSU	SSU
AJ867020	Nitzschia cf. supralitorea NZSU2	SSU	SSU

AJ867021	Nitzschia inconspicua NINC1	SSU	SSU
AJ867277	Nitzschia amphibia FDCC L602	SSU	SSU
AJ867278	Nitzschia communis FDCC L408	SSU	SSU
AJ867279	Nitzschia sigma FDCC L1546	SSU	SSU
AJ867280	Nitzschia vitrea FDCC L1276	SSU	SSU
AM182191	Nitzschia fonticola A-RT24	LSU	LSU+*rbcL*
AM182193	Nitzschia fonticola C-RT26	LSU	four-gene, LSU+*rbcL*, LSU
AM182194	Nitzschia amphibia amphibia-RT5	LSU	four-gene, LSU+*rbcL*, LSU
AM182195	Nitzschia inconspicua incons-RT10	LSU	LSU
AM182196	Nitzschia supralitorea supralit-RT11	LSU	LSU
AM183228	Nitzschia palea Jp013-ND3	LSU	LSU+*rbcL*, LSU
AM183229	Nitzschia palea Jp014-ND4	LSU	LSU+*rbcL*, LSU
AM183230	Nitzschia palea Jp030-K12	LSU	LSU+*rbcL*, LSU
AM183231	Nitzschia palea Jp030-K12	LSU	four-gene, LSU+*rbcL*, LSU
AM183232	Nitzschia palea Jp052-FU6	LSU	LSU+*rbcL*, LSU
AM183233	Nitzschia palea Mayama	LSU	four-gene, LSU+*rbcL*, LSU
AM183235	Nitzschia palea SLA [SriLanka1]	LSU	four-gene, LSU+*rbcL*, LSU
AM183236	Nitzschia palea SLB [SriLanka2]	LSU	four-gene, LSU+*rbcL*, LSU
AM183238	Nitzschia palea Nil	LSU	LSU
AM183239	Nitzschia palea PY	LSU	LSU+*rbcL*, LSU
AM183240	Nitzschia palea BB2b	LSU	four-gene, LSU+*rbcL*, LSU
AM183242	Nitzschia palea Aitor5	LSU	four-gene, LSU+*rbcL*, LSU
AM183245	Nitzschia palea Nit B2	LSU	four-gene, LSU+*rbcL*, LSU
AM183246	Nitzschia palea Nit C	LSU	four-gene, LSU+*rbcL*, LSU
AM183247	Nitzschia palea Nit B4	LSU	four-gene
AM183248	Nitzschia palea Victor 02-9E	LSU	four-gene
AM183586	Nitzschia cf. bulnheimiana AG	LSU	four-gene, LSU+*rbcL*, LSU
AM235380	Pseudo-nitzschia multiseries Nparl	SSU	SSU
AM235381	Pseudo-nitzschia multiseries TKA 2-28	SSU	SSU
AM235382	Pseudo-nitzschia multiseries POMX	SSU	SSU
AM501963	Eunotia sp. AT-73Gel02	SSU	SSU
AM502001	Eunotia implicata AT-219 07	SSU	SSU
AM502040	Eunotia formica AT-111Gel09	SSU	SSU
AM710428	Eunotia formica AT-111Gel09	*rbcL*	LSU+*rbcL*
AM710429	Eunotia sp. AT-73Gel02	*rbcL*	LSU+*rbcL*
AM710468	Eunotia implicata AT-219.07	*rbcL*	LSU+*rbcL*
AM710517	Eunotia formica AT-111Gel09	LSU	LSU+*rbcL*, LSU

AM710518	Eunotia sp. AT-73Gel02	LSU	LSU+*rbcL*, LSU
AM710557	Eunotia implicata AT-219.07	LSU	LSU+*rbcL*, LSU
AM909631	Nitzschia capitellata strain 262	LSU	four-gene
AP018505	Nitzschia sp. PL3-2	genome	*cox1*
AP018507	Nitzschia sp. PL1-4	genome	*cox1*
AP018509	Nitzschia sp. NIES-3576	genome	*cox1*
AP018510	Nitzschia sp. NIES-3581	genome	*cox1*
AP018512	Nitzschia palea NIES-2729	genome	*cox1*
AY081136	Pseudo-nitzschia galaxiae Mex 23	LSU	LSU
AY081137	Pseudo-nitzschia galaxiae Sydney 4	LSU	LSU
AY221947	Pseudo-nitzschia multiseries CLN125	SSU	SSU
AY485457	Cylindrotheca fusiformis CCMP339	SSU	SSU
AY485458	Nitzschia thermalis HP	SSU	SSU
AY485467	Fragilariopsis cylindrus CCMP1102	SSU	SSU+*rbcL*
AY550126	Pseudo-nitzschia pseudodelicatissima SZN-B109	LSU	LSU
AY550127	Pseudo-nitzschia pseudodelicatissima SZN-B112	LSU	LSU
AY571744	Eunotia minor E3318	*rbcL*	*rbcL*
AY764136	Pseudo-nitzschia arenysensis 14V	LSU	LSU
AY866415	Cylndrotheca closterium MGB0402	*rbcL*	SSU+*rbcL*, *rbcL*
AY866416	Cylndrotheca closterium MGB0401	*rbcL*	SSU+*rbcL*
AY866417	Cylndrotheca closterium MGB0401	SSU	SSU+*rbcL*, SSU
AY866418	Cylndrotheca closterium MGB0402	SSU	SSU+*rbcL*, SSU
AY881967	Nitzschia longissima	*rbcL*	SSU+*rbcL*, *rbcL*
AY881968	Nitzschia longissima	SSU	SSU+*rbcL*, SSU
DQ019445	Cylindrotheca closterium MGB0501	*rbcL*	SSU+*rbcL*, *rbcL*
DQ019446	Cylindrotheca closterium MGB0501	SSU	SSU+*rbcL*, SSU
DQ082738	Cylindrotheca closterium MGB0502	SSU	SSU+*rbcL*, SSU
DQ082739	Cylindrotheca closterium MGB0503	SSU	SSU
DQ082740	Cylindrotheca closterium MGB0504	SSU	SSU
DQ082741	Cylindrotheca closterium MGB0505	SSU	SSU+*rbcL*, SSU
DQ082742	Cylindrotheca closterium MGB0506	SSU	SSU+*rbcL*, SSU
DQ082743	Cylindrotheca closterium MGB0502	*rbcL*	SSU+*rbcL*
DQ082744	Cylindrotheca closterium MGB0503	*rbcL*	SSU+*rbcL*, *rbcL*
DQ082745	Cylindrotheca closterium MGB0504	*rbcL*	SSU+*rbcL*
DQ082746	Cylindrotheca closterium MGB0505	*rbcL*	SSU+*rbcL*, *rbcL*

DQ082747	Cylindrotheca closterium MGB0506	*rbcL*	SSU+*rbcL*, *rbcL*
DQ143045	Cylindrotheca closterium JZB-28	*rbcL*	SSU+*rbcL*
DQ143046	Cylindrotheca closterium JZB-3A	*rbcL*	SSU+*rbcL*, *rbcL*
DQ143047	Cylindrotheca closterium JZB-3C	*rbcL*	SSU+*rbcL*, *rbcL*
DQ178392	Cylindrotheca closterium JZB-3A	SSU	SSU+*rbcL*
DQ178393	Cylindrotheca closterium JZB-3C	SSU	SSU+*rbcL*, SSU
DQ178394	Cylindrotheca closterium JZB-28	SSU	SSU+*rbcL*, SSU
DQ813808	Pseudo-nitzschia pseudodelicatissima AL-15	LSU	LSU+*rbcL*, LSU
DQ813811	Pseudo-nitzschia arenysensis AL-24	LSU	LSU+*rbcL*
DQ813812	Pseudo-nitzschia caciantha AL-56	LSU	LSU+*rbcL*, LSU
DQ813813	Pseudo-nitzschia dolorosa AL-59	LSU	LSU+*rbcL*, LSU
DQ813814	Pseudo-nitzschia mannii AL-101	LSU	LSU+*rbcL*, LSU
DQ813816	Pseudo-nitzschia mannii P4	LSU	LSU
DQ813817	Pseudo-nitzschia pseudodelicatissima AL-15	LSU	LSU+*rbcL*, LSU
DQ813818	Pseudo-nitzschia delicatissima AL-22	*rbcL*	*rbcL*
DQ813819	Pseudo-nitzschia arenysensis AL-24	*rbcL*	SSU+*rbcL*, LSU+*rbcL*, *rbcL*
DQ813820	Pseudo-nitzschia cuspidata AL-28	*rbcL*	SSU+*rbcL*, *rbcL*
DQ813821	Pseudo-nitzschia caciantha AL-56	*rbcL*	SSU+*rbcL*, LSU+*rbcL*, *rbcL*
DQ813822	Pseudo-nitzschia dolorosa AL-59	*rbcL*	LSU+*rbcL*, *rbcL*
DQ813823	Pseudo-nitzschia arenysensis AL-64	*rbcL*	*rbcL*
DQ813824	Pseudo-nitzschia mannii AL-101	*rbcL*	LSU+*rbcL*, *rbcL*
DQ813825	Pseudo-nitzschia calliantha AL-117	*rbcL*	SSU+*rbcL*, *rbcL*
DR026462	Fragilariopsis cylindrus FcylESTa38f08.s1	SSU	SSU
EF140623	Fragilariopsis curta 3	SSU	SSU
EF140624	Fragilariopsis cylindrus 3	SSU	SSU
EF164960	Eunotia sp. EUN392T	*cox1*	*cox1*
EF417282	Uncultured organism from Habroleptoides confusa	LSU	LSU
EF423498	Nitzschia cf. pusilla CCMP558 [Nitzschia frustulum]	*rbcL*	LSU+*rbcL*, *rbcL*
EF423499	Fragilariopsis cylindrus E8C2	*rbcL*	*rbcL*
EF423500	Fragilariopsis kerguelensis E13B2	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL*
EF423501	Fragilariopsis kerguelensis PA_P6B3	*rbcL*	*rbcL*
EF423502	Pseudo-nitzschia fraudulenta AL50	*rbcL*	SSU+*rbcL*, *rbcL*
EF423504	Pseudo-nitzschia americana FBJun06.6	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL*
EF423505	Pseudo-nitzschia multistriata 19A	*rbcL*	*rbcL*

EF423506	Pseudo-nitzschia pungens FBA1D5	*rbcL*	*rbcL*
EF423507	Pseudo-nitzschia pungens FBA2A11	*rbcL*	SSU+*rbcL*
EF423508	Pseudo-nitzschia turgiduloides 7A1	*rbcL*	*rbcL*
EF423509	Pseudo-nitzschia galaxiae FB06.17	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
EF423510	Pseudo-nitzschia galaxiae SM60	*rbcL*	*rbcL*
EF423511	Pseudo-nitzschia galaxiae SM1	*rbcL*	*rbcL*
EF423512	Pseudo-nitzschia galaxiae SM3	*rbcL*	*rbcL*
EF423513	Pseudo-nitzschia galaxiae SM55	*rbcL*	*rbcL*
EF423514	Pseudo-nitzschia galaxiae SM54	*rbcL*	*rbcL*
EF423515	Pseudo-nitzschia galaxiae AL8	*rbcL*	*rbcL*
EF423516	Pseudo-nitzschia delicatissima AY11	*rbcL*	*rbcL*
EF432521	Bacillariophyta sp. SL64/78c	SSU	SSU
EF432527	Bacillariophyta sp. W5-1	SSU	SSU
EF506606	Pseudo-nitzschia galaxiae SM10	LSU	LSU
EF506608	Pseudo-nitzschia decipiens Mex13	LSU	LSU
EF520304	Fragilariopsis cylindrus E8C2	*psbC*	*psbC*
EF520305	Fragilariopsis kerguelensis E13B2	*psbC*	four-gene, *psbC*
EF520306	Fragilariopsis kerguelensis 6B3	*psbC*	*psbC*
EF520307	Pseudo-nitzschia turgiduloides 7A1	*psbC*	*psbC*
EF520308	Pseudo-nitzschia calliantha AL11	*psbC*	*psbC*
EF520309	Pseudo-nitzschia calliantha AL112	*psbC*	*psbC*
EF520311	Pseudo-nitzschia calliantha AL117	*psbC*	*psbC*
EF520312	Pseudo-nitzschia caciantha AL43	*psbC*	*psbC*
EF520313	Pseudo-nitzschia fraudulenta AL50	*psbC*	*psbC*
EF520314	Pseudo-nitzschia fraudulenta BB19	*psbC*	*psbC*
EF520315	Pseudo-nitzschia cuspidata AL28	*psbC*	*psbC*
EF520316	Pseudo-nitzschia pseudodelicatissima AL20	*psbC*	*psbC*
EF520317	Pseudo-nitzschia sp. CLA1.D4	*psbC*	*psbC*
EF520318	Pseudo-nitzschia sp. CLA1.D2	*psbC*	four-gene
EF520319	Pseudo-nitzschia pungens FBA1B2	*psbC*	*psbC*
EF520320	Pseudo-nitzschia pungens FBA2.A11	*psbC*	*psbC*
EF520321	Pseudo-nitzschia americana FBJUN06	*psbC*	four-gene, *psbC*
EF520322	Pseudo-nitzschia multistriata DD1	*psbC*	*psbC*
EF520323	Pseudo-nitzschia multistriata DD4	*psbC*	*psbC*
EF520324	Pseudo-nitzschia multistriata DD22	*psbC*	*psbC*
EF520325	Pseudo-nitzschia multistriata 279	*psbC*	*psbC*
EF520326	Pseudo-nitzschia galaxiae FB06	*psbC*	four-gene, *psbC*

EF520328	Pseudo-nitzschia galaxiae CLA1.D5	*psbC*	*psbC*
EF520329	Pseudo-nitzschia dolorosa AL59	*psbC*	*psbC*
EF520330	Pseudo-nitzschia delicatissima AL38	*psbC*	*psbC*
EF520331	Pseudo-nitzschia delicatissima CLA1.A1	*psbC*	four-gene, *psbC*
EF520332	Pseudo-nitzschia delicatissima AY7	*psbC*	*psbC*
EF520333	Pseudo-nitzschia fraudulenta AL75	*rbcL*	*rbcL*
EF520334	Pseudo-nitzschia multistriata CLA1.B3	*rbcL*	*rbcL*
EF520335	Pseudo-nitzschia multistriata DD22	*rbcL*	*rbcL*
EF520337	Pseudo-nitzschia multistriata 279	*rbcL*	*rbcL*
EF520338	Pseudo-nitzschia sp. CLA1.D2	*rbcL*	four-gene, LSU+*rbcL*, *rbcL*
EF520339	Pseudo-nitzschia sp. CLA1.D4	*rbcL*	*rbcL*
EF520340	Pseudo-nitzschia delicatissima CLA1.A1	*rbcL*	four-gene, LSU+*rbcL*, *rbcL*
EF520341	Pseudo-nitzschia delicatissima CLA1.A2	*rbcL*	*rbcL*
EF522108	Pseudo-nitzschia americana FBJUN06.1.6	LSU	four-gene, LSU+*rbcL*
EF522112	Pseudo-nitzschia galaxiae MOZ06.1.A3	LSU	LSU
EF522113	Pseudo-nitzschia galaxiae FB06.1.17	LSU	four-gene
EF522114	Pseudo-nitzschia delicatissima CLA1.A1	LSU	four-gene, LSU+*rbcL*, LSU
EF522115	Pseudo-nitzschia sp. CLA1.D2	LSU	four-gene, LSU+*rbcL*, LSU
EF531709	Pseudo-nitzschia turgiduloides 124C	LSU	LSU
EF566016	Pseudo-nitzschia delicatissima AR1	LSU	LSU+*rbcL*, LSU
EF642975	Pseudo-nitzschia fraudulenta AR3	LSU	LSU
EU090031	Nitzschia sp. AnM0026	SSU	SSU
EU090049	Nitzschia sp. AnM0026	*rbcL*	*rbcL*
FJ002104	Cylindrotheca closterium C27	*rbcL*	*rbcL*
FJ002125	Psammodictyon panduriforme C24	*rbcL*	*rbcL*
FJ002138	Fragilariopsis cylindrus C50	*rbcL*	SSU+*rbcL*
FJ150714	Pseudo-nitzschia calliantha ICMB-109	LSU	LSU+*rbcL*
FJ150720	Pseudo-nitzschia pungens ICMB-143	LSU	LSU+*rbcL*
FJ150732	Pseudo-nitzschia galaxiae ICMB-174	LSU	LSU+*rbcL*
FJ150734	Pseudo-nitzschia brasiliana ICMB-176	LSU	LSU+*rbcL*
FJ150735	Pseudo-nitzschia multistriata CM2	LSU	LSU+*rbcL*
FJ150737	Pseudo-nitzschia galaxiae ICMB-177	LSU	LSU+*rbcL*
FJ150740	Pseudo-nitzschia brasiliana ICMB-172	*rbcL*	SSU+*rbcL*
FJ150751	Pseudo-nitzschia galaxiae ICMB-174	*rbcL*	LSU+*rbcL*
FJ150752	Pseudo-nitzschia brasiliana ICMB-175	*rbcL*	*rbcL*
FJ150753	Pseudo-nitzschia brasiliana ICMB-176	*rbcL*	LSU+*rbcL*
FJ150754	Pseudo-nitzschia galaxiae ICMB-177	*rbcL*	LSU+*rbcL*

FJ150757	Pseudo-nitzschia multistriata CM2	*rbcL*	LSU+*rbcL*
FJ150758	Pseudo-nitzschia calliantha ICMB-109	*rbcL*	LSU+*rbcL*, *rbcL*
FJ150759	Pseudo-nitzschia pungens ICMB-143	*rbcL*	LSU+*rbcL*, *rbcL*
FJ150764	Pseudo-nitzschia delicatissima AR1	*rbcL*	LSU+*rbcL*
FJ214163	Nitzschia cf. pusilla ND 53	LSU	LSU
FJ489631	Pseudo-nitzschia linea ICMB-156	*rbcL*	LSU+*rbcL*
FJ489633	Pseudo-nitzschia linea ICMB-156	LSU	LSU+*rbcL*, LSU
FM207547	Pseudo-nitzschia pungens NA108	*rbcL*	*rbcL*
FM207548	Pseudo-nitzschia pungens NA213	*rbcL*	*rbcL*
FN557017	Nitzschia palea Brazil	*rbcL*	*rbcL*
FN557018	Nitzschia palea Japan A1	*rbcL*	*rbcL*
FN557019	Nitzschia palea Japan B1	*rbcL*	LSU+*rbcL*
FN557020	Nitzschia palea Japan E	*rbcL*	LSU+*rbcL*, *rbcL*
FN557021	Nitzschia palea Paraguay	*rbcL*	LSU+*rbcL*
FN557022	Nitzschia palea Spain A3	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
FN557023	Nitzschia palea Spain A4	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL*
FN557025	Nitzschia palea Spain C	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL*
FN557026	Nitzschia palea Belgium1	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
FN557029	Nitzschia palea Belgium4	*rbcL*	LSU+*rbcL*
FN557030	Nitzschia capitellata capitellata Scot1	*rbcL*	four-gene, LSU+*rbcL*
FN557031	Nitzschia capitellata capitellata Scot2	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*
FN557032	Nitzschia capitellata capitellata Spain	*rbcL*	four-gene, SSU+*rbcL*
FN557033	Nitzschia sigmoidea sigmoidea RBGE	*rbcL*	*rbcL*
FN557039	Nitzschia palea Brazil	*cox1*	*cox1*
FN557042	Nitzschia palea Japan F	*cox1*	*cox1*
FN557043	Nitzschia palea Japan E	*cox1*	*cox1*
FN557045	Nitzschia palea New Scot2	*cox1*	*cox1*
FN557046	Nitzschia palea New Spain1	*cox1*	*cox1*
FN557048	Nitzschia palea Paraguay	*cox1*	*cox1*
FN557049	Nitzschia palea Spain A3	*cox1*	*cox1*
FN557052	Nitzschia palea Spain C	*cox1*	*cox1*
FN557053	Nitzschia palea Japan B2	*cox1*	*cox1*
FN557054	Nitzschia palea Japan C	*cox1*	*cox1*
FN557055	Nitzschia palea Japan D	*cox1*	*cox1*
FN557057	Nitzschia palea Egypt	*cox1*	*cox1*

FN557058	Nitzschia palea SriLanka1	*cox1*	*cox1*
FN557059	Nitzschia palea UK	*cox1*	*cox1*
FN557060	Nitzschia cf. fonticola cf. fonticola 1	*cox1*	*cox1*
FN557061	Nitzschia cf. fonticola cf. fonticola 2	*cox1*	*cox1*
FN557062	Nitzschia cf. recta cf. recta	*cox1*	*cox1*
FN557063	Nitzschia palea SriLanka2	*cox1*	*cox1*
FR865501	Nitzschia epithemioides CCAP 1052/18	SSU	SSU
FR865513	Psammodictyon sp. CCAP 1062/1	SSU	SSU
GAKA01002849	Nitzschia sp. ChengR-2013 comp7_c0_seq1	SSU	SSU
GAPN01000170	Cylindrotheca closterium mira_c170	SSU	SSU
GAPN01002192	Cylindrotheca closterium mira_c2195	SSU	SSU
GAPN01006912	Cylindrotheca closterium mira_rep_c6950	SSU	SSU
GQ246179	Nitzschia sp. MD1	SSU	SSU
GQ396799	Nitzschia sp. DMST	SSU	SSU
GQ468529	Cylindrotheca closterium KMMCC:B-9	SSU	SSU
GQ468534	Cylindrotheca closterium KMMCC:B-88	SSU	SSU
GQ468535	Cylindrotheca closterium KMMCC:B-110	SSU	SSU
GQ468536	Cylindrotheca closterium KMMCC:B-119	SSU	SSU
GQ468539	Cylindrotheca closterium KMMCC:B-181	SSU	SSU
GQ468542	Cylindrotheca closterium KMMCC:B-361	SSU	SSU
GQ468545	Cylindrotheca closterium KMMCC:B-552	SSU	SSU
GQ844253	Cylindrotheca fusiformis CCMP344	*cox1*	*cox1*
GQ844270	Pseudo-nitzschia delicatissima DIAT223-07	*cox1*	*cox1*
GU254065	Pseudo-nitzschia brasiliana MMDL50424	LSU	LSU
GU373961	Pseudo-nitzschia australis SPC21	SSU	SSU
GU373964	Pseudo-nitzschia multiseries CCMP1660	SSU	SSU+*rbcL*, SSU
GU373965	Pseudo-nitzschia pseudodelicatissima SPC22	SSU	SSU
GU373968	Pseudo-nitzschia pungens CL205	SSU	SSU
GU373969	Pseudo-nitzschia seriata CCMP1440	SSU	SSU
GU373970	Pseudo-nitzschia sp. CCMP1309	SSU	SSU
GU591327	Durinskia baltica CS-38 ENDOSYMBIONT	*rbcL*	SSU+*rbcL*, *rbcL*, *psbC*
GU591328	Kryptoperidinium foliaceum CCMP1326	*rbcL*	SSU+*rbcL*, *rbcL*, *psbC*
GU732414	Nitzschia cf. pusilla YSW06	LSU	LSU
GU734794	Neodenticula seminae Broad-2001	LSU	LSU
GU734795	Neodenticula seminae Narrow-SP	LSU	LSU
HE798209	Nitzschia lembiformis R1	LSU	four+gene, LSU

HF675061	Nitzschia cf. ardua L44	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL*
HF675062	Nitzschia cf. aequorea DM1004CAT	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL*
HF675063	Nitzschia cf. bulnheimiana AG	*rbcL*	four-gene, LSU+*rbcL*, *rbcL*
HF675065	Nitzschia cf. fonticola cf. fonticola 2	*rbcL*	LSU+*rbcL*
HF675066	Nitzschia fonticola A-RT24	*rbcL*	LSU+*rbcL*
HF675068	Nitzschia fonticola C-RT26	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL*
HF675069	Nitzschia frustulum Nit24	*rbcL*	*rbcL*
HF675071	Nitzschia inconspicua G1_1	*rbcL*	*rbcL*
HF675072	Nitzschia inconspicua G1_2	*rbcL*	four-gene, SSU+*rbcL*
HF675073	Nitzschia inconspicua G1_3	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*
HF675074	Nitzschia inconspicua G2_1	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
HF675075	Nitzschia inconspicua G2_2	*rbcL*	four-gene, SSU+*rbcL*
HF675076	Nitzschia inconspicua G2_3	*rbcL*	LSU+*rbcL*
HF675080	Nitzschia inconspicua G3_1	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
HF675081	Nitzschia inconspicua G3_2	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*
HF675082	Nitzschia inconspicua G3_3	*rbcL*	four-gene, SSU+*rbcL*
HF675083	Nitzschia inconspicua G3_4	*rbcL*	four-gene, SSU+*rbcL*
HF675084	Nitzschia inconspicua G4_1	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL*
HF675085	Nitzschia inconspicua G4_2	*rbcL*	four-gene, SSU+*rbcL*
HF675087	Nitzschia inconspicua G5_1	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
HF675088	Nitzschia inconspicua G5_2	*rbcL*	four-gene, SSU+*rbcL*
HF675089	Nitzschia inconspicua G5-3	*rbcL*	LSU+*rbcL*
HF675102	Nitzschia inconspicua G6_1	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL*
HF675103	Nitzschia cf. microcephala L56	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
HF675104	Nitzschia palea L15	*rbcL*	*rbcL*
HF675107	Nitzschia palea laia46	*rbcL*	*rbcL*
HF675108	Nitzschia pusilla L1	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
HF675109	Nitzschia pusilla L3	*rbcL*	four-gene, SSU+*rbcL*
HF675110	Nitzschia pusilla L25	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL*
HF675111	Nitzschia soratensis DM1009MK	*rbcL*	four-gene, SSU+*rbcL*

HF675112	Nitzschia soratensis DM1008MK	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL*
HF675116	Nitzschia sp. s0819	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
HF675117	Tryblionella sp. s0863	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL*
HF675118	Nitzschia amphibia amphibia-RT5	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL*
HF675119	Nitzschia cf. pusilla Nit44	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
HF675120	Nitzschia palea Spain A1	*rbcL*	*rbcL*
HF675121	Nitzschia palea SriLanka1	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
HF675122	Nitzschia palea SriLanka2	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
HF675123	Nitzschia palea Japan F	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*
HF675124	Nitzschia palea Spain A2	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL*
HF675125	Nitzschia palea Japan D	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL*
HF675127	Nitzschia palea New Spain2	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL*
HF675128	Nitzschia palea New Scot2	*rbcL*	LSU+*rbcL*, *rbcL*
HF675129	Nitzschia cf. pusilla CCMP558	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
HF679146	Nitzschia cf. aequorea Nit1004CAT	LSU	four-gene, LSU+*rbcL*, LSU
HF679147	Nitzschia cf. ardua L44	LSU	four-gene, LSU+*rbcL*, LSU
HF679148	Nitzschia capitellata capitellata Scot1	LSU	four-gene
HF679149	Nitzschia capitellata capitellata Scot2	LSU	four-gene, LSU
HF679151	Nitzschia cf. fonticola cf. fonticola 2	LSU	LSU+*rbcL*, LSU
HF679152	Nitzschia inconspicua G1_2	LSU	four-gene
HF679153	Nitzschia inconspicua G1_3	LSU	four-gene, LSU+*rbcL*, LSU
HF679154	Nitzschia inconspicua G2_1	LSU	four-gene
HF679155	Nitzschia inconspicua G2_2	LSU	four-gene
HF679156	Nitzschia inconspicua G2_3	LSU	LSU+*rbcL*, LSU
HF679160	Nitzschia inconspicua G3_2	LSU	four-gene, LSU+*rbcL*, LSU
HF679161	Nitzschia inconspicua G3_3	LSU	four-gene
HF679163	Nitzschia inconspicua G4_1	LSU	four-gene, LSU+*rbcL*, LSU
HF679164	Nitzschia inconspicua G4_2	LSU	four-gene
HF679166	Nitzschia inconspicua G5_1	LSU	four-gene
HF679167	Nitzschia inconspicua G5_2	LSU	four-gene
HF679168	Nitzschia inconspicua G5_3	LSU	LSU+*rbcL*
HF679175	Nitzschia inconspicua G5_11	LSU	LSU

HF679184	Nitzschia inconspicua G6_1	LSU	four-gene, LSU+*rbcL*, LSU
HF679185	Nitzschia inconspicua G7_1	LSU	four-gene, LSU+*rbcL*, LSU
HF679186	Nitzschia cf. microcephala L56	LSU	four-gene
HF679190	Nitzschia palea L18	LSU	LSU
HF679192	Nitzschia palea New Spain 1	LSU	LSU
HF679193	Nitzschia pusilla L1	LSU	four-gene
HF679195	Nitzschia pusilla L3	LSU	four-gene
HF679196	Nitzschia pusilla L25	LSU	four-gene, LSU+*rbcL*, LSU
HF679197	Nitzschia soratensis DM1008MK	LSU	four-gene
HF679198	Nitzschia soratensis DM1009MK	LSU	four-gene, LSU+*rbcL*, LSU
HF679199	Nitzschia cf. pusilla Nit 44	LSU	four-gene, LSU
HF679201	Nitzschia palea New Spain2	LSU	four-gene, LSU+*rbcL*
HF679202	Nitzschia palea Belgium 4	LSU	LSU+*rbcL*, LSU
HF679203	Nitzschia palea New Scot2	LSU	LSU+*rbcL*, LSU
HF679204	Nitzschia cf. pusilla CCMP558	LSU	four-gene, LSU+*rbcL*, LSU
HM627325	Koernerella recticostata	*psbC*	*psbC*
HM805020	Bacillaria cf. paxillifer BA14c	SSU	SSU
HM805036	Nitzschia cf. fonticola BA34	SSU	SSU
HM805040	Nitzschia microcephala BA85	SSU	SSU
HQ111378	Pseudo-nitzschia brasiliana PnPm07	LSU	LSU
HQ111396	Pseudo-nitzschia dolorosa PnKk08	LSU	LSU
HQ317078	Nitzschia cf. promare CCMP:1116	*cox1*	*cox1*
HQ317079	Nitzschia sp. BOLD:AAX5147	*cox1*	*cox1*
HQ317080	Fragilariopsis curta CCMP:553	*cox1*	*cox1*
HQ317081	Fragilariopsis cylindrus CCMP:557	*cox1*	*cox1*
HQ317084	Nitzschia sp. CCMP581	*cox1*	*cox1*
HQ317085	Nitzschia sp. CCMP1532	*cox1*	*cox1*
HQ317086	Nitzschia sp. CCMP2533	*cox1*	*cox1*
HQ317087	Pseudo-nitzschia subcurvata CCMP:1431	*cox1*	*cox1*
HQ337558	Nitzschia cf. incrustans CCMP:1086	*rbcL*	LSU+*rbcL*
HQ337561	Nitzschia cf. promare CCMP:1116	*rbcL*	LSU+*rbcL*
HQ337572	Nitzschia laevis CCMP:559	*rbcL*	LSU+*rbcL*
HQ337573	Tryblionella compressa CCMP:561	*rbcL*	LSU+*rbcL*
HQ396820	Nitzschia cf. incrustans CCMP:1086	LSU	LSU+*rbcL*, LSU
HQ396835	Nitzschia laevis CCMP:559	LSU	LSU+*rbcL*
HQ396837	Tryblionella compressa CCMP:561	LSU	LSU+*rbcL*, LSU
HQ656837	Cylindrotheca closterium PCC:610	*rbcL*	*rbcL*

HQ912279	Eunotia glacialis UTEX FD46	*psbC*	four-gene, *psbC*
HQ912282	Nitzschia filiformis UTEX FD267	*psbC*	four-gene, *psbC*
HQ912287	Achnanthes coarctata UTEX FD185	*psbC*	four-gene, *psbC*
HQ912292	Eunotia bilunaris UTEX FD412	*psbC*	four-gene, *psbC*
HQ912293	Tryblionella apiculata UTEX FD465	*psbC*	four-gene, *psbC*
HQ912303	Denticula kuetzingii UTEX FD135	*psbC*	four-gene, *psbC*
HQ912320	Bacillaria paxillifera UTEX FD468	*psbC*	four-gene, *psbC*
HQ912329	Eunotia pectinalis NIES461	*psbC*	four-gene, *psbC*
HQ912338	Cylindrotheca closterium CCMP1855	*psbC*	four-gene
HQ912376	Hantzschia amphioxys var. major A4	*psbC*	four-gene, *psbC*
HQ912390	Hantzschia amphioxys var. major A4	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
HQ912404	Hantzschia amphioxys var. major A4	SSU	four-gene, SSU+*rbcL*, SSU
HQ912450	Eunotia glacialis UTEX FD46	*rbcL*	four-gene
HQ912453	Nitzschia filiformis UTEX FD267	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
HQ912458	Achnanthes coarctata UTEX FD185	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
HQ912463	Eunotia bilunaris UTEX FD412	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
HQ912464	Tryblionella apiculata UTEX FD465	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
HQ912474	Denticula kuetzingii UTEX FD135	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
HQ912491	Bacillaria paxillifera UTEX FD468	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
HQ912500	Eunotia pectinalis NIES461	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
HQ912509	Cylindrotheca closterium CCMP1855	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
HQ912586	Eunotia glacialis UTEX FD46	SSU	four-gene, SSU+*rbcL*, SSU
HQ912589	Nitzschia filiformis UTEX FD267	SSU	four-gene, SSU+*rbcL*, SSU
HQ912594	Achnanthes coarctata UTEX FD185	SSU	four-gene, SSU+*rbcL*
HQ912599	Eunotia bilunaris UTEX FD412	SSU	four-gene, SSU+*rbcL*, SSU
HQ912600	Tryblionella apiculata UTEX FD465	SSU	four-gene, SSU+*rbcL*, SSU
HQ912610	Denticula kuetzingii UTEX FD135	SSU	four-gene, SSU+*rbcL*, SSU
HQ912627	Bacillaria paxillifera UTEX FD468	SSU	four-gene, SSU+*rbcL*, SSU
HQ912636	Eunotia pectinalis NIES461	SSU	four-gene, SSU+*rbcL*, SSU
HQ912645	Cylindrotheca closterium CCMP1855	SSU	four-gene, SSU+*rbcL*
JF790980	"Cymbella cistuliformis" 1113	SSU	SSU
JF790983	"Cymbella cistuliformis" 1120	SSU	SSU
JF794052	Nitzschia sp. RCC2276	SSU	SSU
JN050293	Pseudo-nitzschia calliantha NL2	LSU	LSU
JN050296	Pseudo-nitzschia fryxelliana NWFSC 241	LSU	LSU+*rbcL*, LSU
JN050298	Pseudo-nitzschia hasleana NWFSC 186	LSU	LSU+*rbcL*
JN050300	Pseudo-nitzschia lineola NWFSC 188	LSU	LSU

JN050301	Pseudo-nitzschia cf. turgidula NWFSC 255	LSU	LSU
JN050302	Pseudo-nitzschia fryxelliana NWFSC 241	*rbcL*	LSU+*rbcL*, *rbcL*
JN050304	Pseudo-nitzschia hasleana NWFSC 186	*rbcL*	LSU+*rbcL*, *rbcL*
JN050306	Pseudo-nitzschia cuspidata NWFSC 194	*cox1*	*cox1*
JN050307	Pseudo-nitzschia cuspidata Sydney1	*cox1*	*cox1*
JN050308	Pseudo-nitzschia fryxelliana NWFSC 241	*cox1*	*cox1*
JN050310	Pseudo-nitzschia hasleana NWFSC 186	*cox1*	*cox1*
JN050311	Pseudo-nitzschia hasleana NWFSC 252	*cox1*	*cox1*
JN050312	Pseudo-nitzschia lineola NWFSC 188	*cox1*	*cox1*
JN091716	Pseudo-nitzschia calliantha NWFSC185	SSU	SSU+*rbcL*
JN378735	Durinskia baltica ENDOSYMBIONT	*cox1*	*cox1*
JN599166	Pseudo-nitzschia australis 10249 10AB	SSU	SSU
JQ582669	Nitzschia frigida NF11	SSU	SSU
JQ776550	Pseudo-nitzschia calliantha CAWD114	LSU	LSU
JQ995391	Pseudo-nitzschia sp. MALINA_E10N1	LSU	LSU
JQ995403	Cylindrotheca closterium RCC1985	LSU	LSU
JQ995416	Pseudo-nitzschia arctica RCC2002	LSU	LSU+*rbcL*
JQ995421	Pseudo-nitzschia sp. RCC2008	LSU	LSU
JQ995450	Nitzschia sp. RCC2276	LSU	LSU
JX316762	Hantzschia sp. CCAP 1030/1	SSU	SSU
JX970999	Cylindrotheca closterium lineage V Mid15	*rbcL*	*rbcL*
JX971000	Cylindrotheca closterium lineage V D8	*rbcL*	*rbcL*
JX971011	Cylindrotheca sp. lineage IV OS1	*rbcL*	*rbcL*
JX971016	Cylindrotheca sp. lineage III OS9b	*rbcL*	*rbcL*
KC017445	Pseudo-nitzschia micropora PS90	LSU	LSU
KC017452	Pseudo-nitzschia calliantha TURB	LSU	LSU
KC017454	Pseudo-nitzschia cuspidata MER	LSU	LSU
KC017455	Pseudo-nitzschia delicatissima CHA	LSU	LSU
KC017456	Pseudo-nitzschia delicatissima CHB	LSU	LSU
KC017457	Pseudo-nitzschia fraudulenta PH25F	LSU	LSU
KC017458	Pseudo-nitzschia multiseries COOG	LSU	LSU
KC017459	Pseudo-nitzschia multistriata PH25D	LSU	LSU
KC017461	Pseudo-nitzschia americana PH25	LSU	LSU
KC017462	Pseudo-nitzschia pungens DR	LSU	LSU
KC147533	Pseudo-nitzschia circumpora PnSb58	LSU	LSU
KC147534	Pseudo-nitzschia batesiana PnTb19	LSU	LSU
KC147537	Pseudo-nitzschia fukuyoi PnTb72	LSU	LSU

KC147544	Pseudo-nitzschia lundholmiae PnTb48	LSU	LSU
KC309473	Achnanthes sp. MPA-2013 SanNic1Achnan	SSU	four-gene, SSU+*rbcL*
KC309474	Achnanthes sp. MPA-2013 ECT3883Achnan	SSU	four-gene, SSU+*rbcL*, SSU
KC309475	Achnanthes sp. MPA-2013 ECT3911Achnan	SSU	four-gene, SSU+*rbcL*, SSU
KC309476	Achnanthes sp. MPA-2013 ECT3684Achnan	SSU	four-gene, SSU+*rbcL*, SSU
KC309480	Eunotia sp. MPA-2013 ECT3676Eunotia	SSU	four-gene, SSU+*rbcL*
KC309545	Achnanthes sp. MPA-2013 SanNic1Achnan	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
KC309546	Achnanthes sp. MPA-2013 ECT3883Achnan	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
KC309547	Achnanthes sp. MPA-2013 ECT3911Achnan	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
KC309548	Achnanthes sp. MPA-2013 ECT3684Achnan	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
KC309552	Eunotia sp. MPA-2013 ECT3676Eunotia	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
KC309617	Achnanthes sp. MPA-2013 SanNic1Achnan	*psbC*	four-gene, *psbC*
KC309618	Achnanthes sp. MPA-2013 ECT3883Achnan	*psbC*	four-gene, *psbC*
KC309619	Achnanthes sp. MPA-2013 ECT3911Achnan	*psbC*	four-gene, *psbC*
KC309620	Achnanthes sp. MPA-2013 ECT3684Achnan	*psbC*	four-gene, *psbC*
KC309623	Eunotia sp. MPA-2013 ECT3676Eunotia	*psbC*	four-gene, *psbC*
KC509522	Cylindrotheca closterium CCMP1855	genome	*rbcL*, *psbC*
KC736602	Nitzschia acidoclinata TCC537	*rbcL*	SSU+*rbcL*
KC736604	Nitzschia costei TCC521 **ex N. cf. frustulum**	*rbcL*	SSU+*rbcL*, *rbcL*
KC736605	Nitzschia draveillensis TCC700	*rbcL*	SSU+*rbcL*, *rbcL*
KC736606	Nitzschia inconspicua TCC481	*rbcL*	*rbcL*
KC736607	Nitzschia inconspicua TCC487	*rbcL*	SSU+*rbcL*, *rbcL*
KC736608	Nitzschia lorenziana TCC516	*rbcL*	SSU+*rbcL*, *rbcL*
KC736609	Nitzschia palea TCC435	*rbcL*	four-gene, SSU+*rbcL*
KC736610	Nitzschia palea TCC570	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
KC736611	Nitzschia palea TCC583	*rbcL*	SSU+*rbcL*
KC736632	Nitzschia acidoclinata TCC537	SSU	four-gene, SSU+*rbcL*
KC736633	Nitzschia acidoclinata TCC543	SSU	SSU
KC736634	Nitzschia costei TCC521 **ex N. cf. frustulum**	SSU	SSU+*rbcL*, SSU+*rbcL*
KC736635	Nitzschia draveillensis TCC700	SSU	four-gene, SSU+*rbcL*, SSU
KC736636	Nitzschia inconspicua TCC487	SSU	four-gene, SSU+*rbcL*, SSU
KC736637	Nitzschia lorenziana TCC516	SSU	SSU+*rbcL*
KC736638	Nitzschia palea TCC435	SSU	four-gene, SSU+*rbcL*
KC736639	Nitzschia palea TCC570	SSU	four-gene, SSU+*rbcL*
KC736640	Nitzschia palea TCC583	SSU	SSU+*rbcL*
KC736648	Nitzschia acidoclinata TCC543	*cox1*	*cox1*
KC736649	Nitzschia inconspicua TCC481	*cox1*	*cox1*

KC736650	Nitzschia palea TCC435	*cox1*	*cox1*
KC736651	Nitzschia palea TCC570	*cox1*	*cox1*
KC759159	Nitzschia microcephala Som	SSU	SSU
KC801036	Pseudo-nitzschia arenysensis SZN-B487	*rbcL*	*rbcL*
KC801037	Pseudo-nitzschia cf. delicatissima SZN-B507	*rbcL*	LSU+*rbcL*, *rbcL*
KC801039	Pseudo-nitzschia pseudodelicatissima SZN-B317	*rbcL*	*rbcL*
KC801040	Pseudo-nitzschia multiseries NWFSC-316	*rbcL*	SSU+*rbcL*
KC801041	Pseudo-nitzschia cf. delicatissima SZN-B507	LSU	LSU+*rbcL*, LSU
KC832999	Fragilariopsis kerguelensis MM_E13B2	LSU	four-gene, LSU+*rbcL*, LSU
KF006838	Pseudo-nitzschia subpacifica Pn252-07E7	LSU	LSU
KF177695	Bacillariophyta sp. 1 MAB-2013 GSP108-1	SSU	SSU
KF177708	Bacillariophyta sp. 1 MAB-2013 GSP127-1	SSU	SSU
KF177730	Bacillariophyta sp. MAB-2013 GSP162-1	SSU	SSU
KF177731	Bacillariophyta sp. MAB-2013 GSP163-1	SSU	SSU
KF177772	Bacillariophyta sp. MAB-2013 GSPBP-1	SSU	SSU
KF177774	Navicula pulchripora UTEX 2604	SSU	SSU
KF177775	Nitzschia laevis UTEX 2047	SSU	SSU
KF241715	Pseudo-nitzschia multistriata SZN-B531	LSU	LSU
KF417684	Nitzschia dissipata 05DB2_22	SSU	SSU
KF417685	Nitzschia fonticola Wb1b1	SSU	SSU
KF417686	Nitzschia fonticola 05DB3_20	SSU	SSU
KF417687	Nitzschia palea TPA1	SSU	SSU
KF417688	Nitzschia pusilla QB21	SSU	SSU
KF482043	Pseudo-nitzschia kodamae PnPd31	LSU	LSU
KF482045	Pseudo-nitzschia kodamae PnPd36	LSU	LSU
KF482046	Pseudo-nitzschia kodamae PnPd39	LSU	LSU
KF482048	Pseudo-nitzschia caciantha PnSL03	LSU	LSU
KF482049	Pseudo-nitzschia caciantha PnSL05	LSU	LSU
KF733443	Eunotia naegelii UTEX FD354	genome	*rbcL*, *psbC*
KF955284	Nitzschia bizertensis BD2	LSU	LSU
KF955285	Nitzschia bizertensis BD2	SSU	SSU
KF959639	Nitzschia palea TCC139-2	*rbcL*	SSU+*rbcL*
KF959653	Nitzschia palea TCC139-2	SSU	SSU+*rbcL*
KJ463434	Amphora laevissima 7314-AMPH085	SSU	four-gene, SSU+*rbcL*, SSU
KJ463436	Amphora obtusa_var_crassa 6951-AMPH070	SSU	four-gene, SSU+*rbcL*, SSU
KJ463464	Amphora laevissima 7314-AMPH085	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*

KJ463466	Amphora obtusa_var_crassa 6951-AMPH070	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
KJ463494	Amphora laevissima 7314-AMPH085	*psbC*	four-gene, *psbC*
KJ463496	Amphora obtusa_var_crassa 6951-AMPH070	*psbC*	four-gene, *psbC*
KJ542393	Nitzschia palea TCC531	LSU	LSU+*rbcL*
KJ542395	Nitzschia palea TCC563	LSU	LSU+*rbcL*, LSU
KJ542397	Nitzschia palea TCC570	LSU	four-gene
KJ542400	Nitzschia palea TCC480	LSU	LSU+*rbcL*, LSU
KJ542401	Nitzschia palea TCC486	LSU	LSU+*rbcL*, LSU
KJ542402	Nitzschia palea TCC476	LSU	LSU+*rbcL*, LSU
KJ542411	Nitzschia palea TCC703	LSU	LSU+*rbcL*, LSU
KJ542412	Nitzschia palea TCC468	LSU	LSU+*rbcL*, LSU
KJ542413	Nitzschia palea TCC456	LSU	LSU+*rbcL*
KJ542414	Nitzschia palea TCC435	LSU	four-gene
KJ542416	Nitzschia palea DM1010	LSU	LSU+*rbcL*, LSU
KJ542420	Nitzschia palea TCC620	LSU	LSU+*rbcL*, LSU
KJ542426	Nitzschia palea TCC603	LSU	LSU+*rbcL*
KJ542428	Nitzschia palea TCC588	LSU	LSU+*rbcL*
KJ542429	Nitzschia palea R12	LSU	four-gene
KJ542431	Nitzschia palea TCC139-1	LSU	LSU+*rbcL*, LSU
KJ542452	Nitzschia palea TCC603	*cox1*	*cox1*
KJ542457	Nitzschia palea TCC531	*rbcL*	LSU+*rbcL*
KJ542460	Nitzschia palea TCC563	*rbcL*	LSU+*rbcL*, *rbcL*
KJ542465	Nitzschia palea TCC480	*rbcL*	LSU+*rbcL*, *rbcL*
KJ542468	Nitzschia palea TCC476	*rbcL*	LSU+*rbcL*, *rbcL*
KJ542483	Nitzschia palea TCC703	*rbcL*	LSU+*rbcL*, *rbcL*
KJ542484	Nitzschia palea TCC468	*rbcL*	LSU+*rbcL*, *rbcL*
KJ542485	Nitzschia palea TCC456	*rbcL*	LSU+*rbcL*
KJ542486	Nitzschia palea TCC425	*rbcL*	LSU+*rbcL*, *rbcL*
KJ542489	Nitzschia palea DM1010	*rbcL*	LSU+*rbcL*
KJ542493	Nitzschia palea TCC620	*rbcL*	LSU+*rbcL*
KJ542494	Nitzschia palea TCC623	*rbcL*	*rbcL*
KJ542499	Nitzschia palea TCC603	*rbcL*	LSU+*rbcL*, *rbcL*
KJ542501	Nitzschia palea TCC588	*rbcL*	LSU+*rbcL*, *rbcL*
KJ542502	Nitzschia palea R12	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
KJ542504	Nitzschia palea Japan A2	*rbcL*	*rbcL*
KJ542505	Nitzschia palea Japan B2	*rbcL*	LSU+*rbcL*, *rbcL*
KJ542506	Nitzschia palea Japan C	*rbcL*	LSU+*rbcL*

KJ542515	Nitzschia palea SriLanka1	*rbcL*	LSU+*rbcL*
KJ542516	Nitzschia palea SriLanka2	*rbcL*	LSU+*rbcL*
KJ542517	Nitzschia palea BB2b	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL*
KJ542519	Nitzschia palea TCC 139-1	*rbcL*	SSU+*rbcL*
KJ577899	Nitzschia martiana TN-2014 3VIII07N.martyana [as Navicula]	*rbcL*	*rbcL*
KJ577933	Nitzschia martiana TN-2014 3VIII07N.martyana [as Navicula]	*psbC*	*psbC*
KJ608078	Pseudo-nitzschia galaxiae SZN-B606	SSU	four-gene, SSU+*rbcL*
KJ671730	Cylindrotheca closterium 10	*cox1*	*cox1*
KJ671736	Nitzschia longissima 33	*cox1*	*cox1*
KJ671737	Psammodictyon panduriforme L	*cox1*	*cox1*
KJ671739	Pseudo-nitzschia sp. A2ni	*cox1*	*cox1*
KJ866907	Pseudo-nitzschia granii UNC1102	SSU	SSU+*rbcL*, SSU+*rbcL*
KJ866919	Fragilariopsis kerguelensis L26-C5	SSU	four-gene, SSU+*rbcL*, SSU
KJ961684	Eunotia sp. 2A LKM-2015	SSU	SSU
KJ961686	Eunotia sp. 8 LKM-2015	SSU	SSU
KJ961687	Eunotia sp. 17	SSU	SSU
KJ961688	Eunotia sp. 5	SSU	SSU
KJ961689	Eunotia sp. 13	SSU	SSU
KJ961690	Eunotia sp. 6 LKM-2015	SSU	SSU
KJ961692	Eunotia sp. 116	SSU	SSU
KJ961694	Eunophora sp. 107	SSU	SSU
KJ961695	Eunotia sp. 18	SSU	SSU
KJ961696	Eunotia sp. 44	SSU	SSU
KJ961697	Eunotia sp. 41	SSU	SSU
KJ961699	Eunotia sp. 30	SSU	SSU
KJ961700	Actinella sp. 111	SSU	SSU
KJ961701	Actinella sp. 99	SSU	SSU
KJ961706	Eunotia sp. 60	SSU	SSU
KJ961707	Eunotia sp. 62	SSU	SSU
KJ961709	Eunotia sp. 63	SSU	SSU
KM116079	Hantzschia sp. LFS-2014 D03	SSU	SSU
KM116080	Hantzschia sp. LFS-2014 D04	SSU	SSU
KM116081	Hantzschia amphioxys var. major D06	SSU	SSU
KM116083	Hantzschia amphioxys var. major D08	SSU	SSU
KM116084	Hantzschia elongata D11	SSU	SSU

KM116085	Hantzschia amphioxys FLA02	SSU	SSU
KM116086	Hantzschia amphioxys FLA03	SSU	SSU
KM116087	Hantzschia amphioxys FLA04	SSU	SSU
KM116088	Hantzschia amphioxys E01	SSU	SSU
KM116089	Hantzschia amphioxys A06	SSU	SSU
KM116090	Hantzschia amphioxys A07	SSU	SSU
KM116091	Hantzschia amphioxys A08	SSU	SSU
KM116092	Hantzschia amphioxys E06	SSU	SSU
KM116093	Hantzschia amphioxys E07	SSU	SSU
KM116094	Hantzschia sigma F01	SSU	SSU
KM116101	Hantzschia spectabilis E08	SSU	SSU
KM116105	Nitzschia commutata B02	SSU	SSU
KM116106	Hantzschia amphioxys f. muelleri FLA05	SSU	SSU
KM116107	Hantzschia amphioxys FLA06	SSU	SSU
KM116110	Hantzschia sp. FLA09	SSU	SSU
KM116111	Hantzschia sp. FLA10	SSU	SSU
KM116112	Hantzschia sp. FLA11	SSU	SSU
KM386874	Pseudo-nitzschia brasiliana CCMA405	SSU	SSU
KM387719	Nitzschia cf. communis T6-NC11	SSU	SSU
KM400622	Pseudo-nitzschia sabit PnPd76	LSU	LSU
KM400623	Pseudo-nitzschia sabit PnPd75	LSU	LSU
KM407565	Hantzschia sp. Ant005-E01	LSU	LSU
KM407568	Hantzschia amphioxys Ant025-E04	LSU	LSU
KM407571	Hantzschia amphioxys UTEX-FD339-E07	LSU	LSU
KM407572	Hantzschia amphioxys UTEX-FD339-E08	LSU	LSU
KM407574	Hantzschia elongata UTEX-FD421-E10	LSU	LSU
KM407578	Hantzschia amphioxys var. major UTEX-FD348-F02	LSU	LSU
KM407579	Hantzschia amphioxys var. major UTEX-FD348-F03	LSU	LSU
KM407583	Hantzschia sigma UTEX-FD313-F11	LSU	LSU
KM407587	Hantzschia spectabilis UTEX-FD269-G06	LSU	LSU
KM407588	Hantzschia spectabilis UTEX-FD269-G07	LSU	LSU
KM407589	Hantzschia spectabilis UTEX-FD269-G08	LSU	LSU
KM999113	Nitzschia cf. sigmoidea KEL-2015 JAR89_G2Run12	*rbcL*	*rbcL*
KM999114	Hantzschia elongata JAR79_D8Run13	*rbcL*	*rbcL*
KM999115	Eunotia sp. KEL 2015 JAR78_D2Run13	*rbcL*	*rbcL*

KP099755	Uncultured Nitzschia a70	LSU	LSU
KP101078	Pseudo-nitzschia plurisecta Ner-A1	*cox1*	*cox1*
KP101081	Pseudo-nitzschia abrensis Ner-J2	*cox1*	*cox1*
KP288520	Pseudo-nitzschia sabit Ps102	*cox1*	*cox1*
KP288521	Pseudo-nitzschia sabit Ps277	*cox1*	*cox1*
KP288522	Pseudo-nitzschia sabit Ps283	*cox1*	*cox1*
KP337356	Pseudo-nitzschia decipiens PnKk38	LSU	LSU
KP708987	Pseudo-nitzschia arenysensis PnKk40	SSU	SSU+*rbcL*, SSU
KP708989	Pseudo-nitzschia batesiana PnTb19	SSU	SSU
KP708990	Pseudo-nitzschia brasiliana PnSm07	SSU	SSU+*rbcL*
KP708992	Pseudo-nitzschia caciantha PnSL05	SSU	SSU+*rbcL*
KP708993	Pseudo-nitzschia circumpora PnPd27	SSU	SSU
KP708995	Pseudo-nitzschia cuspidata PnPd29	SSU	SSU+*rbcL*, SSU
KP708996	Pseudo-nitzschia decipiens PnKk38	SSU	SSU
KP708999	Pseudo-nitzschia fukuyoi PnTb39	SSU	SSU
KP709000	Pseudo-nitzschia kodamae PnPd31	SSU	SSU
KP709002	Pseudo-nitzschia lundholmiae PnTb28	SSU	SSU
KP709003	Pseudo-nitzschia micropora PnKk14	SSU	SSU
KP709004	Pseudo-nitzschia pungens PnKd05	SSU	SSU+*rbcL*
KP709006	Pseudo-nitzschia sabit PnPd83	SSU	SSU
KP750173	Pseudo-nitzschia multistriata Ps143	*cox1*	*cox1*
KP750174	Pseudo-nitzschia multistriata Ps91	*cox1*	*cox1*
KP750176	Pseudo-nitzschia brasiliana Ps148	*cox1*	*cox1*
KP750177	Pseudo-nitzschia delicatissima Ps101	*cox1*	*cox1*
KP941049	Pseudo-nitzschia brasiliana Ps148	LSU	LSU
KP941050	Pseudo-nitzschia delicatissima Ps101	LSU	LSU
KR048205	Simonsenia aveniformis	*rbcL*	*rbcL*
KR709240	Pseudo-nitzschia multiseries	genome	*rbcL*, *psbC*
KR871383	Pseudo-nitzschia pungens PnKL16	*cox1*	*cox1*
KR871387	Pseudo-nitzschia pungens PnSb63	*cox1*	*cox1*
KR871388	Pseudo-nitzschia brasiliana PnSm07	*cox1*	*cox1*
KR871390	Pseudo-nitzschia batesiana PnTb19	*cox1*	*cox1*
KR871391	Pseudo-nitzschia fukuyoi PnTb25	*cox1*	*cox1*
KT072921	Nitzschia fonticola TCC533	*rbcL*	four-gene, SSU+*rbcL*
KT072924	Nitzschia capitellata TCC579	*rbcL*	SSU+*rbcL*
KT072926	Nitzschia cf. pusilla TCC586	*rbcL*	four-gene, SSU+*rbcL*

KT072967	Nitzschia inconspicua TCC510 **ex N hantzschiana**	SSU	four-gene, SSU+*rbcL*, SSU
KT072971	Nitzschia acidoclinata TCC538	SSU	four-gene, SSU+*rbcL*
KT072978	Nitzschia capitellata TCC579	SSU	SSU+*rbcL*, SSU
KT072985	Nitzschia palea TCC609	SSU	SSU
KT189135	Pseudo-nitzschia hasleana 208	LSU	LSU
KT189138	Pseudo-nitzschia fraudulenta 339b	LSU	LSU
KT288116	Eunotia cf. mucophila PV-2015 LB2	*rbcL*	*rbcL*
KT288118	Eunotia cf. mucophila PV-2015 BST1	*rbcL*	*rbcL*
KT288119	Eunotia cf. mucophila PV-2015 BST10	*rbcL*	*rbcL*
KT288120	Eunotia cf. mucophila PV-2015 JP11	*rbcL*	*rbcL*
KT288121	Eunotia bilunaris labile DM33-5	*rbcL*	*rbcL*
KT288122	Eunotia bilunaris labile DM33-9	*rbcL*	*rbcL*
KT288123	Eunotia bilunaris labile DM33-18	*rbcL*	*rbcL*
KT288124	Eunotia bilunaris labile DM33_08_2	*rbcL*	*rbcL*
KT288125	Eunotia bilunaris labile WAR_60	*rbcL*	*rbcL*
KT288127	Eunotia bilunaris slender DM33-15	*rbcL*	*rbcL*
KT288130	Eunotia bilunaris slender DM33-17	*rbcL*	*rbcL*
KT288131	Eunotia bilunaris robust DM33-1	*rbcL*	*rbcL*
KT288132	Eunotia bilunaris robust DM33-3	*rbcL*	*rbcL*
KT288135	Eunotia bilunaris robust DM22-5	*rbcL*	*rbcL*
KT288136	Eunotia bilunaris robust DM22-12	*rbcL*	*rbcL*
KT288141	Eunotia bilunaris robust WAR_63	*rbcL*	*rbcL*
KT288142	Eunotia bilunaris robust ROUS_1	*rbcL*	*rbcL*
KT288148	Eunotia bilunaris robust LADm_24	*rbcL*	*rbcL*
KT288152	Eunotia cf. latitaenia PV-2015 LADm_23	*rbcL*	*rbcL*
KT288155	Eunotia cf. latitaenia PV-2015 LADm_57	*rbcL*	*rbcL*
KT288157	Eunotia cf. latitaenia PV-2015 LADm_62	*rbcL*	*rbcL*
KT693309	Cymbellonitzschia banzuensis 10928-CN01	*rbcL*	SSU+*rbcL*, *rbcL*
KT693310	Cymbellonitzschia banzuensis 10928-CN01	SSU	SSU+*rbcL*, SSU
KT808257	Pseudo-nitzschia arctica RCC2002	*rbcL*	LSU+*rbcL*
KT860972	Nitzschia sp. RCC466	SSU	SSU
KT860982	Nitzschia sp. RCC826	SSU	SSU
KT861012	Nitzschia sp. RCC2934	SSU	SSU
KT861018	Psammodictyon sp. RCC3091	SSU	SSU
KT861227	Nitzschia sp. RCC80	SSU	SSU
KT886104	Nitzschia sp. KAS622	SSU	SSU

KT943601	Achnanthes sp. SZCZCH113	SSU	four-gene, SSU+*rbcL*, SSU
KT943602	Achnanthes sp. SZCZM119	SSU	four-gene, SSU+*rbcL*
KT943615	Achnanthes sp. SZCZCH113	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
KT943616	Achnanthes sp. SZCZM119	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
KT943626	Achnanthes sp. SZCZCH113	*psbC*	four-gene, *psbC*
KT943627	Achnanthes sp. SZCZM119	*psbC*	four-gene, *psbC*
KT943638	Tryblionella gaoana SZCZCH97	SSU	four-gene, SSU+*rbcL*, SSU
KT943639	Nitzschia aurariae SZCZCH966	SSU	four-gene, SSU+*rbcL*, SSU
KT943640	Nitzschia valdestriata SZCZCH969	SSU	four-gene, SSU+*rbcL*, SSU
KT943641	Nitzschia cf. volvendirostrata SZCZCH845	SSU	four-gene, SSU+*rbcL*, SSU
KT943642	Nitzschia traheaformis SZCZCH970	SSU	four-gene, SSU+*rbcL*
KT943643	Nitzschia traheaformis SZCZCH971	SSU	four-gene, SSU+*rbcL*, SSU
KT943644	Nitzschia traheaformis SZCZCH972	SSU	four-gene, SSU+*rbcL*
KT943648	Amphora vixvisibilis SZCZCH967	SSU	four-gene, SSU+*rbcL*, SSU
KT943651	Nitzschia sp. SZCZCH658	SSU	SSU
KT943663	Nitzschia aurariae SZCZCH966	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
KT943664	Nitzschia valdestriata SZCZCH969	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
KT943665	Nitzschia cf. volvendirostrata SZCZCH845	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
KT943666	Nitzschia traheaformis SZCZCH970 [Nitzschia cf. dubiiformis]	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
KT943667	Nitzschia traheaformis SZCZCH971 [Nitzschia cf. dubiiformis]	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*
KT943668	Nitzschia traheaformis SZCZCH972 [Nitzschia cf. dubiiformis]	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
KT943670	Amphora vixvisibilis SZCZCH967	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
KT943675	Nitzschia nanodissipata SZCZCH974	*rbcL*	*rbcL*
KT943683	Tryblionella gaoana SZCZCH97	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL*
KT943697	Tryblionella gaoana SZCZCH97	*psbC*	four-gene
KT943698	Nitzschia aurariae SZCZCH966	*psbC*	four-gene, *psbC*
KT943699	Nitzschia valdestriata SZCZCH969	*psbC*	four-gene, *psbC*
KT943700	Nitzschia cf. volvendirostrata SZCZCH845 [Nitzschia sp.]	*psbC*	four-gene, *psbC*
KT943701	Nitzschia traheaformis SZCZCH970 [Nitzschia cf. dubiiformis]	*psbC*	four-gene, *psbC*
KT943702	Nitzschia traheaformis SZCZCH971 [Nitzschia cf. dubiiformis]	*psbC*	four-gene
KT943706	Amphora vixvisibilis SZCZCH967	*psbC*	four-gene, *psbC*
KT943712	Nitzschia nanodissipata SZCZCH974	*psbC*	*psbC*

KU179112	Nitzschia volvendirostrata KSA0039	*rbcL*	*rbcL*
KU179114	Nitzschia volvendirostrata SZCZP36	*rbcL*	*rbcL*
KU179115	Nitzschia sp. SZCZM117	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
KU179116	Nitzschia sp. KSA0035	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
KU179128	Nitzschia sp. KSA0035	SSU	four-gene, SSU+*rbcL*, SSU
KU179129	Nitzschia sp. SZCZM117	SSU	four-gene, SSU+*rbcL*
KU179141	Nitzschia volvendirostrata SZCZP36	*psbC*	*psbC*
KU179141	Nitzschia volvendirostrata KSA0039	*psbC*	*psbC*
KU179142	Nitzschia sp. SZCZM117	*psbC*	four-gene, *psbC*
KU179143	Nitzschia sp. KSA0035	*psbC*	four-gene, *psbC*
KU183494	Pseudo-nitzschia granii RCC:2006	*rbcL*	SSU+*rbcL*
KU212806	Pseudonitzschia arctica P2F2	LSU	LSU
KU561119	Nitzschia ovalis DHmm1W3	SSU	SSU
KU561133	Nitzschia palea Xmm20S5	SSU	SSU
KU561134	Nitzschia ovalis Xmm12S2	SSU	SSU
KU561139	Nitzschia dubiiformis Xmm11S4	SSU	SSU
KU561152	Nitzschia microcephala Xmm1251	SSU	SSU
KU561172	Bacillaria cf. paxillifera XY-2016 Xmm24S4	SSU	SSU
KU561184	Nitzschia ovalis Xmm10W3	SSU	SSU
KU561195	Nitzschia capitellata Xmm16S2	SSU	SSU
KU561204	Cylindrotheca closterium Xmm18W1	SSU	SSU
KU561207	Cylindrotheca closterium Xmm37S2	SSU	SSU
KU561219	Psammodictyon constrictum Xmm23S3	SSU	SSU
KX229689	Pseudo-nitzschia americana UNC1412	SSU	four-gene, SSU+*rbcL*, SSU
KX229690	Pseudo-nitzschia fraudulenta UNC1413	SSU	SSU+*rbcL*, SSU
KX290859	Pseudo-nitzschia americana 427b	LSU	LSU
KX290867	Pseudo-nitzschia arenysensis 221b	LSU	LSU
KX290871	Pseudo-nitzschia australis HAB-400	LSU	LSU
KX290877	Pseudo-nitzschia cuspidata 133b	LSU	LSU
KX290881	Pseudo-nitzschia fraudulenta HAB-369	LSU	LSU
KX290883	Pseudo-nitzschia hasleana 8b	LSU	LSU
KX290895	Pseudo-nitzschia pungens 3b	LSU	LSU
KX290900	Pseudo-nitzschia seriata HAB-312	LSU	LSU
KX290903	Pseudo-nitzschia sp. A HAB-2017 HAB-484	LSU	LSU
KX290907	Pseudo-nitzschia sp. B HAB-2017 235b	LSU	LSU
KX290913	Pseudo-nitzschia sp. C HAB-2017 HAB-137	LSU	LSU
KX572912	Pseudo-nitzschia abrensis PnMi178	*cox1*	*cox1*

KX572913	Pseudo-nitzschia batesiana PnTb19	*cox1*	*cox1*
KX572914	Pseudo-nitzschia batesiana PnMi32	*cox1*	*cox1*
KX572915	Pseudo-nitzschia batesiana PnMi44	*cox1*	*cox1*
KX572916	Pseudo-nitzschia kodamae PnMi04	*cox1*	*cox1*
KX572920	Pseudo-nitzschia brasiliana PnPd34	*cox1*	*cox1*
KX572922	Pseudo-nitzschia caciantha PnSL05	*cox1*	*cox1*
KX572923	Pseudo-nitzschia circumpora PnPd27	*cox1*	*cox1*
KX572924	Pseudo-nitzschia circumpora PnPd28	*cox1*	*cox1*
KX572925	Pseudo-nitzschia cuspidata NWFSC189	*cox1*	*cox1*
KX572927	Pseudo-nitzschia cuspidata PnPd29	*cox1*	*cox1*
KX572928	Pseudo-nitzschia decipiens PnKk38	*cox1*	*cox1*
KX572932	Pseudo-nitzschia fukuyoi PnTb25	*cox1*	*cox1*
KX572933	Pseudo-nitzschia fukuyoi PnTb31	*cox1*	*cox1*
KX572935	Pseudo-nitzschia subpacifica PnMi16	*cox1*	*cox1*
KX572937	Pseudo-nitzschia lundholmiae PnTb10	*cox1*	*cox1*
KX572941	Pseudo-nitzschia pseudodelicatissima P-11	*cox1*	*cox1*
KX572942	Pseudo-nitzschia subfraudulenta PnMi71	*cox1*	*cox1*
KX572944	Pseudo-nitzschia subfraudulenta PnMi162	*cox1*	*cox1*
KX572946	Pseudo-nitzschia micropora PnKk14	*cox1*	*cox1*
KX575709	Bacillaria paxillifera RVSN23	SSU	SSU
KX889092	Nitzschia cf. paleacea BC0483	*rbcL*	LSU+*rbcL*, *rbcL*
KX889093	Nitzschia varelae NIT952CAT	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL*
KX889094	Nitzschia lembiformis R2	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL*
KX889095	Nitzschia acicularis R20	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
KX889105	Nitzschia cf. paleacea BC0483	LSU	LSU+*rbcL*, LSU
KX889109	Nitzschia cf. sigma NIT1013ABR	LSU	four-gene, LSU+*rbcL*, LSU
KX889110	Nitzschia acicularis Nit56	LSU	four-gene, LSU+*rbcL*, LSU
KX889112	Nitzschia varelae NIT952CAT	LSU	four-gene, LSU+*rbcL*, LSU
KX981791	Craspedostauros alyoubyi UTKSA0083	*psbC*	four-gene, *psbC*
KX981792	Craspedostauros paradoxa GU44BK-1 keeledHcpA25	*psbC*	four-gene, *psbC*
KX981793	Craspedostauros cf. _neoconstrictus CCMP1120	*psbC*	four-gene, *psbC*
KX981795	Diploneis sp. Coz1 peanut penn1	*psbC*	four-gene, *psbC*
KX981798	Pleurosigma sp. UTKSA0019	*psbC*	four-gene, *psbC*
KX981801	Cylindrotheca sp. UTKSA0079	*psbC*	*psbC*

KX981802	Cylindrotheca sp. UTKSA0082	*psbC*	*psbC*
KX981803	Nitzschia sp. KSA0120	*psbC*	*psbC*
KX981804	Nitzschia sp. 9vi08- 5F BToxNitz	*psbC*	*psbC*
KX981805	Psammodictyon constrictum GU7X-7 peanut5	*psbC*	*psbC*
KX981806	Staurotropis khiyamii UTKSA0047	*psbC*	four-gene, *psbC*
KX981807	Staurotropis americana Coz4 cfUnd-5	*psbC*	four-gene, *psbC*
KX981808	Staurotropis americana FishPassMangrove staurosA1	*psbC*	four-gene, *psbC*
KX981814	Craspedostauros alyoubyi UTKSA0083	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
KX981815	Craspedostauros amphoroides CCMP797	*rbcL*	*rbcL*
KX981816	Craspedostauros paradoxa GU44BK-1 keeledHcpA25	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
KX981817	Craspedostauros cf. neoconstrictus CCMP1120	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
KX981819	Diploneis sp. Coz1 peanut penn1	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
KX981822	Pleurosigma sp. UTKSA0019	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
KX981824	Trachyneis sp. SantaRosaCor green Nav3	*rbcL*	*rbcL*
KX981826	Cylndrotheca sp. UTKSA0079	*rbcL*	SSU+*rbcL*, *rbcL*
KX981827	Cylndrotheca sp. UTKSA0082	*rbcL*	SSU+*rbcL*, *rbcL*
KX981828	Nitzschia sp. KSA0120	*rbcL*	SSU+*rbcL*, *rbcL*
KX981829	Nitzschia sp. 9vi08-5F BToxNitz	*rbcL*	SSU+*rbcL*, *rbcL*
KX981830	Psammodictyon constrictum GU7X-7 peanut5	*rbcL*	SSU+*rbcL*, *rbcL*
KX981831	Undatella quadrata 19vi08-1A Und	*rbcL*	SSU+*rbcL*, *rbcL*
KX981832	Staurotropis khiyamii UTKSA0047	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
KX981833	Staurotropis americana Coz4 cfUnd_5	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
KX981834	Staurotropis americana FishPassMangrove staurosA1	*rbcL*	four-gene, SSU+*rbcL*, *rbcL*
KX981839	Diploneis sp. Coz1 peanut penn1	SSU	four-gene, SSU+*rbcL*, SSU
KX981840	Pleurosigma sp. UTKSA0019	SSU	four-gene, SSU+*rbcL*, SSU
KX981847	Cylndrotheca sp. UTKSA0079	SSU	SSU+*rbcL*, SSU
KX981848	Cylndrotheca sp. UTKSA0082	SSU	SSU+*rbcL*
KX981849	Nitzschia sp. KSA0120	SSU	SSU+*rbcL*
KX981850	Nitzschia sp. 9vi08-5F BToxNitz	SSU	SSU+*rbcL*
KX981851	Psammodictyon constrictum GU7X-7 peanut5	SSU	SSU+*rbcL*
KX981852	Undatella quadrata 19vi08-1A Und	SSU	SSU+*rbcL*
KX981853	Staurotropis khiyamii UTKSA0047	SSU	four-gene, SSU+*rbcL*, SSU
KX981854	Staurotropis americana Coz4 cfUnd-5	SSU	four-gene, SSU+*rbcL*, SSU
KX981855	Staurotropis americana FishPassMangrove staurosA1	SSU	four-gene, SSU+*rbcL*, SSU

KX981857	Craspedostauros alyoubyi UTKSA0083	SSU	four-gene, SSU+*rbcL*
KX981858	Craspedostauros paradoxa GU44BK-1 keeledHcpA25	SSU	four-gene, SSU+*rbcL*
KX981860	Craspedostauros cf. neoconstrictus CCMP1120	SSU	four-gene, SSU+*rbcL*, SSU
KY320312	Cylndrotheca closterium TA256	*rbcL*	SSU+*rbcL*, *rbcL*
KY320313	Cylndrotheca gracilis TA46	*rbcL*	SSU+*rbcL*, *rbcL*
KY320314	Cylndrotheca sp. TA198	*rbcL*	SSU+*rbcL*, *rbcL*
KY320315	Bacillaria paxillifera EW234	*rbcL*	SSU+*rbcL*, *rbcL*
KY320316	Bacillaria sp. SH349	*rbcL*	SSU+*rbcL*, *rbcL*
KY320317	Nitzschia liebetruthii TA353	*rbcL*	SSU+*rbcL*, *rbcL*
KY320318	Nitzschia bergii TA139	*rbcL*	SSU+*rbcL*, *rbcL*
KY320319	Nitzschia cf. paleacea TA406	*rbcL*	SSU+*rbcL*, *rbcL*
KY320320	Nitzschia dubia TA37	*rbcL*	SSU+*rbcL*, *rbcL*
KY320321	Nitzschia dubiiformis SH366	*rbcL*	*rbcL*
KY320322	Nitzschia paleaeformis TA394	*rbcL*	SSU+*rbcL*, *rbcL*
KY320323	Nitzschia pusilla TA45	*rbcL*	SSU+*rbcL*, *rbcL*
KY320324	Nitzschia sigma TA377	*rbcL*	SSU+*rbcL*, *rbcL*
KY320325	Nitzschia sigmaformis TA311	*rbcL*	SSU+*rbcL*, *rbcL*
KY320326	Nitzschia sp. Dillu16	*rbcL*	SSU+*rbcL*, *rbcL*
KY320327	Nitzschia sp. TA61	*rbcL*	SSU+*rbcL*, *rbcL*
KY320328	Nitzschia pellucida EW229	*rbcL*	*rbcL*
KY320329	Nitzschia pusilla TA420	*rbcL*	SSU+*rbcL*, *rbcL*
KY320330	Nitzschia aequorea Dillu38	*rbcL*	SSU+*rbcL*, *rbcL*
KY320331	Nitzschia ligowskii TA426	*rbcL*	SSU+*rbcL*, *rbcL*
KY320332	Nitzschia dissipata TA44	*rbcL*	SSU+*rbcL*, *rbcL*
KY320333	Nitzschia dissipata TA192	*rbcL*	SSU+*rbcL*, *rbcL*
KY320334	Tryblionella apiculata TA-85	*rbcL*	SSU+*rbcL*, *rbcL*
KY320337	Nitzschia sigma TA341	*rbcL*	SSU+*rbcL*, *rbcL*
KY320338	Nitzschia sp. TA409	*rbcL*	SSU+*rbcL*, *rbcL*
KY320373	Cylndrotheca closterium TA256	SSU	SSU+*rbcL*, SSU
KY320374	Cylndrotheca gracilis TA46	SSU	SSU+*rbcL*, SSU
KY320375	Cylndrotheca sp. TA198	SSU	SSU+*rbcL*, SSU
KY320376	Bacillaria paxillifera EW234	SSU	SSU+*rbcL*, SSU
KY320377	Bacillaria sp. SH349	SSU	SSU+*rbcL*, SSU
KY320378	Nitzschia liebetruthii TA353	SSU	SSU+*rbcL*, SSU
KY320379	Nitzschia bergii TA139	SSU	SSU+*rbcL*, SSU
KY320380	Nitzschia cf. paleacea TA406	SSU	SSU+*rbcL*, SSU

KY320381	Nitzschia dubia TA37	SSU	SSU+*rbcL*, SSU
KY320382	Nitzschia dubiiformis SH366	SSU	SSU
KY320383	Nitzschia paleaeformis TA394	SSU	SSU+*rbcL*, SSU
KY320384	Nitzschia pusilla TA-45	SSU	SSU+*rbcL*, SSU
KY320385	Nitzschia sigma TA377	SSU	SSU+*rbcL*, SSU
KY320386	Nitzschia sigmaformis TA311	SSU	SSU+*rbcL*, SSU
KY320387	Nitzschia sp. Dillu16	SSU	SSU+*rbcL*, SSU
KY320388	Nitzschia sp. TA61	SSU	SSU+*rbcL*, SSU
KY320389	Nitzschia pellucida EW229	SSU	SSU+*rbcL*, SSU
KY320390	Nitzschia pusilla TA420	SSU	SSU+*rbcL*, SSU
KY320391	Nitzschia aequorea Dillu38	SSU	SSU+*rbcL*, SSU
KY320392	Nitzschia ligowskii TA426	SSU	SSU+*rbcL*, SSU
KY320393	Nitzschia dissipata TA44	SSU	SSU+*rbcL*, SSU
KY320394	Nitzschia dissipata TA192	SSU	SSU+*rbcL*, SSU
KY320395	Nitzschia sigma TA341	SSU	SSU+*rbcL*, SSU
KY320396	Nitzschia sp. TA409	SSU	SSU+*rbcL*, SSU
KY320397	Tryblionella apiculata TA-85	SSU	SSU+*rbcL*, SSU
KY799138	Nitzschia palea TCC851	*rbcL*	SSU+*rbcL*
KY799139	Nitzschia palea TCC852	*rbcL*	SSU+*rbcL*
KY799140	Nitzschia palea TCC855	*rbcL*	SSU+*rbcL*
KY799146	Nitzschia pusilla TCC896	*rbcL*	SSU+*rbcL*, *rbcL*
KY863472	Nitzschia palea TCC139-1	SSU	SSU+*rbcL*
KY863474	Nitzschia palea TCC851	SSU	SSU+*rbcL*
KY863475	Nitzschia palea TCC852	SSU	SSU+*rbcL*
KY863477	Nitzschia palea TCC855	SSU	SSU+*rbcL*
KY863478	Nitzschia cf. pusilla TCC894	SSU	SSU+*rbcL*
KY863479	Nitzschia pusilla TCC896	SSU	SSU+*rbcL*
KY863480	Nitzschia cf. pusilla TCC898	SSU	SSU+*rbcL*
KY863493	Nitzschia cf. pusilla TCC894	*rbcL*	SSU+*rbcL*
KY863494	Nitzschia cf. pusilla TCC898	*rbcL*	SSU+*rbcL*
LC054952	Nitzschia sp. NY060	SSU	SSU
LC126284	Nitzschia sp. TS-2016b	SSU	SSU
LC189151	Fragilariopsis cylindrus NIES-3887	SSU	SSU
LC192325	Durinskia kwazulunatalensis Cx18 ENDOSYMBIONT	*rbcL*	SSU+*rbcL*, *rbcL*
LC192326	Durinskia kwazulunatalensis HG181 ENDOSYMBIONT	*rbcL*	*rbcL*

LC192327	Durinskia kwazulunatalensis Cx22 ENDOSYMBIONT	*rbcL*	SSU+*rbcL*
LC192328	Dinophyta sp. HG180 ENDOSYMBIONT	*rbcL*	SSU+*rbcL*, *rbcL*
LC192329	Dinophyta sp. HG204 ENDOSYMBIONT	*rbcL*	SSU+*rbcL*, *rbcL*
LC192331	Durinskia capensis Kommetjie 6-B ENDOSYMBIONT	*rbcL*	*rbcL*
LC192332	Durinskia capensis Kommetjie 2-B ENDOSYMBIONT	*rbcL*	*rbcL*
LC192333	Durinskia capensis Kommetjie 2-A ENDOSYMBIONT	*rbcL*	SSU+*rbcL*, *rbcL*
LC192334	Durinskia capensis Kommetjie 6-A ENDOSYMBIONT	*rbcL*	*rbcL*
LC192335	Durinskia cf. baltica HG171 ENDOSYMBIONT	*rbcL*	*rbcL*
LC192336	Durinskia cf. baltica HG265 ENDOSYMBIONT	*rbcL*	*rbcL*
LC192337	Durinskia kwazulunatalensis Cx22 ENDOSYMBIONT	SSU	SSU+*rbcL*
LC192338	Durinskia kwazulunatalensis Cx18 ENDOSYMBIONT	SSU	SSU+*rbcL*
LC192339	Dinophyta sp. HG180 ENDOSYMBIONT	SSU	SSU+*rbcL*
LC192340	Dinophyta sp. HG204 ENDOSYMBIONT	SSU	SSU+*rbcL*
LC192342	Durinskia capensis Kommetjie 2-A ENDOSYMBIONT	SSU	SSU+*rbcL*
LC192343	Durinskia baltica CS-38 ENDOSYMBIONT	SSU	SSU+*rbcL*
M59080	Cylindrotheca sp.	*rbcL*	*rbcL*
M87325	Bacillaria paxillifer	SSU	SSU
M87326	Cylindrotheca closterium	SSU	SSU
M87334	Nitzschia apiculata	SSU	SSU
MF374776	Pseudo-nitzschia simulans MC940	LSU	LSU
MF374778	Pseudo-nitzschia simulans MC3038	LSU	LSU
MF997422	Nitzschia alba CCMP2426	genome	*cox1*
MG182051	Nitzschia sp. Nitz4	genome	*cox1*
MG271845	Cylindrotheca closterium CCMP1855	genome	*cox1*
MG271846	Eunotia naegelii UTEX FD354	genome	*cox1*
MH297491	Nitzschia palea Wise	genome	*cox1*
MH794250	Simonsenia paucistriata SZCZCH839	*rbcL*	*rbcL*
MH794251	Simonsenia paucistriata SZCZCH839	*psbC*	*psbC*
NC_027265	Pseudo-nitzschia multiseries	genome	*cox1*
U18240	Pseudo-nitzschia pungens F310	SSU	SSU
U18241	Pseudo-nitzschia multiseries tka2	SSU	SSU

U412621	Pseudo-nitzschia pungens	LSU	LSU
U413901	Pseudo-nitzschia americana	LSU	LSU
Y10566	Peridinium balticum ENDOSYMBIONT	SSU	SSU
Y10567	Peridinium foliaceum ENDOSYMBIONT	SSU	SSU, ,

Supplementary Table 2. Sequences newly deposited in GenBank (**bold**) and sequences taken from public sources other than GenBank (Roman). The *Hantzschia* clones with clone names in the format HANT*xxx*-11 were obtained from the public data portal of the BOLD database (http://www.boldsystems.org/index.php/Public_BINSearch?searchtype=records).

Taxon and clone name	Clone name	GenBank #	Sequence author	Gene	Use of sequence
Bacillaria sp. BAC901CAT	**BAC901CAT**	**MN750428**	**C. Li**	**LSU**	**four-gene, LSU+*rbcL*, LSU**
Bacillaria sp. BAC901CAT	**BAC901CAT**	**MN734007**	**C. Li**	***psbC***	**four-gene, *psbC***
Bacillaria sp. BAC901CAT	**BAC901CAT**	**MN734075**	**C. Li**	***rbcL***	**four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL***
Bacillaria sp. BAC901CAT	**BAC901CAT**	**MN750450**	**C. Li**	**SSU**	**four-gene, SSU+*rbcL*, SSU**
Bacillaria sp. SZCZP613	**SZCZP613**	**MN944012**	**C. Li**	**LSU**	**four-gene**
Bacillaria sp. SZCZP613	**SZCZP613**	**MN920690**	**C. Li**	***psbC***	**four-gene, *psbC***
Bacillaria sp. SZCZP613	**SZCZP613**	**MN920681**	**C. Li**	***rbcL***	**four-gene, SSU+*rbcL*, *rbcL***
Bacillaria sp. SZCZP613	**SZCZP613**	**MN944000**	**C. Li**	**SSU**	**four-gene, SSU+*rbcL*, SSU**
Cylindrotheca sp. SZCZCH50	**SZCZCH50**	**MN944004**	**C. Li**	**LSU**	**four-gene, LSU+*rbcL*, LSU**
Cylindrotheca sp. SZCZCH50	**SZCZCH50**	**MN920684**	**C. Li**	***psbC***	**four-gene, *psbC***
Cylindrotheca sp. SZCZCH50	**SZCZCH50**	**MN920674**	**C. Li**	***rbcL***	**four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL***
Cylindrotheca sp. SZCZCH50	**SZCZCH50**	**MN943995**	**C. Li**	**SSU**	**four-gene, SSU+*rbcL*, SSU**
Cylindrotheca sp. SZCZCH690	**SZCZCH690**	**MN944005**	**C. Li**	**LSU**	**four-gene, LSU+*rbcL*, LSU**
Cylindrotheca sp. SZCZCH690	**SZCZCH690**	**MN920685**	**C. Li**	***psbC***	**four-gene, *psbC***
Cylindrotheca sp. SZCZCH690	**SZCZCH690**	**MN920676**	**C. Li**	***rbcL***	**four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL***
Cylindrotheca sp. SZCZCH690	**SZCZCH690**	**MN943996**	**C. Li**	**SSU**	**four-gene, SSU+*rbcL*, SSU**
Hantzschia abundans HANT024-11	HANT024-11	[BOLD database]		LSU	LSU+*rbcL*, LSU
Hantzschia abundans HANT024-11	HANT024-11	[BOLD]		*rbcL*	LSU+*rbcL*, *rbcL*

Hantzschia abundans HANT025-11	HANT025-11	[BOLD database]		LSU	LSU+*rbcL*, LSU
Hantzschia abundans HANT025-11	HANT025-11	[BOLD]		*rbcL*	LSU+*rbcL*
Hantzschia abundans HANT026-11	HANT026-11	[BOLD]		*rbcL*	*rbcL*
Hantzschia amphioxys HANT011-11	HANT011-11	[BOLD database]		LSU	LSU+*rbcL*, LSU
Hantzschia amphioxys HANT011-11	HANT011-11	[BOLD]		*rbcL*	LSU+*rbcL*, *rbcL*
Hantzschia amphioxys HANT017-11	HANT017-11	[BOLD database]		LSU	LSU+*rbcL*, LSU
Hantzschia amphioxys HANT017-11	HANT017-11	[BOLD]		*rbcL*	LSU+*rbcL*, *rbcL*
Hantzschia amphioxys HANT018-11	HANT018-11	[BOLD database]		LSU	LSU+*rbcL*, LSU
Hantzschia amphioxys HANT018-11	HANT018-11	[BOLD]		*rbcL*	LSU+*rbcL*, *rbcL*
Hantzschia amphioxys HANT019-11	HANT019-11	[BOLD]		*rbcL*	*rbcL*
Hantzschia amphioxys HANT028-11	HANT028-11	[BOLD database]		LSU	LSU+*rbcL*, LSU
Hantzschia amphioxys HANT028-11	HANT028-11	[BOLD]		*rbcL*	LSU+*rbcL*, *rbcL*
Hantzschia amphioxys TCC901	**TCC901**	**MN696780**	**F. Rimet**	***rbcL***	***rbcL***
Hantzschia amphioxys TCC901	**TCC901**	**MN696729**	**F. Rimet**	**SSU**	**SSU**
Hantzschia cf. amphioxys HANT012-11	HANT012-11	[BOLD database]		LSU	LSU+*rbcL*, LSU
Hantzschia cf. amphioxys HANT012-11	HANT012-11	[BOLD]		*rbcL*	LSU+*rbcL*, *rbcL*
Hantzschia cf. amphioxys HANT013-11	HANT013-11	[BOLD database]		LSU	LSU+*rbcL*, LSU
Hantzschia cf. amphioxys HANT013-11	HANT013-11	[BOLD]		*rbcL*	LSU+*rbcL*, *rbcL*
Hantzschia cf. amphioxys HANT015-11	HANT015-11	[BOLD database]		LSU	LSU+*rbcL*, LSU

Hantzschia cf. amphioxys HANT015-11	HANT015-11	[BOLD]		*rbcL*	LSU+*rbcL*, *rbcL*
Hantzschia sp HANT009-11	HANT009-11	[BOLD]		*rbcL*	*rbcL*
Hantzschia sp. HANT001-11	HANT001-11	[BOLD database]		LSU	LSU+*rbcL*, LSU
Hantzschia sp. HANT001-11	HANT001-11	[BOLD]		*rbcL*	LSU+*rbcL*, *rbcL*
Hantzschia sp. HANT002-11	HANT002-11	[BOLD database]		LSU	LSU+*rbcL*, LSU
Hantzschia sp. HANT002-11	HANT002-11	[BOLD]		*rbcL*	LSU+*rbcL*, *rbcL*
Hantzschia sp. HANT005-11	HANT005-11	[BOLD database]		LSU	LSU+*rbcL*, LSU
Hantzschia sp. HANT005-11	HANT005-11	[BOLD]		*rbcL*	LSU+*rbcL*, *rbcL*
Hantzschia sp. HANT006-11	HANT006-11	[BOLD database]		LSU	LSU+*rbcL*, LSU
Hantzschia sp. HANT006-11	HANT006-11	[BOLD]		*rbcL*	LSU+*rbcL*, *rbcL*
Hantzschia sp. HANT021-11	HANT021-11	[BOLD database]		LSU	LSU+*rbcL*, LSU
Hantzschia sp. HANT021-11	HANT021-11	[BOLD]		*rbcL*	LSU+*rbcL*, *rbcL*
Hantzschia vivax TCC940	**TCC940**	**MN696730**	**F. Rimet**	**SSU**	**SSU**
Nitzschia acicularis Nit56	**Nit56**	**MN734045**	**C. Li**	***psbC***	**four-gene, *psbC***
Nitzschia acicularis Nit56	**Nit56**	**MN734084**	**R. Trobajo**	***rbcL***	**four-gene, SSU+*rbcL***
Nitzschia acicularis Nit56	**Nit56**	**MN750489**	**C. Li**	**SSU**	**four-gene, SSU+*rbcL***
Nitzschia acicularis R20	**R20**	**MN750438**	**R. Trobajo**	**LSU**	**four-gene**
Nitzschia acicularis R20	**R20**	**MN734050**	**C. Li**	***psbC***	**four-gene**
Nitzschia acicularis R20	**R20**	**MN750494**	**C. Li**	**SSU**	**four-gene, SSU+*rbcL***
Nitzschia acicularis TCC375	**TCC375**	**MN696690**	**F. Rimet**	**SSU**	**SSU**
Nitzschia acidoclinata BC0098	**BC0098**	**MN718753**	**S. Sato**	***rbcL***	***rbcL***

Nitzschia acidoclinata BC0619	**BC0619**	**MN725797**	**R. Hollands**	**LSU**	**LSU+*rbcL*, LSU**
Nitzschia acidoclinata BC0619	**BC0619**	**MN718774**	**S. Sato**	***rbcL***	**LSU+*rbcL*, *rbcL***
Nitzschia acidoclinata TCC537	**TCC537**	**MN696740**	**F. Rimet**	**LSU**	**four-gene**
Nitzschia acidoclinata TCC538	**TCC538**	**MN696741**	**F. Rimet**	**LSU**	**four-gene**
Nitzschia acidoclinata TCC538	**TCC538**	**MN696763**	**F. Rimet**	***rbcL***	**four-gene, SSU+*rbcL***
Nitzschia acidoclinata TCC560	**TCC560**	**MN696743**	**F. Rimet**	**LSU**	**four-gene**
Nitzschia acidoclinata TCC560	**TCC560**	**MN696765**	**F. Rimet**	***rbcL***	**four-gene, SSU+*rbcL***
Nitzschia acidoclinata TCC560	**TCC560**	**MN696711**	**F. Rimet**	**SSU**	**four-gene, SSU+*rbcL***
Nitzschia acidoclinata TCC619	**TCC619**	**MN696749**	**F. Rimet**	**LSU**	**four-gene**
Nitzschia acidoclinata TCC619	**TCC619**	**MN696770**	**F. Rimet**	***rbcL***	**four-gene, SSU+*rbcL***
Nitzschia acidoclinata TCC619	**TCC619**	**MN696720**	**F. Rimet**	**SSU**	**four-gene, SSU+*rbcL***
Nitzschia aff. sublinearis BC0850	**BC0850**	**MN718797**	**S. Sato**	***rbcL***	***rbcL***
Nitzschia alicae BC0330	**BC0330**	**MN718762**	**S. Sato**	***rbcL***	***rbcL***
Nitzschia amphibia BC0486	**BC0486**	**MN718768**	**S. Sato**	***rbcL***	***rbcL***
Nitzschia amphibia BC0503	**BC0503**	**MN725796**	**R. Hollands**	**LSU**	**LSU+*rbcL*, LSU**
Nitzschia amphibia BC0503	**BC0503**	**MN718771**	**S. Sato**	***rbcL***	**LSU+*rbcL*, *rbcL***
Nitzschia amphibia BC0701	**BC0701**	**MN725803**	**R. Hollands**	**LSU**	**LSU+*rbcL*, LSU**
Nitzschia amphibia BC0701	**BC0701**	**MN718781**	**S. Sato**	***rbcL***	**LSU+*rbcL***
Nitzschia amphibia RT5 [Nit239]	**RT5 [Nit239]**	**MN734051**	**C. Li**	***psbC***	**four-gene, *psbC***
Nitzschia amphibia RT5 [Nit239]	**RT5 [Nit239]**	**MN750495**	**C. Li**	**SSU**	**four-gene, SSU+*rbcL*, SSU**
Nitzschia capitellata BC0713	**BC0713**	**MN725805**	**R. Hollands**	**LSU**	**LSU+*rbcL*, LSU**
Nitzschia capitellata BC0713	**BC0713**	**MN718783**	**S. Sato**	***rbcL***	**LSU+*rbcL*, *rbcL***
Nitzschia capitellata capitellata-Scot1	**capitellata-Scot1**	**MN734010**	**C. Li**	***psbC***	**four-gene, *psbC***

Nitzschia capitellata capitellata-Scot1	**capitellata-Scot1**	**MN750453**	**C. Li**	**SSU**	**four-gene, SSU+*rbcL***
Nitzschia capitellata capitellata-Scot2	**capitellata-Scot2**	**MN734011**	**C. Li**	***psbC***	**four-gene, *psbC***
Nitzschia capitellata capitellata-Scot2	**capitellata-Scot2**	**MN750454**	**C. Li**	**SSU**	**four-gene, SSU+*rbcL***
Nitzschia capitellata capitellata-Spain	**capitellata-Spain**	**MN734012**	**C. Li**	***psbC***	**four-gene, *psbC***
Nitzschia capitellata capitellata-Spain	**capitellata-Spain**	**MN750455**	**C. Li**	**SSU**	**four-gene, SSU+*rbcL*, SSU**
Nitzschia cf. aequorea NIT1004CAT	**NIT1004CAT**	**MN734034**	**C. Li**	***psbC***	**four-gene, *psbC***
Nitzschia cf. aequorea NIT1004CAT	**NIT1004CAT**	**MN750480**	**C. Li**	**SSU**	**four-gene, SSU+*rbcL***
Nitzschia cf. ardua L44	**L44**	**MN734030**	**C. Li**	***psbC***	**four-gene, *psbC***
Nitzschia cf. ardua L44	**L44**	**MN750476**	**C. Li**	**SSU**	**four-gene, SSU+*rbcL*, SSU**
Nitzschia cf. bulnheimiana AG	**AG**	**MN750449**	**C. Li**	**SSU**	**four-gene, SSU+*rbcL*, SSU**
Nitzschia cf. dissipata var. media BC0470	**BC0470**	**MN725794**	**R. Hollands**	**LSU**	**four-gene**
Nitzschia cf. dissipata var. media BC0470	**BC0470**	**MN718802**	**M.P. Ashworth**	***psbC***	**four-gene, *psbC***
Nitzschia cf. dissipata var. media BC0470	**BC0470**	**MN718767**	**S. Sato**	***rbcL***	**four-gene, SSU+*rbcL*, *rbcL***
Nitzschia cf. dissipata var. media BC0470	**BC0470**	**MN750422**	**M.P. Ashworth**	**SSU**	**four-gene, SSU+*rbcL*, SSU**
Nitzschia cf. dissipata var. media BC0649	**BC0649**	**MN725798**	**R. Hollands**	**LSU**	**LSU+*rbcL*, LSU**
Nitzschia cf. dissipata var. media BC0649	**BC0649**	**MN718775**	**S. Sato**	***rbcL***	**LSU+*rbcL*, *rbcL***
Nitzschia cf. dissipata var. media BC0866	**BC0866**	**MN725816**	**R. Hollands**	**LSU**	**LSU+*rbcL*, LSU**
Nitzschia cf. dissipata var. media BC0866	**BC0866**	**MN718798**	**S. Sato**	***rbcL***	**LSU+*rbcL*, *rbcL***
Nitzschia cf. fonticola BC0053	**BC0053**	**MN718749**	**S. Sato**	***rbcL***	***rbcL***

Nitzschia cf. gracilis Nit51	**Nit51**	**MN734043**	**C. Li**	***psbC***	**four-gene, *psbC***
Nitzschia cf. gracilis Nit51	**Nit51**	**MN734082**	**R. Trobajo**	***rbcL***	**four-gene, SSU+*rbcL*, *rbcL***
Nitzschia cf. gracilis Nit51	**Nit51**	**MN750487**	**C. Li**	**SSU**	**four-gene, SSU+*rbcL*, SSU**
Nitzschia cf. hantzschiana NIT337TM	**NIT337TM**	**MN734074**	**G.E. Simpson**	***rbcL***	***rbcL***
Nitzschia cf. longissima Cylin clos	**Cylin clos**	**MN734068**	**G.E. Simpson**	***rbcL***	***rbcL***
Nitzschia cf. palea BC0799	**BC0799**	**MN725812**	**R. Hollands**	**LSU**	**LSU+*rbcL*, LSU**
Nitzschia cf. palea BC0799	**BC0799**	**MN718792**	**S. Sato**	***rbcL***	**LSU+*rbcL*, *rbcL***
Nitzschia cf. palea TCC886	**TCC886**	**MN696778**	**F. Rimet**	***rbcL***	**SSU+*rbcL*, *rbcL***
Nitzschia cf. palea TCC886	**TCC886**	**MN696727**	**F. Rimet**	**SSU**	**SSU+*rbcL*, SSU**
Nitzschia cf. perminuta BC0730	**BC0730**	**MN725806**	**R. Hollands**	**LSU**	**LSU+*rbcL*, LSU**
Nitzschia cf. perminuta BC0730	**BC0730**	**MN718784**	**S. Sato**	***rbcL***	**LSU+*rbcL*, *rbcL***
Nitzschia cf. perminuta BC0838	**BC0838**	**MN725815**	**R. Hollands**	**LSU**	**LSU+*rbcL*, LSU**
Nitzschia cf. perminuta BC0838	**BC0838**	**MN718795**	**S. Sato**	***rbcL***	**LSU+*rbcL*, *rbcL***
Nitzschia cf. pumila Nit57	**Nit57**	**MN750434**	**R. Trobajo**	**LSU**	**LSU+*rbcL*, LSU**
Nitzschia cf. pumila Nit57	**Nit57**	**MN734085**	**C. Li**	***rbcL***	**LSU+*rbcL*, *rbcL***
Nitzschia cf. pusilla BC0333	**BC0333**	**MN725792**	**R. Hollands**	**LSU**	**LSU+*rbcL*, LSU**
Nitzschia cf. pusilla BC0333	**BC0333**	**MN718763**	**S. Sato**	***rbcL***	**LSU+*rbcL*, *rbcL***
Nitzschia cf. pusilla CCMP558	**CCMP558**	**MN734013**	**C. Li**	***psbC***	**four-gene, *psbC***
Nitzschia cf. pusilla CCMP558	**CCMP558**	**MN750456**	**C. Li**	**SSU**	**four-gene, SSU+*rbcL***
Nitzschia cf. pusilla L1	**L1**	**MN734027**	**C. Li**	***psbC***	**four-gene, *psbC***
Nitzschia cf. pusilla L1	**L1**	**MN750473**	**C. Li**	**SSU**	**four-gene, SSU+*rbcL*, SSU**
Nitzschia cf. pusilla L25	**L25**	**MN734028**	**C. Li**	***psbC***	**four-gene, *psbC***
Nitzschia cf. pusilla L25	**L25**	**MN750474**	**C. Li**	**SSU**	**four-gene, SSU+*rbcL*, SSU**
Nitzschia cf. pusilla L3	**L3**	**MN734029**	**C. Li**	***psbC***	**four-gene, *psbC***

Nitzschia cf. pusilla L3	L3	MN750475	C. Li	SSU	four-gene, SSU+*rbcL*, SSU
Nitzschia cf. pusilla NIT1003CAT	NIT1003CAT	MN750429	R. Trobajo	LSU	four-gene, LSU+*rbcL*, LSU
Nitzschia cf. pusilla NIT1003CAT	NIT1003CAT	MN734033	C. Li	*psbC*	four-gene, *psbC*
Nitzschia cf. pusilla NIT1003CAT	NIT1003CAT	MN734077	R. Trobajo	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL*
Nitzschia cf. pusilla NIT1003CAT	NIT1003CAT	MN750479	C. Li	SSU	four-gene, SSU
Nitzschia cf. pusilla Nit44	Nit44	MN734041	C. Li	*psbC*	four-gene, *psbC*
Nitzschia cf. pusilla Nit44	Nit44	MN750485	C. Li	SSU	four-gene, SSU+*rbcL*
Nitzschia cf. pusilla NIT945CAT	NIT945CAT	MN750435	C. Li	LSU	LSU
Nitzschia cf. pusilla TCC396	TCC396	MN696700	F. Rimet	SSU	SSU
Nitzschia cf. pusilla TCC586	TCC586	MN696747	F. Rimet	LSU	four-gene
Nitzschia cf. pusilla TCC586	TCC586	MN696717	F. Rimet	SSU	four-gene, SSU+*rbcL*
Nitzschia cf. pusilla TCC665	TCC665	MN696751	F. Rimet	LSU	four-gene, LSU+*rbcL*, LSU
Nitzschia cf. pusilla TCC665	TCC665	MN696772	F. Rimet	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL*
Nitzschia cf. pusilla TCC665	TCC665	MN696723	F. Rimet	SSU	four-gene, SSU+*rbcL*
Nitzschia cf. pusilla TCC900	TCC900	MN696779	F. Rimet	*rbcL*	SSU+*rbcL*
Nitzschia cf. pusilla TCC900	TCC900	MN696728	F. Rimet	SSU	SSU+*rbcL*, SSU
Nitzschia cf. recta BC0769	BC0769	MN725808	R. Hollands	LSU	LSU+*rbcL*, LSU
Nitzschia cf. recta BC0769	BC0769	MN718786	S. Sato	*rbcL*	LSU+*rbcL*, *rbcL*
Nitzschia cf. recta BC0795	BC0795	MN725811	R. Hollands	LSU	four-gene, LSU+*rbcL*, LSU
Nitzschia cf. recta BC0795	BC0795	MN718804	M.P. Ashworth	*psbC*	four-gene, *psbC*
Nitzschia cf. recta BC0795	BC0795	MN718791	S. Sato	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL*
Nitzschia cf. recta BC0795	BC0795	MN750424	M.P. Ashworth	SSU	four-gene, SSU+*rbcL*, SSU
Nitzschia cf. romana BC0650	BC0650	MN725799	R. Hollands	LSU	LSU+*rbcL*, LSU

Nitzschia cf. romana BC0650	BC0650	MN718776	S. Sato	*rbcL*	LSU+*rbcL*, *rbcL*
Nitzschia cf. sigma BC0308	BC0308	MN718759	S. Sato	*rbcL*	*rbcL*
Nitzschia cf. sigma NIT1013ABR	NIT1013ABR	MN734038	C. Li	*psbC*	four-gene, *psbC*
Nitzschia cf. sigma NIT1013ABR	NIT1013ABR	MN734080	R. Trobajo	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL*
Nitzschia cf. sigma NIT1013ABR	NIT1013ABR	MN750484	C. Li	SSU	four-gene, SSU+*rbcL*, SSU
Nitzschia cf. soratensis BC0501	BC0501	MN725795	R. Hollands	LSU	LSU+*rbcL*, LSU
Nitzschia cf. soratensis BC0501	BC0501	MN718769	S. Sato	*rbcL*	LSU+*rbcL*, *rbcL*
Nitzschia communis TCC853	TCC853	MN696775	F. Rimet	*rbcL*	*rbcL*
Nitzschia costei BC0469	BC0469	MN725793	R. Hollands	LSU	LSU+*rbcL*, LSU
Nitzschia costei BC0469	BC0469	MN718766	S. Sato	*rbcL*	LSU+*rbcL*, *rbcL*
Nitzschia costei TCC521	TCC521	MN696738	F. Rimet	LSU	four-gene
Nitzschia costei TCC550	TCC550	MN696742	F. Rimet	LSU	four-gene, LSU+*rbcL*, LSU
Nitzschia costei TCC550	TCC550	MN696764	F. Rimet	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL*
Nitzschia costei TCC550	TCC550	MN696710	F. Rimet	SSU	four-gene, SSU+*rbcL*
Nitzschia dissipata TCC378	TCC378	MN696691	F. Rimet	SSU	SSU
Nitzschia dissipata TCC632	TCC632	MN696750	F. Rimet	LSU	four-gene
Nitzschia dissipata TCC632	TCC632	MN696771	F. Rimet	*rbcL*	four-gene, SSU+*rbcL*
Nitzschia dissipata TCC632	TCC632	MN696722	F. Rimet	SSU	four-gene, SSU+*rbcL*, SSU
Nitzschia dissipata TCC707	TCC707	MN696753	F. Rimet	LSU	four-gene, LSU+*rbcL*, LSU
Nitzschia dissipata TCC707	TCC707	MN696773	F. Rimet	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL*
Nitzschia dissipata TCC707	TCC707	MN696724	F. Rimet	SSU	four-gene, SSU+*rbcL*
Nitzschia dissipata var. media TCC876	TCC876	MN696725	F. Rimet	SSU	SSU
Nitzschia draveillensis BC0325	BC0325	MN725791	R. Hollands	LSU	LSU+*rbcL*, LSU
Nitzschia draveillensis BC0325	BC0325	MN718761	S. Sato	*rbcL*	LSU+*rbcL*, *rbcL*

Nitzschia draveillensis Nit50	**Nit50**	**MN750432**	**R. Trobajo**	**LSU**	**four-gene, LSU+*rbcL*, LSU**
Nitzschia draveillensis Nit50	**Nit50**	**MN734042**	**C. Li**	***psbC***	**four-gene, *psbC***
Nitzschia draveillensis Nit50	**Nit50**	**MN734081**	**R. Trobajo**	***rbcL***	**four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL***
Nitzschia draveillensis Nit50	**Nit50**	**MN750486**	**C. Li**	**SSU**	**four-gene, SSU+*rbcL*, SSU**
Nitzschia draveillensis TCC700	**TCC700**	**MN696752**	**F. Rimet**	**LSU**	**four-gene**
Nitzschia fonticola C	**C**	**MN734009**	**C. Li**	***psbC***	**four-gene, *psbC***
Nitzschia fonticola C	**C**	**MN750452**	**C. Li**	**SSU**	**four-gene, SSU+*rbcL*, SSU**
Nitzschia fonticola TCC380	**TCC380**	**MN696692**	**F. Rimet**	**SSU**	**SSU**
Nitzschia fonticola TCC533	**TCC533**	**MN696739**	**F. Rimet**	**LSU**	**four-gene**
Nitzschia fonticola TCC533	**TCC533**	**MN696709**	**F. Rimet**	**SSU**	**four-gene, SSU+*rbcL***
Nitzschia frustulum Nit24	**Nit24**	**MN734039**	**C. Li**	***psbC***	***psbC***
Nitzschia frustulum Nit25	**Nit25**	**MN734040**	**C. Li**	***psbC***	***psbC***
Nitzschia gracilis TCC576	**TCC576**	**MN696746**	**F. Rimet**	**LSU**	**four-gene, LSU+*rbcL*, LSU**
Nitzschia gracilis TCC576	**TCC576**	**MN696768**	**F. Rimet**	***rbcL***	**four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL***
Nitzschia gracilis TCC576	**TCC576**	**MN696715**	**F. Rimet**	**SSU**	**four-gene, SSU+*rbcL***
Nitzschia heufleriana BC0307	**BC0307**	**MN718758**	**S. Sato**	***rbcL***	***rbcL***
Nitzschia inconspicua G1_2 [L54]	**G1_2 [L54]**	**MN734014**	**C. Li**	***psbC***	**four-gene, *psbC***
Nitzschia inconspicua G1_2 [L54]	**G1_2 [L54]**	**MN750457**	**C. Li**	**SSU**	**four-gene, SSU+*rbcL*, SSU**
Nitzschia inconspicua G1_3 [L55]	**G1_3 [L55]**	**MN734015**	**C. Li**	***psbC***	**four-gene, *psbC***
Nitzschia inconspicua G1_3 [L55]	**G1_3 [L55]**	**MN750458**	**C. Li**	**SSU**	**four-gene, SSU+*rbcL*, SSU**
Nitzschia inconspicua G2_1 [L46]	**G2_1 [L46]**	**MN734016**	**C. Li**	***psbC***	**four-gene, *psbC***
Nitzschia inconspicua G2_1 [L46]	**G2_1 [L46]**	**MN750459**	**C. Li**	**SSU**	**four-gene, SSU+*rbcL*, SSU**
Nitzschia inconspicua G2_2 [L47]	**G2_2 [L47]**	**MN734017**	**C. Li**	***psbC***	**four-gene, *psbC***
Nitzschia inconspicua G2_2 [L47]	**G2_2 [L47]**	**MN750460**	**C. Li**	**SSU**	**four-gene, SSU+*rbcL***

Nitzschia inconspicua G3_1 [L53]	G3_1 [L53]	MN734018	C. Li	*psbC*	four-gene, *psbC*
Nitzschia inconspicua G3_1 [L53]	G3_1 [L53]	MN750461	C. Li	SSU	four-gene, SSU+*rbcL*, SSU
Nitzschia inconspicua G3_2 [L58]	G3_2 [L58]	MN750462	C. Li	SSU	four-gene, SSU+*rbcL*, SSU
Nitzschia inconspicua G3_3 [L61]	G3_3 [L61]	MN734019	C. Li	*psbC*	four-gene
Nitzschia inconspicua G3_3 [L61]	G3_3 [L61]	MN750463	C. Li	SSU	four-gene, SSU+*rbcL*
Nitzschia inconspicua G3_4 [L62]	G3_4 [L62]	MN734020	C. Li	*psbC*	four-gene, *psbC*
Nitzschia inconspicua G3_4 [L62]	G3_4 [L62]	MN750464	C. Li	SSU	four-gene, SSU+*rbcL*, SSU
Nitzschia inconspicua G4_1 [L44]	G4_1 [L44]	MN734021	C. Li	*psbC*	four-gene, *psbC*
Nitzschia inconspicua G4_1 [L44]	G4_1 [L44]	MN750465	C. Li	SSU	four-gene, SSU+*rbcL*, SSU
Nitzschia inconspicua G4_2 [L5]	G4_2 [L5]	MN750466	C. Li	SSU	four-gene, SSU+*rbcL*, SSU
Nitzschia inconspicua G5_1 [NIT1002CAT]	G5_1 [NIT1002CAT]	MN734022	C. Li	*psbC*	four-gene, *psbC*
Nitzschia inconspicua G5_1 [NIT1002CAT]	G5_1 [NIT1002CAT]	MN750467	C. Li	SSU	four-gene, SSU+*rbcL*, SSU
Nitzschia inconspicua G5_2 [NIT1005CAT]	G5_2 [NIT1005CAT]	MN734023	C. Li	*psbC*	four-gene, *psbC*
Nitzschia inconspicua G5_2 [NIT1005CAT]	G5_2 [NIT1005CAT]	MN750468	C. Li	SSU	four-gene, SSU+*rbcL*, SSU
Nitzschia inconspicua G6_1 [NIT950CAT]	G6_1 [NIT950CAT]	MN734024	C. Li	*psbC*	four-gene, *psbC*
Nitzschia inconspicua G6_1 [NIT950CAT]	G6_1 [NIT950CAT]	MN750469	C. Li	SSU	four-gene, SSU+*rbcL*, SSU
Nitzschia inconspicua G7_1 [NIT948CAT]	G7_1 [NIT948CAT]	MN734076	C. Li	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL*
Nitzschia inconspicua G7_1 [NIT948CAT]	G7_1 [NIT948CAT]	MN750470	C. Li	SSU	four-gene, SSU+*rbcL*, SSU
Nitzschia inconspicua TCC474	TCC474	MN696733	F. Rimet	LSU	four-gene, LSU+*rbcL*, LSU

Nitzschia inconspicua TCC474	TCC474	MN696758	F. Rimet	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL*
Nitzschia inconspicua TCC474	TCC474	MN696705	F. Rimet	SSU	four-gene, SSU+*rbcL*, SSU
Nitzschia inconspicua TCC487	TCC487	MN696734	F. Rimet	LSU	four-gene
Nitzschia inconspicua TCC488	TCC488	MN696735	F. Rimet	LSU	four-gene
Nitzschia inconspicua TCC488	TCC488	MN696760	F. Rimet	*rbcL*	four-gene, SSU+*rbcL*
Nitzschia inconspicua TCC488	TCC488	MN696706	F. Rimet	SSU	four-gene, SSU+*rbcL*
Nitzschia inconspicua TCC498	TCC498	MN696736	F. Rimet	LSU	four-gene
Nitzschia inconspicua TCC498	TCC498	MN696761	F. Rimet	*rbcL*	four-gene, SSU+*rbcL*
Nitzschia inconspicua TCC498	TCC498	MN696707	F. Rimet	SSU	four-gene, SSU+*rbcL*
Nitzschia inconspicua TCC510	TCC510	MN696737	F. Rimet	LSU	four-gene, LSU+*rbcL*, LSU
Nitzschia inconspicua TCC510	TCC510	MN696762	F. Rimet	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL*
Nitzschia inconspicua TCC571	TCC571	MN696744	F. Rimet	LSU	four-gene, LSU+*rbcL*
Nitzschia inconspicua TCC571	TCC571	MN696766	F. Rimet	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL*
Nitzschia inconspicua TCC571	TCC571	MN696713	F. Rimet	SSU	four-gene, SSU+*rbcL*
Nitzschia lembiformis R2	R2	MN750437	C. Li	LSU	LSU+*rbcL*
Nitzschia lembiformis R2	R2	MN734049	C. Li	*psbC*	four-gene, *psbC*
Nitzschia lembiformis R2	R2	MN750493	C. Li	SSU	four-gene, SSU+*rbcL*, SSU
Nitzschia linearis BC0083	BC0083	MN725785	R. Hollands	LSU	LSU+*rbcL*, LSU
Nitzschia linearis BC0083	BC0083	MN718751	S. Sato	*rbcL*	LSU+*rbcL*, *rbcL*
Nitzschia linearis BC0273	BC0273	MN725789	R. Hollands	LSU	LSU+*rbcL*, LSU
Nitzschia linearis BC0273	BC0273	MN718756	S. Sato	*rbcL*	LSU+*rbcL*, *rbcL*
Nitzschia linearis BC0669	BC0669	MN718777	S. Sato	*rbcL*	*rbcL*
Nitzschia linearis BC0696	BC0696	MN725802	R. Hollands	LSU	LSU+*rbcL*, LSU
Nitzschia linearis BC0696	BC0696	MN718780	S. Sato	*rbcL*	LSU+*rbcL*

Nitzschia linearis BC0712	**BC0712**	**MN725804**	**R. Hollands**	**LSU**	**LSU+*rbcL*, LSU**
Nitzschia linearis BC0712	**BC0712**	**MN718782**	**S. Sato**	***rbcL***	**LSU+*rbcL*, *rbcL***
Nitzschia linearis BC0815	**BC0815**	**MN725814**	**R. Hollands**	**LSU**	**LSU+*rbcL*, LSU**
Nitzschia linearis BC0815	**BC0815**	**MN718794**	**S. Sato**	***rbcL***	**LSU+*rbcL***
Nitzschia linearis BC0897	**BC0897**	**MN718799**	**S. Sato**	***rbcL***	***rbcL***
Nitzschia linearis Nit53	**Nit53**	**MN750433**	**R. Trobajo**	**LSU**	**four-gene**
Nitzschia linearis Nit53	**Nit53**	**MN734044**	**C. Li**	***psbC***	**four-gene, *psbC***
Nitzschia linearis Nit53	**Nit53**	**MN734083**	**R. Trobajo**	***rbcL***	**four-gene, SSU+*rbcL***
Nitzschia linearis Nit53	**Nit53**	**MN750488**	**C. Li**	**SSU**	**four-gene, SSU+*rbcL*, SSU**
Nitzschia linearis TCC386	**TCC386**	**MN696696**	**F. Rimet**	**SSU**	**SSU**
Nitzschia linearis TCC387	**TCC387**	**MN696697**	**F. Rimet**	**SSU**	**SSU**
Nitzschia linearis TCC512	**TCC512**	**MN696708**	**F. Rimet**	**SSU**	**SSU**
Nitzschia microcephala L56	**L56**	**MN734031**	**C. Li**	***psbC***	**four-gene, *psbC***
Nitzschia microcephala L56	**L56**	**MN750477**	**C. Li**	**SSU**	**four-gene, SSU+*rbcL***
Nitzschia microcephala R10	**R10**	**MN750436**	**R. Trobajo**	**LSU**	**four-gene, LSU+*rbcL*, LSU**
Nitzschia microcephala R10	**R10**	**MN734047**	**C. Li**	***psbC***	**four-gene, *psbC***
Nitzschia microcephala R10	**R10**	**MN734086**	**R. Trobajo**	***rbcL***	**four-gene, SSU+*rbcL*, LSU+*rbcL***
Nitzschia microcephala R10	**R10**	**MN750491**	**C. Li**	**SSU**	**four-gene, SSU+*rbcL***
Nitzschia palea BC0039	**BC0039**	**MN725784**	**R. Hollands**	**LSU**	**LSU+*rbcL*, LSU**
Nitzschia palea BC0039	**BC0039**	**MN718748**	**S. Sato**	***rbcL***	**LSU+*rbcL*, *rbcL***
Nitzschia palea BC0095	**BC0095**	**MN725786**	**R. Hollands**	**LSU**	**LSU+*rbcL*, LSU**
Nitzschia palea BC0095	**BC0095**	**MN718752**	**S. Sato**	***rbcL***	**LSU+*rbcL*, *rbcL***
Nitzschia palea BC0234	**BC0234**	**MN725787**	**R. Hollands**	**LSU**	**LSU+*rbcL*, LSU**
Nitzschia palea BC0234	**BC0234**	**MN718754**	**S. Sato**	***rbcL***	**LSU+*rbcL*, *rbcL***

Nitzschia palea BC0240	BC0240	MN725788	R. Hollands	LSU	LSU+*rbcL*, LSU
Nitzschia palea BC0240	BC0240	MN718755	S. Sato	*rbcL*	LSU+*rbcL*
Nitzschia palea BC0277	BC0277	MN725790	R. Hollands	LSU	LSU+*rbcL*, LSU
Nitzschia palea BC0277	BC0277	MN718757	S. Sato	*rbcL*	LSU+*rbcL*, *rbcL*
Nitzschia palea BC0373	BC0373	MN718764	S. Sato	*rbcL*	*rbcL*
Nitzschia palea BC0375	BC0375	MN718765	S. Sato	*rbcL*	*rbcL*
Nitzschia palea BC0603	BC0603	MN718772	S. Sato	*rbcL*	*rbcL*
Nitzschia palea BC0605	BC0605	MN718773	S. Sato	*rbcL*	*rbcL*
Nitzschia palea BC0670	BC0670	MN725800	R. Hollands	LSU	LSU+*rbcL*, LSU
Nitzschia palea BC0670	BC0670	MN718778	S. Sato	*rbcL*	LSU+*rbcL*, *rbcL*
Nitzschia palea BC0748	BC0748	MN725807	R. Hollands	LSU	LSU+*rbcL*, LSU
Nitzschia palea BC0748	BC0748	MN718785	S. Sato	*rbcL*	LSU+*rbcL*, *rbcL*
Nitzschia palea BC0774	BC0774	MN718787	S. Sato	*rbcL*	*rbcL*
Nitzschia palea BC0776	BC0776	MN725809	R. Hollands	LSU	LSU+*rbcL*, LSU
Nitzschia palea BC0776	BC0776	MN718788	S. Sato	*rbcL*	LSU+*rbcL*
Nitzschia palea BC0786	BC0786	MN718789	S. Sato	*rbcL*	*rbcL*
Nitzschia palea BC0848	BC0848	MN718796	S. Sato	*rbcL*	*rbcL*
Nitzschia palea BC0905	BC0905	MN718800	S. Sato	*rbcL*	*rbcL*
Nitzschia palea BC0912	BC0912	MN725817	R. Hollands	LSU	LSU+*rbcL*, LSU
Nitzschia palea BC0912	BC0912	MN718801	S. Sato	*rbcL*	LSU+*rbcL*, *rbcL*
Nitzschia palea Belgium-1	Belgium-1	MN734008	C. Li	*psbC*	four-gene, *psbC*
Nitzschia palea Belgium-1	Belgium-1	MN750451	C. Li	SSU	four-gene, SSU+*rbcL*, SSU
Nitzschia palea Japan D	Japan D	MN734025	C. Li	*psbC*	four-gene, *psbC*
Nitzschia palea Japan D	Japan D	MN750471	C. Li	SSU	four-gene, SSU+*rbcL*, SSU

Nitzschia palea Japan F	**Japan F**	**MN734026**	**C. Li**	***psbC***	**four-gene, *psbC***
Nitzschia palea Japan F	**Japan F**	**MN750472**	**C. Li**	**SSU**	**four-gene, SSU+*rbcL***
Nitzschia palea New Spain2	**New Spain2**	**MN734032**	**C. Li**	***psbC***	**four-gene, *psbC***
Nitzschia palea New Spain2	**New Spain2**	**MN750478**	**C. Li**	**SSU**	**four-gene, SSU+*rbcL***
Nitzschia palea NIT1011KEL	**NIT1011KEL**	**MN750430**	**R. Trobajo**	**LSU**	**LSU+*rbcL*, LSU**
Nitzschia palea NIT1011KEL	**NIT1011KEL**	**MN734078**	**R. Trobajo**	***rbcL***	**LSU+*rbcL***
Nitzschia palea NIT329TM	**NIT329TM**	**MN734072**	**G.E. Simpson**	***rbcL***	***rbcL***
Nitzschia palea R12	**R12**	**MN734048**	**C. Li**	***psbC***	**four-gene, *psbC***
Nitzschia palea R12	**R12**	**MN750492**	**C. Li**	**SSU**	**four-gene, SSU+*rbcL*, SSU**
Nitzschia palea R8	**R8**	**MN750439**	**R. Trobajo**	**LSU**	**LSU+*rbcL*, LSU**
Nitzschia palea R8	**R8**	**MN734087**	**R. Trobajo**	***rbcL***	**LSU+*rbcL*, *rbcL***
Nitzschia palea Spain A2	**Spain A2**	**MN750499**	**C. Li**	**SSU**	**four-gene, SSU+*rbcL*, SSU**
Nitzschia palea Spain A3	**Spain A3**	**MN734055**	**C. Li**	***psbC***	**four-gene, *psbC***
Nitzschia palea Spain A3	**Spain A3**	**MN750500**	**C. Li**	**SSU**	**four-gene, SSU+*rbcL***
Nitzschia palea Spain A4	**Spain A4**	**MN734056**	**C. Li**	***psbC***	**four-gene, *psbC***
Nitzschia palea Spain A4	**Spain A4**	**MN750501**	**C. Li**	**SSU**	**four-gene, SSU+*rbcL***
Nitzschia palea Spain C	**Spain C**	**MN734057**	**C. Li**	***psbC***	**four-gene, *psbC***
Nitzschia palea Spain C	**Spain C**	**MN750502**	**C. Li**	**SSU**	**four-gene, SSU+*rbcL*, SSU**
Nitzschia palea SriLanka1 [SLA]	**SriLanka1 [SLA]**	**MN750503**	**C. Li**	**SSU**	**four-gene, SSU+*rbcL*, SSU**
Nitzschia palea SriLanka2 [SLB]	**SriLanka2 [SLB]**	**MN734058**	**C. Li**	***psbC***	**four-gene, *psbC***
Nitzschia palea SriLanka2 [SLB]	**SriLanka2 [SLB]**	**MN750504**	**C. Li**	**SSU**	**four-gene, SSU+*rbcL*, SSU**
Nitzschia palea TCC139-2	**TCC139-2**	**MN696731**	**F. Rimet**	**LSU**	**LSU+*rbcL*, LSU**
Nitzschia palea TCC394	**TCC394**	**MN696698**	**F. Rimet**	**SSU**	**SSU**
Nitzschia palea TCC395	**TCC395**	**MN696699**	**F. Rimet**	**SSU**	**SSU**

Nitzschia palea TCC397	TCC397	MN696701	F. Rimet	SSU	SSU
Nitzschia palea TCC403	TCC403	MN696702	F. Rimet	SSU	SSU
Nitzschia palea TCC425	TCC425	MN696732	F. Rimet	LSU	LSU+*rbcL*, LSU
Nitzschia palea TCC468	TCC468	MN696704	F. Rimet	SSU	SSU
Nitzschia palea TCC486	TCC486	MN696759	F. Rimet	*rbcL*	LSU+*rbcL*, *rbcL*
Nitzschia palea TCC563	TCC563	MN696712	F. Rimet	SSU	SSU
Nitzschia palea TCC577	TCC577	MN696716	F. Rimet	SSU	SSU
Nitzschia palea TCC600	TCC600	MN696718	F. Rimet	SSU	SSU
Nitzschia palea TCC620	TCC620	MN696721	F. Rimet	SSU	SSU
Nitzschia palea TCC767	TCC767	MN696774	F. Rimet	*rbcL*	*rbcL*
Nitzschia palea TCC854	TCC854	MN696776	F. Rimet	*rbcL*	*rbcL*
Nitzschia palea TCC945	TCC945	MN696754	F. Rimet	LSU	LSU+*rbcL*, LSU
Nitzschia palea TCC945	TCC945	MN696782	F. Rimet	*rbcL*	LSU+*rbcL*, *rbcL*
Nitzschia palea UK [Nit7=BB2b]	UK [Nit7=BB2b]	MN734066	C. Li	*psbC*	four-gene, *psbC*
Nitzschia palea UK [Nit7=BB2b]	UK [Nit7=BB2b]	MN750512	C. Li	SSU	four-gene, SSU+*rbcL*, SSU
Nitzschia paleacea BC0675	BC0675	MN725801	R. Hollands	LSU	LSU+*rbcL*, LSU
Nitzschia paleacea BC0675	BC0675	MN718779	S. Sato	*rbcL*	LSU+*rbcL*
Nitzschia paleacea BC0806	BC0806	MN725813	R. Hollands	LSU	LSU+*rbcL*, LSU
Nitzschia paleacea BC0806	BC0806	MN718793	S. Sato	*rbcL*	LSU+*rbcL*, *rbcL*
Nitzschia paleaeformis TCC382	TCC382	MN696693	F. Rimet	SSU	SSU
Nitzschia perminuta TCC885	TCC885	MN696777	F. Rimet	*rbcL*	SSU+*rbcL*, *rbcL*
Nitzschia perminuta TCC885	TCC885	MN696726	F. Rimet	SSU	SSU+*rbcL*, SSU
Nitzschia pusilla TCC384	TCC384	MN696694	F. Rimet	SSU	SSU
Nitzschia pusilla TCC385	TCC385	MN696695	F. Rimet	SSU	SSU

Nitzschia rectilonga SZCZE431	**SZCZE431**	**MN944010**	**C. Li**	**LSU**	**four-gene, LSU+*rbcL*, LSU**
Nitzschia rectilonga SZCZE431	**SZCZE431**	**MN920688**	**C. Li**	***psbC***	**four-gene, *psbC***
Nitzschia rectilonga SZCZE431	**SZCZE431**	**MN920679**	**C. Li**	***rbcL***	**four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL***
Nitzschia rectilonga SZCZE431	**SZCZE431**	**MN943999**	**C. Li**	**SSU**	**four-gene, SSU+*rbcL*, SSU**
Nitzschia reskoi TCC949	**TCC949**	**MN696756**	**F. Rimet**	**LSU**	**LSU+*rbcL*, LSU**
Nitzschia reskoi TCC949	**TCC949**	**MN696784**	**F. Rimet**	***rbcL***	**LSU+*rbcL*, *rbcL***
Nitzschia sigmoidea BC0787	**BC0787**	**MN725810**	**R. Hollands**	**LSU**	**four-gene, LSU+*rbcL*, LSU**
Nitzschia sigmoidea BC0787	**BC0787**	**MN718803**	**M.P. Ashworth**	***psbC***	**four-gene, *psbC***
Nitzschia sigmoidea BC0787	**BC0787**	**MN718790**	**S. Sato**	***rbcL***	**four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL***
Nitzschia sigmoidea BC0787	**BC0787**	**MN750423**	**M.P. Ashworth**	**SSU**	**four-gene, SSU+*rbcL*, SSU**
Nitzschia soratensis NIT1008KEL	**NIT1008KEL**	**MN734035**	**C. Li**	***psbC***	**four-gene, *psbC***
Nitzschia soratensis NIT1008KEL	**NIT1008KEL**	**MN750481**	**C. Li**	**SSU**	**four-gene, SSU+*rbcL***
Nitzschia soratensis NIT1009KEL	**NIT1009KEL**	**MN734036**	**C. Li**	***psbC***	**four-gene, *psbC***
Nitzschia soratensis NIT1009KEL	**NIT1009KEL**	**MN750482**	**C. Li**	**SSU**	**four-gene, SSU+*rbcL*, SSU**
Nitzschia sp. BC0076	**BC0076**	**MN718750**	**S. Sato**	***rbcL***	***rbcL***
Nitzschia sp. BC0317	**BC0317**	**MN718760**	**S. Sato**	***rbcL***	***rbcL***
Nitzschia sp. NIT1012CAT	**NIT1012CAT**	**MN750431**	**R. Trobajo**	**LSU**	**four-gene**
Nitzschia sp. NIT1012CAT	**NIT1012CAT**	**MN734037**	**C. Li**	***psbC***	**four-gene, *psbC***
Nitzschia sp. NIT1012CAT	**NIT1012CAT**	**MN734079**	**R. Trobajo**	***rbcL***	**four-gene, SSU+*rbcL***
Nitzschia sp. NIT1012CAT	**NIT1012CAT**	**MN750483**	**C. Li**	**SSU**	**four-gene, SSU+*rbcL***
Nitzschia sp. NIT330TM	**NIT330TM**	**MN734073**	**G.E. Simpson**	***rbcL***	***rbcL***
Nitzschia sp. s0819	**s0819**	**MN734052**	**C. Li**	***psbC***	**four-gene, *psbC***
Nitzschia sp. s0819	**s0819**	**MN750496**	**C. Li**	**SSU**	**four-gene, SSU+*rbcL*, SSU**

Nitzschia sp. s0826	s0826	MN734053	C. Li	*psbC*	*psbC*
Nitzschia sp. s0826	s0826	MN750497	C. Li	SSU	SSU
Nitzschia sp. SZCZCH1090	SZCZCH1090	MN944003	C. Li	LSU	four-gene, LSU+*rbcL*, LSU
Nitzschia sp. SZCZCH1090	SZCZCH1090	MN920683	C. Li	*psbC*	four-gene, *psbC*
Nitzschia sp. SZCZCH1090	SZCZCH1090	MN920673	C. Li	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL*
Nitzschia sp. SZCZCH1090	SZCZCH1090	MN943994	C. Li	SSU	four-gene, SSU+*rbcL*, SSU
Nitzschia sp. SZCZCH54	SZCZCH54	MN920675	C. Li	*rbcL*	*rbcL*
Nitzschia sp. SZCZP71	SZCZP71	MN944013	C. Li	LSU	four-gene, LSU+*rbcL*, LSU
Nitzschia sp. SZCZP71	SZCZP71	MN920691	C. Li	*psbC*	four-gene, *psbC*
Nitzschia sp. SZCZP71	SZCZP71	MN920682	C. Li	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*
Nitzschia sp. SZCZP71	SZCZP71	MN944001	C. Li	SSU	four-gene, SSU+*rbcL*, SSU
Nitzschia supralitorea NIT145D	NIT145D	MN734070	G.E. Simpson	*rbcL*	*rbcL*
Nitzschia supralitorea TCC404	TCC404	MN696703	F. Rimet	SSU	SSU
Nitzschia supralitorea TCC606	TCC606	MN696748	F. Rimet	LSU	four-gene, LSU+*rbcL*, LSU
Nitzschia supralitorea TCC606	TCC606	MN696769	F. Rimet	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL*
Nitzschia supralitorea TCC606	TCC606	MN696719	F. Rimet	SSU	four-gene, SSU+*rbcL*, SSU
Nitzschia supralitorea TCC944	TCC944	MN696781	F. Rimet	*rbcL*	*rbcL*
Nitzschia supralitorea TCC946	TCC946	MN696755	F. Rimet	LSU	LSU+*rbcL*, LSU
Nitzschia supralitorea TCC946	TCC946	MN696783	F. Rimet	*rbcL*	LSU+*rbcL*, *rbcL*
Nitzschia supralitorea TCC950	TCC950	MN696757	F. Rimet	LSU	LSU+*rbcL*, LSU
Nitzschia supralitorea TCC950	TCC950	MN696785	F. Rimet	*rbcL*	LSU+*rbcL*, *rbcL*
Nitzschia traheaformis SZCZCH971	SZCZCH971	MN944007	C. Li	LSU	four-gene, LSU+*rbcL*, LSU
Nitzschia traheaformis SZCZCH972	SZCZCH972	MN920686	C. Li	*psbC*	four-gene, *psbC*
Nitzschia tubicola TCC575	TCC575	MN696745	F. Rimet	LSU	four-gene, LSU+*rbcL*, LSU

Nitzschia tubicola TCC575	TCC575	MN696767	F. Rimet	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL*
Nitzschia tubicola TCC575	TCC575	MN696714	F. Rimet	SSU	four-gene, SSU+*rbcL*, SSU
Nitzschia umbonata NIT327TM	NIT327TM	MN734071	G.E. Simpson	*rbcL*	*rbcL*
Nitzschia varelae NIT952CAT	NIT952CAT	MN734046	C. Li	*psbC*	four-gene, *psbC*
Nitzschia varelae NIT952CAT	NIT952CAT	MN750490	C. Li	SSU	four-gene, SSU+*rbcL*, SSU
Psammodictyon sp. Corsica	Corsica	MN734067	G.E. Simpson	*rbcL*	*rbcL*
Psammodictyon sp. Gillian	Gillian	MN734069	G.E. Simpson	*rbcL*	*rbcL*
Psammodictyon sp. SZCZE328	SZCZE328	MN944008	C. Li	LSU	four-gene, LSU+*rbcL*, LSU
Psammodictyon sp. SZCZE328	SZCZE328	MN920687	C. Li	*psbC*	four-gene, *psbC*
Psammodictyon sp. SZCZE328	SZCZE328	MN920677	C. Li	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL*
Psammodictyon sp. SZCZE328	SZCZE328	MN943997	C. Li	SSU	four-gene, SSU+*rbcL*, SSU
Psammodictyon sp. SZCZE331	SZCZE331	MN944009	C. Li	LSU	four-gene, LSU+*rbcL*, LSU
Psammodictyon sp. SZCZE331	SZCZE331	MN920678	C. Li	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL*
Psammodictyon sp. SZCZE331	SZCZE331	MN943998	C. Li	SSU	four-gene, SSU+*rbcL*, SSU
Psammodictyon sp. SZCZE459	SZCZE459	MN944011	C. Li	LSU	four-gene, LSU+*rbcL*, LSU
Psammodictyon sp. SZCZE459	SZCZE459	MN920689	C. Li	*psbC*	four-gene, *psbC*
Psammodictyon sp. SZCZE459	SZCZE459	MN920680	C. Li	*rbcL*	four-gene, LSU+*rbcL*, *rbcL*
Tryblionella apiculata TRY946CAT	TRY946CAT	MN750443	R. Trobajo	LSU	four-gene, LSU+*rbcL*
Tryblionella apiculata TRY946CAT	TRY946CAT	MN734061	C. Li	*psbC*	four-gene, *psbC*
Tryblionella apiculata TRY946CAT	TRY946CAT	MN734089	R. Trobajo	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL*
Tryblionella apiculata TRY946CAT	TRY946CAT	MN750507	C. Li	SSU	four-gene, SSU+*rbcL*, SSU
Tryblionella apiculata TRY947CAT	TRY947CAT	MN750444	R. Trobajo	LSU	four-gene
Tryblionella apiculata TRY947CAT	TRY947CAT	MN734062	C. Li	*psbC*	four-gene
Tryblionella apiculata TRY947CAT	TRY947CAT	MN734090	R. Trobajo	*rbcL*	four-gene, SSU+*rbcL*

Tryblionella apiculata TRY947CAT	TRY947CAT	MN750508	C. Li	SSU	four-gene, SSU+*rbcL*
Tryblionella apiculata TRY949CAT	TRY949CAT	MN750445	C. Li	LSU	LSU
Tryblionella cf. compressa TRY1006CAT	TRY1006CAT	MN750441	R. Trobajo	LSU	four-gene, LSU
Tryblionella cf. compressa TRY1006CAT	TRY1006CAT	MN734059	C. Li	*psbC*	four-gene, *psbC*
Tryblionella cf. compressa TRY1006CAT	TRY1006CAT	MN750505	C. Li	SSU	four-gene, SSU
Tryblionella cf. compressa TRY1007CAT	TRY1007CAT	MN750442	R. Trobajo	LSU	four-gene, LSU+*rbcL*
Tryblionella cf. compressa TRY1007CAT	TRY1007CAT	MN734060	C. Li	*psbC*	four-gene, *psbC*
Tryblionella cf. compressa TRY1007CAT	TRY1007CAT	MN734088	R. Trobajo	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL*
Tryblionella cf. compressa TRY1007CAT	TRY1007CAT	MN750506	C. Li	SSU	four-gene, SSU+*rbcL*, SSU
Tryblionella debilis BC0502	BC0502	MN718770	S. Sato	*rbcL*	*rbcL*
Tryblionella gaoana SZCZCH97	SZCZCH97	MN944006	C. Li	LSU	four-gene, LSU+*rbcL*, LSU
Tryblionella hungarica TRY951CAT	TRY951CAT	MN750446	R. Trobajo	LSU	four-gene, LSU+*rbcL*, LSU
Tryblionella hungarica TRY951CAT	TRY951CAT	MN734063	C. Li	*psbC*	four-gene, *psbC*
Tryblionella hungarica TRY951CAT	TRY951CAT	MN734091	R. Trobajo	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL*
Tryblionella hungarica TRY951CAT	TRY951CAT	MN750509	C. Li	SSU	four-gene, SSU+*rbcL*, SSU
Tryblionella hungarica TRY981CAT	TRY981CAT	MN750447	R. Trobajo	LSU	four-gene, LSU+*rbcL*, LSU
Tryblionella hungarica TRY981CAT	TRY981CAT	MN734064	C. Li	*psbC*	four-gene, *psbC*
Tryblionella hungarica TRY981CAT	TRY981CAT	MN734092	R. Trobajo	*rbcL*	four-gene, SSU+*rbcL*, LSU+*rbcL*, *rbcL*
Tryblionella hungarica TRY981CAT	TRY981CAT	MN750510	C. Li	SSU	four-gene, SSU+*rbcL*, SSU
Tryblionella hungarica TRY986CAT	TRY986CAT	MN750448	R. Trobajo	LSU	four-gene
Tryblionella hungarica TRY986CAT	TRY986CAT	MN734065	C. Li	*psbC*	four-gene, *psbC*
Tryblionella hungarica TRY986CAT	TRY986CAT	MN734093	R. Trobajo	*rbcL*	four-gene, SSU+*rbcL*
Tryblionella hungarica TRY986CAT	TRY986CAT	MN750511	C. Li	SSU	four-gene, SSU+*rbcL*
Tryblionella sp. s0863	s0863	MN750440	C. Li	LSU	four-gene, LSU+*rbcL*, LSU

Tryblionella sp. s0863	**s0863**	**MN734054**	**C. Li**	***psbC***	**four-gene, *psbC***
Tryblionella sp. s0863	**s0863**	**MN750498**	**C. Li**	**SSU**	**four-gene, SSU+*rbcL***

Supplementary Table 3. Bootstrap support values for the main clades and subclades of Bacillariaceae in the concatenated and single-gene trees (Figs 3, 4, Supplementary Figs 2–7). **Bold** = support >70%, Roman = 50% < support < 70%, [Roman] = support < 50%, – = clade not present, singleton = only one terminal represented.

Clade/subclade	4-gene	*rbcL*–SSU	*rbcL–LSU*	*rbcL*	SSU	LSU	*psbC*	*cox1*
1	**100**	**81**	singleton	**89**	**78**	**90**	**71**	–
2	**100**	**99**	**100**	**98**	[11]	**100**	**72**	singleton
3	singleton	singleton	**100**	**100**	**98**	**100**	singleton	–
4	**92**	–	[47]	[30]	–	–	–	–
4A	singleton	**100**	singleton	**100**	**97**	singleton	**100**	–
4B	**100**	**100**	**94**	**98**	**84**	**95**	**75**	65
4B-I	**100**	**100**	**100**	**100**	**100**	**99**	–	–
4B-II	**100**	58	**81**	–	–	[17]	**96**	[45]
5	**88**	–	**84**	–	–	69	–	–
5A	singleton	singleton	singleton	[20]	**89**	singleton	–	–
5B	**100**	**99**	**100**	**99**	**96**	**100**	[44]	–
6	**89**	–	[36]	–	–	–	[2]	–
6A	singleton	**99**	singleton	**97**	–	singleton	singleton	–
6B	**98**	**94**	**98**	**93**	[7]	[27]	[4]	[38]
7	**100**	**99**	**83**	**97**	58	[37]	**90**	77
8	**99**	65	**100**	**86**	**97**	**98**	**81**	81
8A	**88**	–	50	[45]	[49]	–	–	–
8A-I	**100**	**100**	**100**	**96**	**100**	**97**	**94**	**99**
8A-II	**100**	**100**	**100**	**98**	**99**	**95**	**93**	–
8B	**99**	**76**	**88**	[46]	[24]	–	**86**	**99**
8C	**100**	**86**	**100**	**98**	**100**	**98**	**95**	**86**
8C-I	singleton	**99**	singleton	**99**	**82**	–	**100**	**100**
8C-II	**100**	**100**	**100**	**99**	**41**	–	–	59

SUPPLEMENTARY FILE 1. Materials and methods

1. Isolation and culturing

1.1. *Szczecin*: Material was collected from a variety of substrata (sand, sediment, rock, macrophytes, seaweeds, and 20-µm plankton net hauls) in marine habitats in widely separated regions (Table 1). Samples were placed in 10 ml plastic tubes and a few milliliters of f/2 culture medium (Guillard, 1975) added to help keep diatoms alive during transport to the laboratory. Subsequently, enrichment cultures were established by transferring part of each sample to Petri dishes (50-mm diameter) with f/2 medium. Three weeks to one month later, single cells were isolated by pipette into a small volume of f/2 culture medium and washed by three or four serial transfers into fresh f/2 medium. The culture was then placed close to a north-facing window or in a batch incubator at 18°C under a 16:8 h light:dark (L:D) cycle, illuminated with 50 µmol photons m^{-2} $s^{-1}$of white light.

1.2. *Edinburgh*: Samples from freshwater, brackish and marine habitats (source localities are given in Table 1 here and also in the metadata in GenBank: see Supplementary Table 2 for accessions) were placed in 50 mm Petri dishes, sometimes diluted with medium (WC medium for freshwater diatoms, R medium for marine diatoms, and mixtures of the two for brackish diatoms [for the composition of WC medium, see Guillard & Lorenzen, 1972; for R medium, see Roshchin, 1994; Chepurnov & Mann, 1997]). Individual cells of diatoms were isolated by micropipette or by streaking on 2–3% agar plates; with streaked material, single cells were sometimes isolated immediately by pipette from the agar surface, but in other cases plates were incubated for 2–4 weeks and cells transferred from discrete small colonies of clonal cells. Micropipette isolations were made with either a Zeiss inverted microscope or a stereomicroscope. With the inverted microscope, higher magnifications (of up to 400×) were possible and preliminary identifications could sometimes be made. Selected cells were transferred into small volumes of medium in the wells of 96-well plates. For freshwaters, a general-purpose freshwater medium was initially used (WC medium with silicate, adjusted to pH 7:). However, trials indicated that this was unsuitable for diatoms from more oligotrophic and acid habitats. For these, modified WC medium was used, containing lower N and/or P (one-tenth of the usual WC additions), or a modified Grundgloeodinium II medium (von Stosch & Fecher, 1979), in which the SiO_2 used in the original formulation was replaced with the sodium metasilicate addition of WC medium. After a few days of incubation, the health and clonality of each culture was confirmed under an inverted microscope. Successfully established clonal cultures were then grown in 90 mm Petri dishes for DNA extraction and preparation for voucher slides. Clones were grown at 15–22°C under cool-white fluorescent light on a 14:10 h L:D cycle at a photon flux density of 5–20 µmol photons m^{-2} s^{-1}.

1.3. *Thonon culture collection (TCC)*: Samples from various freshwater habitats (source localities are given in Table 1 and in the spreadsheets available at https://www6.inrae.fr/carrtel-collection_eng/Barcoding-database/Database-download) were sampled and placed in 50 ml sterile flasks and then were stored in a cool place (5°C). Then, in the lab, drops were introduced in 12-well microplate with a mixture of synthetic (same modified WC medium as in Edinburgh) and water from the field (previously sterilized on a 0.2 µm filter for Schott bottles). Then they were allowed to grow for a few days. After this period, the microplates were observed on inverted microscope (up to 400×). Then cells were isolated with micropipettes and put in new 12-well microplates with modified WC medium. They were allowed to grow for a few days more and then were checked for health and clonality. Successfully established clonal cultures were then grown in 50 ml flasks (20°C, 14:10h L:D, under cool-white fluorescent light).

2. DNA preparation and sequencing

2.1. Harvesting

2.1.1. *Szczecin*: The cultured cells were examined under light microscopy to check their growth condition within one month after isolation. For well-growing clones, 1.5 ml of suspension was harvested and centrifuged for 20 min at 5000 rpm using a Centrifuge 5424R (Eppendorf, Germany).The supernatant was discarded and the pellet rinsed twice with sterile distilled water to remove residual salts.

2.1.2. *Edinburgh*: Where necessary, cells from exponentially growing cultures were brought into suspension by gently scraping them off the bottom of Petri dishes using short pieces of sterile silicone rubber tubing. A few ml of suspension were centrifuged to concentrate the diatoms into a pellet, which was then washed twice with sterile distilled water to remove residual salts.

2.1.3. *Thonon Culture Collection*: After the cultures were grown in sterile 50 ml fasks, they were then registered in the TCC after sufficient some material could be kept (untreated material kept at -80°C, treated material in 10 ml vials and microscopic slides). Each culture received a unique TCC number which is searchable at: https://www6.inra.fr/carrtel-collection_eng/Culture-search

2.2. DNA extraction

2.2.1. *Szczecin*: For high density cultures, 200 µl of 10% (g/ml) SDS (Bio-rad, Japan) and one sterile metal bead (4mm diameter) were added to pellets of harvested cells and this solution was mixed using a shaker (Retsch, Poland) at frequency 20 s^{-1} for 30 s to 1 min. Genomic DNA was then extracted using High Pure PCR Template Preparation Kit (Roche, Mannheim, Germany) following the protocol for isolation of nucleic acids from bacteria or yeasts given by the manufacturer. As for low-density cultures, genomic DNA was obtained with Chelex method: a few cells were harvested, centrifuged, the supernatant discarded, and 150 ml of 10% (m/v) Chelex® 100 Resin (Bio-Rad, USA) added to the pellet. The mixture was then heated for 20 min at 95° C using a Thermomixer comfort (Eppendorf, Germany), followed by centrifugation for 20 min at 4000 rpm at 10°C. The supernatant was transferred to a new 1.5 ml Eppendorf tube (Eppendorf, Germany) and used as the DNA template for PCR.

2.2.2. *Edinburgh*: DNA was extracted from each pellet using using a DNeasy Plant Kit (Qiagen, Crawley, UK), or a high-throughput genomic DNA extraction instrument QIAxtractor (Qiagen).

2.2.3. *Thonon Culture Collection*: Two protocols were used, either the same extraction kit was used as Edinburgh (DNeasy Plant Kit), or the GenEluteTM-LPA (Sigma–Aldrich) protocol

2.3. PCR amplification

Four target DNA markers were used: nuclear-encoded small subunit (nSSU) and partial large subunit (nLSU) ribosomal DNAs, and chloroplast-encoded *rbcL* and *psbC*. Sequences of *cox1* were obtained from GenBank. The expected sizes of the PCR products were 1600–1700 bp (SSU rDNA), 1400–1500 bp (*rbcL*), 1100–1200 bp (*psbC*), and 500–600 bp (nLSU).

2.3.1. *Szczecin.* The PCR and sequencing primers are listed in Table 2. The volume of each PCR was 25 µL: 3 µL DNA template; 2.5 µL 10x Dream Taq buffer (includes 20 mM $MgCl_2$); 1 µL Ultrapure dNTPs Set (5 mM each dATP, dCTP, dGTP, dTTP); 0.5 µL each primer (10 µM); 0.15 µL Dream Taq DNA polymerase (5 U/µL); and sterile ddH_2O to a final volume of 25 µL. PCR conditions for SSU were as follows: 94°C for 2 min, 35 cycles of {94°C for 15 s, 55°C for 15 s, 72°C for 1 min 35 seconds}, and a final extension at 72°C for 7 min. PCR conditions for *psbC* and *rbcL* were the same as with SSU but with 53°C for annealing temperature and 1 min 15 seconds extension time. If the first PCR reaction failed, a second PCR reaction was performed with the first PCR product as the template (diluted 10 times) using another pair of primers (Table 2), with annealing temperatures of 58°C, 53°C and 45°C respectively for SSU, *rbcL* and *psbC*. PCR conditions for LSU were: 95°C for 3 min, 35 cycles of {95°C for 15 s, 43°C for 15 s, 72°C for 45 seconds}, and a final extension at 72°C for 7 min. The presence of amplification products was verified with 1% agarose (Maximus, Poland) gel in an electrophoresis chamber model 40-1214 (Peqlab Biotechnologie GmbH, Germany) and imaged and visualized by G: BOX (SYNGENE). Successful reactions were purified using a Exonuclease I & Polar-BAP (EURx, Gdańsk, Poland) protocol, then sent to oligo.pl DNA Sequencing Laboratory IBB PAS, Warsaw, Poland for Sanger sequencing with use of BigDye Terminator v. 3.1 chemistry and ABI3730 xl sequencer.

2.3.2. *Edinburgh*: For *rbcL*, the forward and reverse primers used (Table 3) were the ones reported by Jones et al. (2005), DPrbcL1 and DPrbcL7, which amplified a region of ~1400 bp, covering the *rbcL* gene. The PCR reaction for the amplification of *rbcL* was in 25μl volumes containing 10ng DNA, 1 mM deoxynucleotides (dNTPs), 1× Roche diagnostics PCR reaction buffer (Roche Diagnostics GmbH, Mannheim, Germany), 1 unit Taq DNA polymerase (Roche) and 0.5 μM of each primer. The PCR cycling comprised an initial denaturing phase for 3 minutes (94ºC), followed by 30–40 cycles of 94°C for 1 minute, 55°C for 1 minute and 72°C for 1.5 minutes, with a final extension of 72°C for 5 minutes.

The quantity and length of the PCR products were examined by agarose gel electrophoresis against known standards. PCR products were purified using ExoSAP-IT (USB Corporation, Ohio, USA). Sequencing was conducted in 10μl volumes using 0.32 μM of PCR primer or sequencing primers NDrbcL5: CTCAACCATTYATGCG and DrbcL11: CTGTGTAACCCATWAC (Jones et al. 2005), 1μl of BigDye v3.1 and 2μl of sequencing reaction buffer (Applied Biosystems). Sequencing PCR conditions were 25 cycles of 95°C for 30 seconds, 50°C for 20 seconds and 60°C for 4 minutes. Excess dye-labelled nucleotides were removed using the Performa DTR V3 clean-up system (EdgeBio) and sequence products were run on an ABI 3730 DNA sequencer (Applied Biosystems) at the University of Edinburgh.

Sequencing reads were edited and assembled using SeqMan (DNASTAR, Madison, WI). Each *rbcL* region was sequenced by 4 reads (using primers DPrbcL1, DPrbcL7, NDrbcL5 and DrbcL11) and the whole region was sequenced by at least 2 overlapping reads.

2.3.3. *Thonon Culture Collection*: Methodology for PCR amplification is detailed in Table 4 (Rimet et al. 2011, Kermarrec et al. 2013): 5 gene fragments were amplified: D1–D2 region of the LSU rDNA gene, ITS1-5.8S-ITS2, partial rbcL and cox1 genes and 18S. All PCRs were performed using the primers listed in Table 4, and according to the authors' specifications in a PCR thermal cycler (T personal, Biometra, Göttingen, Germany). Additional internal sequencing primers were used to retrieve the complete sequences of rbcL and 18S (Table 4). Sanger sequencing was performed by Beckman Coulter Genomics (Takeley, United Kingdom), GATC (Konstanz, Germany), and Genoscope (Evry, France).

2.4. Alignment, trimming and phylogenetic analysis

SSU sequences were aligned by the SSUalign program (Nawrocki, 2009), with the covariance model based on the 10 diatoms included with the program download and supplemented with secondary structure models from 23 additional diatoms from the CRW website (Cannone et al.,

2002) available from E.C. Theriot. LSU sequences were manually aligned against secondary structure models available from the CRW website. Protein encoding chloroplast genes were aligned using MUSCLE in Seaview 4.0 (Edgar, 2004; Gouy et al., 2010). SSU and LSU data were partitioned into paired and unpaired sites. Protein encoding genes were partitioned into 1st, 2nd, and 3rd codon positions. Phylogenetic analyses run using the GTR+G model under maximum likelihood using RAxML ver. 8.2.9 (Stamatakis, 2014) compiled as the pthread-AVX version on an Intel i7 based processor in Linux Mint 18. Twenty replicates were run each with 500 rapid BS replicates with ML optimization. Bootstrap support was assessed using the BS replicates from the run producing the optimal ML score.

For single-gene maximum likelihood (ML) analyses of *rbcL* and *psbC* and the concatenated *rbcL*–LSU analysis, ambiguously aligned sites with a posterior probability less than 0.95 were removed. Protein-encoding sequences were trimmed at both ends in case the sites were highly gappy (e.g. ca > 70% of OTUs had gaps) and phylogenetically uninformative. The alignments were partitioned into different codon positions (for *rbcL* and *psbC*), or paired and unpaired in the secondary structure model (for rDNA). Phylogenetic trees were conducted using GTRCAT model, with 10,000 bootstrap replicates using rapid Bootstrap analysis in RAxML 8.2 (Stamatakis, 2014). The best-scoring ML tree was chosen as the final tree and bootstrap values were added to the nodes.

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Table 1. Source localities and isolation information for clones from which new sequences were obtained for this paper. ND = no data. For the GenBank accession numbers of the new sequences, see Supplementary Table 2. Details of Thonon Culture Collection (TCC) clones are given in the spreadsheets available at https://www6.inrae.fr/carrtel-collection_eng/Barcoding-database/Database-download

Clone	Identity	Type of sample	Source locality	Latitude	Longitude	Isolated by
Szczecin clones						
SZCZCH1090	*Nitzschia* sp.	shallow water sediment	Chałupy, Puck Bay, Baltic Sea, Poland	54° 45′ 31″ N	18 30′ 34″ E	C. Li
SZCZCH50	*Cylindrotheca* sp.	sediment	Haian Bay, Xuwen county, SE Guangdong, China	ND	ND	C. Li
SZCZCH54	*Nitzschia* sp.	sediment	Haian Bay, Xuwen county, SE Guangdong, China	ND	ND	C. Li
SZCZCH690	*Cylindrotheca* sp.	plankton net	Fish Pass, Corpus Christi, Gulf of Mexico, USA	27° 40′ 48″ N	91° 10′ 22.8″ W	C. Li
SZCZCH97	*Tryblionella gaoana*	shallow water sediment	Chang Dao Island, Bohai Sea, China	37° 57.17′ N	120° 44.04′ E	C. Li
SZCZCH970	*Nitzschia traheaformis*	water sample	Laizhou Bay, Bohai Sea, China[1]	37° 27.362′ N	121° 42.215′ E	C. Li
SZCZCH971	*Nitzschia traheaformis*	water sample	Laizhou Bay, Bohai Sea, China[1]	37° 27.362′ N	121° 42.215′ E	C. Li

SZCZCH972	*Nitzschia traheaformis*	shallow water sediment	Laizhou Bay, Bohai Sea, China[1]	37° 27.362′ N	121° 42.215′ E	C. Li
SZCZCH966	*Nitzschia aurariae*	exposed microbial mat	Muping, Yantai, Yellow Sea, China[1]	37° 27′ 19.37″ N	121° 42′ 7.27″ E	C. Li
SZCZCH969	*Nitzschia aurariae*	sand	Muping, Yantai, Yellow Sea, China[1]	37° 27′ 19.37″ N	121° 42′ 7.27″ E	C. Li
SZCZCH845	*Nitzschia* cf. *volvendirostrata*	sand	Yantai, Moon Bay, public beach Yellow Sea, China[1]	ND	ND	C. Li
SZCZCH967	*Amphora vixvisibilis*	fine sand	Muping, Yantai, Yellow Sea, China[1]	37° 27′ 19.37″ N	121° 42′ 7.27″ E	C. Li
SZCZCH658	*Nitzschia* sp.	sea cucumber aquaculture sediment	Yantai, Yellow Sea, China[1]	37° 26′ 7″ N	121° 32′ 59″ E	C. Li
SZCZCH113	*Achnanthes* sp.	beach	Gdańsk Bay, Baltic Sea	54° 20′ 44″ N	18° 52′ 36″ E	C. Li
SZCZCH974	*Nitzschia nanodissipata*	water sample	Laizhou Bay, Bohai Sea, China[1]	37° 27.362′ N	121° 42.215′ E	C. Li
SZCZE328	*Psammodictyon* sp.	seaweeds	Nosy Be, NW Madagascar	13°24.834′ S	48° 20.048′ E	E. Górecka
SZCZE331	*Psammodictyon* sp.	rock scrape	Nosy Be, NW Madagascar	13° 29.083′ S	48°14.223′ E	E. Górecka
SZCZE431	*Nitzschia rectilonga*	sediment	Corpus Christii, Gulf of Mexico, USA	ND	ND	N. Davidovich

SZCZE459	*Psammodictyon* sp.	rock scrape	Nosy Be, NW Madagascar	13° 24.081’ S	48° 12.449’ E	E. Górecka
SZCZM117	*Nitzschia* sp.	sediment	King George Island, Antarctic Peninsula	c. 58° 55’ W	c. 62° 12’ S	M. Krzywda
SZCZP613	*Bacillaria* sp.	beach	Azores, Sao Miguel, Ponta Delgada	37° 44’14.86” N	25° 40’ 12.56” W	P. Dąbek
SZCZP71	*Nitzschia* sp.	sediment from shallow water	Sandwich Harbour, lagoon, Namibia	23° 21’ 332” S	14° 29.800” E	P. Dąbek
SZCZP36	*Nitzschia volvendirostrata*	sand from sublittoral	Indian Ocean, Mozambique coast, Tofo Sand	24° 55’ 18” S	35° 30’ 25” E	P. Dąbek
SZCZM119	*Achnanthes* sp.	seaweed fragments, Chlorophyta	Portugal, Tejo Estuary, Alcochete beach	38° 44’ 31.69” N	8° 59’ 44.44” W	M. Krzywda
KSA0039	*Nitzschia volvendirostrata*	ND	Durrah, Saudi Arabia Red Sea coast[1]	21° 93.58’ N	38° 94.51’ E	M. Ashworth
KSA0035	*Nitzschia* sp.	ND	Markaz Al Shoiabah (Al Qatan resort) Saudi Arabia Red Sea coast[1]	20° 50.474' N	39° 24.046’ E	M. Ashworth
‘Edinburgh’ clones, including clones isolated for previous studies (Trobajo et al. 2006, 2009, 2010; Rovira 2015; Kelly et al. 2020), with clone synonyms where applicable [in square brackets, column 1]						
AG [AG1=Argentina	Nitzschia cf.	ND	Pond, Estancia el	26° 17’ 8.95” S	58° 49’ 46.2” W	R. Trobajo

fru]	bulnheimiana		Bagual, Formosa, Argentina			
BAC901CAT [BAC DM901]	Bacillaria sp.	lagoon sediment	IRTA aquaculture lagoon, Ebro Delta, Catalonia, Spain	40° 37′ 38.88″ N	0° 39′ 39.26″ E	D.G. Mann
BC0039 [039NitP04]	*Nitzschia palea*	periphyton	Green Cleuch streams, Pentland Hills, Scotland, UK	55.844216 N	-3.311093 E	S. Sato, May 2012
BC0053 [053NitP04]	*Nitzschia* cf. *fonticola*	periphyton	Green Cleuch streams, Pentland Hills, Scotland, UK	55.844216 N	-3.311093 E	S. Sato, May 2012
BC0076 [076NitP07]	*Nitzschia* sp.	periphyton	Green Cleuch streams, Pentland Hills, Scotland, UK	55.844216 N	-3.311093 E	S. Sato, May 2012
BC0083 [083NitP07]	*Nitzschia linearis*	periphyton	Green Cleuch streams, Pentland Hills, Scotland, UK	55.844216 N	-3.311093 E	S. Sato, May 2012
BC0095 [095NitP09]	*Nitzschia palea*	periphyton	Green Cleuch streams, Pentland Hills, Scotland, UK	55.844216 N	-3.311093 E	S. Sato, May 2012
BC0098 [098NitP09]	*Nitzschia acidoclinata*	periphyton	Green Cleuch streams, Pentland Hills, Scotland, UK	55.844216N	-3.311093 E	S. Sato, May 2012
BC0234 [234NitB08]	*Nitzschia palea*	periphyton	Allt a ‘Bhalachain stream, Argyll & Bute, Scotland, UK,	56.206051 N	-4.790649 E	S. Sato, May 2012
BC0240 [240NitB08]	*Nitzschia palea*	periphyton	United Kingdom:Scotland, Argyll & Bute, Allt a	56.206051 N	-4.790649 E	S. Sato, May 2012

			'Bhalachain,			
BC0273 [273NitC06]	*Nitzschia linearis*	periphyton	River Almond, Edinburgh, Scotland, UK	55.973614 N	-3.31066 E	S. Sato, June 2012
BC0277 [277NitC06]	*Nitzschia palea*	periphyton	River Almond, Edinburgh, Scotland, UK	55.973614 N	-3.31066 E	S. Sato, June 2012
BC0307 [307NitC07]	*Nitzschia heufleriana*	periphyton	River Almond, Edinburgh, Scotland, UK	55.973614 N	-3.31066 E	S. Sato, June 2012
BC0308 [308NitC07]	*Nitzschia* cf. *sigma*	periphyton	River Almond, Edinburgh, Scotland, UK	55.973614 N	-3.31066 E	S. Sato, June 2012
BC0317 [317NitW02]	*Nitzschia* sp.	periphyton	Water of Leith, Currie, Edinburgh, Scotland, UK	55.895467 N	-3.308024 E	S. Sato, June 2012
BC0325 [325NitW02]	*Nitzschia draveillensis*	periphyton	Water of Leith, Currie, Edinburgh, Scotland, UK	55.895467 N	-3.308024 E	S. Sato, June 2012
BC0330 [330NitW02]	*Nitzschia alicae*	periphyton	Water of Leith, Currie, Edinburgh, Scotland, UK	55.895467 N	-3.308024 E	S. Sato, June 2012
BC0333 [333NitW02]	*Nitzschia pusilla*	periphyton	Water of Leith, Currie, Edinburgh, Scotland, UK	55.895467 N	-3.308024 E	S. Sato, June 2012
BC0373 [373NitW01]	*Nitzschia palea*	periphyton	Water of Leith, Currie, Edinburgh, Scotland, UK	55.895467 N	-3.308024 E	S. Sato, June 2012
BC0375	*Nitzschia palea*	periphyton	Water of Leith,	55.895467 N	-3.308024 E	S. Sato, June 2012

[375NitW01]			Currie, Edinburgh, Scotland, UK			
BC0469 [469NitR03]	*Nitzschia costei*	sediment and periphyton	The main pond, Royal Botanic Garden Edinburgh, Edinburgh, Scotland, UK	55.965416 N	-3.206233 E	S. Sato, June 2012
BC0470 [470NitR03]	*Nitzschia* cf. *dissipata* var. *media*	sediment and periphyton	The main pond, Royal Botanic Garden Edinburgh, Edinburgh, Scotland, UK	55.965416 N	-3.206233 E	S. Sato, June 2012
BC0486 [486NitR03]	*Nitzschia amphibia*	sediment and periphyton	The main pond, Royal Botanic Garden Edinburgh, Edinburgh, Scotland, UK	55.965416 N	-3.206233 E	S. Sato, June 2012
BC0501 [501NitR04]	*Nitzschia* cf. *soratensis*	periphyton	Artificial stream, Royal Botanic Garden Edinburgh, Edinburgh, Scotland, UK	55.964232 N	-3.205196 E	S. Sato, June 2012
BC0502 [502TryR04]	*Tryblionella debilis*	periphyton	Artificial stream, Royal Botanic Garden Edinburgh, Edinburgh, Scotland, UK	55.964232 N	-3.205196 E	S. Sato, June 2012
BC0503 [503NitR04]	*Nitzschia amphibia*	periphyton	Artificial stream, Royal Botanic	55.964232 N	-3.205196 E	S. Sato, June 2012

			Garden Edinburgh, Edinburgh, Scotland, UK			
BC0603 [603NitK02]	*Nitzschia palea*	periphyton	River Browney, Sunderland Bridge, Co. Durham, England, UK	54.737885 N	-1.5860622 E	S. Sato, June 2012
BC0605 [605NitK02]	*Nitzschia palea*	periphyton	River Browney, Sunderland Bridge, Co. Durham, England, UK	54.737885 N	-1.5860622 E	S. Sato, June 2012
BC0619 [619NitP11]	*Nitzschia acidoclinata*	periphyton	River Tay, Pitlochry, Perth & Kinross, Scotland, UK	56.70746 N	-3.750611 E	S. Sato, July 2012
BC0649 [649NitK07]	*Nitzschia* cf. *dissipata* var. *media*	periphyton	River Dever, Bransbury, Hampshire, England, UK	51.177758 N	-1.3984013 E	S. Sato, September 2012
BC0650 [650NitK07]	*Nitzschia* cf. *romana*	periphyton	River Dever, Bransbury, Hampshire, England, UK	51.177758 N	-1.3984013 E	S. Sato, September 2012
BC0669 [669NitK09]	*Nitzschia linearis*	periphyton	River Anton, Andover, Hampshire, England, UK	51.215536 N	-1.4795755 E	S. Sato, September 2012
BC0670 [670NitK09]	*Nitzschia palea*	periphyton	River Anton, Andover, Hampshire,	51.215536 N	-1.4795755 E	S. Sato, September 2012

			England, UK			
BC0675 [675NitK09]	*Nitzschia* cf. *paleacea*	periphyton	River Anton, Andover, Hampshire, England, UK	51.215536 N	-1.4795755 E	S. Sato, September 2012
BC0696 [696NitK10]	*Nitzschia linearis*	periphyton	River Lambourn, Bagnor, Berkshire, England, UK	51.420638 N	-1.3496305 E	S. Sato, September 2012
BC0701 [701NitK11]	*Nitzschia amphibia*	periphyton	River Kennet, Stitchcombe Mill, Wiltshire, England, UK	51.424326 N	-1.6739029 E	S. Sato, September 2012
BC0712 [712NitK13]	*Nitzschia linearis*	periphyton	River Wylye, Henford Marsh, Wiltshire, England, UK	51.193109 N	-2.1752506 E	S. Sato, September 2012
BC0713 [713NitK13]	*Nitzschia capitellata*	periphyton	River Wylye, Henford Marsh, Wiltshire, England, UK	51.193109 N	-2.1752506 E	S. Sato, September 2012
BC0730 [730NitB12]	*Nitzschia* cf. *perminuta*	periphyton	Inveruglas Water, by Ben Vane, Argyll & Bute, Scotland, UK	55.369836 N	-3.12179 E	S. Sato, September 2012
BC0748 [748NitR05]	*Nitzschia palea*	sediment and periphyton	The main pond, Royal Botanic Garden Edinburgh, Edinburgh, Scotland, UK	55.964797 N	-3.20623 E	S. Sato, September 2012

BC0769 [769NitN01]	*Nitzschia* cf. *recta*	periphyton	Wooler Water, near Wooler, Northumbria, England, UK	55.5185 N	-2.0174 E	S. Sato, October 2012
BC0774 [774NitN01]	*Nitzschia palea*	periphyton	Wooler Water, near Wooler, Northumbria, England, UK	55.5185 N	-2.0174 E	S. Sato, October 2012
BC0776 [776NitN01]	*Nitzschia palea*	periphyton	Wooler Water, near Wooler, Northumbria, England, UK	55.5185 N	-2.0174 E	S. Sato, October 2012
BC0786 [786NitN01]	*Nitzschia palea*	periphyton	Wooler Water, near Wooler, Northumbria, England, UK	55.5185 N	-2.0174 E	S. Sato, October 2012
BC0787 [787NitN01]	*Nitzschia sigmoidea*	periphyton	Wooler Water, near Wooler, Northumbria, England, UK	55.5185 N	-2.0174 E	S. Sato, October 2012
BC0795 [795NitN01]	*Nitzschia* cf. *recta*	periphyton	Wooler Water, near Wooler, Northumbria, England, UK	55.5185 N	-2.0174 E	S. Sato, October 2012
BC0799 [799NitN02]	*Nitzschia* cf. *palea*	periphyton	Wooler Water, near Wooler, Northumbria, England, UK	55.5185 N	-2.0174 E	S. Sato, October 2012
BC0806	*Nitzschia* cf.	periphyton	Wooler Water,	55.5185 N	-2.0174 E	S. Sato, October

[806NitN02]	*paleacea*		near Wooler, Northumbria, England, UK			2012
BC0815 [815NitN02]	*Nitzschia linearis*	periphyton	Wooler Water, near Wooler, Northumbria, England, UK	55.5185 N	-2.0174 E	S. Sato, October 2012
BC0838 [838NitN05]	*Nitzschia* cf. *perminuta*	periphyton	United Kingdom:England, Northumbria, Harthope Burn,	55.51515 N	-2.044313 E	S. Sato, October 2012
BC0848 [848NitN04]	*Nitzschia palea*	periphyton	United Kingdom:England, Northumbria, Harthope Burn,	55.51515 N	-2.044313 E	S. Sato, October 2012
BC0850 [850NitN04]	*Nitzschia* aff. *sublinearis*	periphyton	United Kingdom:England, Northumbria, Harthope Burn,	55.51515 N	-2.044313 E	S. Sato, October 2012
BC0866 [866NitR05]	*Nitzschia* cf. *dissipata* var. *media*	sediment and periphyton	The main pond, Royal Botanic Garden Edinburgh, Edinburgh, Scotland, UK	55.964797 N	-3.20623 E	S. Sato, September 2012
BC0897 [897NitR05]	*Nitzschia linearis*	sediment and periphyton	The main pond, Royal Botanic Garden Edinburgh, Edinburgh, Scotland, UK	55.964797 N	-3.20623 E	S. Sato, September 2012

BC0905 [905NitR05]	*Nitzschia palea*	sediment and periphyton	The main pond, Royal Botanic Garden Edinburgh, Edinburgh, Scotland, UK	55.964797 N	-3.20623 E	S. Sato, September 2012
BC0912 [912NitR05]	*Nitzschia palea*	sediment and periphyton	The main pond, Royal Botanic Garden Edinburgh, Edinburgh, Scotland, UK	55.964797 N	-3.20623 E	S. Sato, September 2012
Belgium-1 [Victor 02-9E]	Nitzschia palea	ND	Secondary clarifier, wastewater treatment plant, Destelbergen, Ghent, Belgium	51° 3′ N	3° 48′ E	V. Chepurnov
capitellata Scot1 [Nit54]	Nitzschia capitellata	sediment	East shore, Loch of Forfar, Forfar, Scotland, UK	ND	ND	R. Trobajo
capitellata Scot2 [Nit55]	Nitzschia capitellata	sediment	East shore, Loch of Forfar, Forfar, Scotland, UK	ND	ND	R. Trobajo
capitellata Spain [Spain cap=Terri F222=262]	Nitzschia capitellata	periphyton	Terri stream, Cornella de Terri, Girona, Spain	ND	ND	R. Trobajo
CCMP558	Nitzschia cf. pusilla	rock pool	Prospect, Nova Scotia, Canada	45.2° N	64.3° W	J. Lewin and R.A. Lewin
Corsica	Psammodictyon sp.	marine shore	Mediterranean, Corsica, France	ND	ND	D.G. Mann and G.E. Simpson
Cylin clos	Nitzschia cf.	marine	Florida, USA	ND	ND	W.H.C.F Kooistra

	longissima					
fonticola C [RT26]	Nitzschia fonticola	periphyton	artificial stream, Royal Botanic Garden, Edinburgh, Scotland, UK	55° 57′ 51.62″ N	3° 12′ 19.04″ W	R. Trobajo
G1_2 [L54]	Nitzschia inconspicua	periphyton	Set River, by Albagés, Catalonia, Spain	41° 26′ 53.1″ N	0° 46′ 42.0″ E	L. Rovira
G1_3 [L55]	Nitzschia inconspicua	periphyton	Set River, by Albagés, Catalonia, Spain	41° 26′ 53.1″ N	0° 46′ 42.0″ E	L. Rovira
G2_1 [L46]	Nitzschia inconspicua	periphyton	Set River, by Albagés, Catalonia, Spain	41° 26′ 53.1″ N	0° 46′ 42.0″ E	L. Rovira
G2_2 [L47]	Nitzschia inconspicua	periphyton	Set River, by Albagés, Catalonia, Spain	41° 26′ 53.1″ N	0° 46′ 42.0″ E	L. Rovira
G3_1 [L53]	Nitzschia inconspicua	periphyton	Lower Ebro River, by Ascó, Catalonia, Spain	41° 12′ 44.4″ N	0° 33′ 17.8″ E	L. Rovira
G3_2 [L58]	Nitzschia inconspicua	periphyton	Lower Ebro River, by Xerta , Catalonia, Spain	40° 52′ 58.5″ N	0° 30′ 27.6″ E	L. Rovira
G3_3 [L61]	Nitzschia inconspicua	periphyton	Lower Ebro River, by Xerta , Catalonia, Spain	40° 52′ 58.5″ N	0° 30′ 27.6″ E	L. Rovira
G3_4 [L62]	Nitzschia inconspicua	periphyton	Lower Ebro River, by Xerta , Catalonia, Spain	40° 52′ 58.5″ N	0° 30′ 27.6″ E	L. Rovira

G4_1 [L44]	Nitzschia inconspicua	periphyton	Ebro Estuary, Ebro Delta, Catalonia, Spain	40° 43’ 46.34” N	0° 52’ 8.45” E	L. Rovira
G4_2 [L5]	Nitzschia inconspicua	periphyton	Ebro Estuary, Ebro Delta, Catalonia, Spain	40° 43’ 46.34” N	0° 52’ 8.45” E	L. Rovira
G5_1 [NIT1002CAT=DM1002cat]	Nitzschia inconspicua	sediment	La Trinitat salt works, Ebro Delta, Catalonia, Spain	40° 35’ 19.65” N	0° 41’ 21.69” E	D.G. Mann
G5_2 [NIT1005CAT=DM1005cat]]	Nitzschia inconspicua	sediment	La Trinitat salt works, Ebro Delta, Catalonia, Spain	40° 35’ 19.65” N	0° 41’ 21.69” E	D.G. Mann
G6_1 [NIT950CAT=DM950cat]]	Nitzschia inconspicua	sediment and periphyton	El Clot lagoon, Ebro Delta, Catalonia, Spain	40° 38’ 58.4” N	0° 41’ 27.1” E	D.G. Mann
G7_1 [NIT948CAT=DM948cat]	Nitzschia inconspicua	sediment and periphyton	IRTA aquaculture lagoon, Ebro Delta, Catalonia, Spain	40° 37’ 38.88” N	0° 39’ 39.26” E	D.G. Mann
Gillian	Psammodictyon sp.	marine shore	Scotland, UK	ND	ND	D.G. Mann
Japan D [Jp037-O6=265]]	Nitzschia palea	periphyton	Sakura River, Tokyo, Japan	ND	ND	R. Trobajo
Japan F [Mayama=235]	Nitzschia palea	periphyton	stream, Okinawa, Japan	ND	ND	R. Trobajo
L1	Nitzschia cf. pusilla	sediment	La Trinitat salt works, Ebro Delta, Catalonia, Spain	40° 35’ 19.65” N	0° 41’ 21.69” E	L. Rovira
L25	Nitzschia cf. pusilla	sediment	La Trinitat salt works, Ebro Delta, Catalonia, Spain	40° 35’ 19.65” N	0° 41’ 21.69” E	L. Rovira

L3	Nitzschia cf. pusilla	sediment	La Trinitat salt works, Ebro Delta, Catalonia, Spain	40° 35′ 19.65″ N	0° 41′ 21.69″ E	L. Rovira
L44	Nitzschia cf. ardua	ND	Alfacada Bay, Ebro Delta, Catalonia, Spain	40° 46′ 18.97″ N	0° 46′ 53.80″ E	L. Rovira
L56	Nitzschia microcephala	periphyton	Lower Ebro River (by Flix, Catalonia, Spain)	41° 14′ 25.2″ N	0° 33′ 13.0″ E	L. Rovira
New Spain 2 [RieraSMV]	Nitzschia palea	periphyton	stream, Sant Martí Vell, near Girona, Catalonia, Spain	ND	ND	R. Trobajo
NIT1003CAT [DM1003]	Nitzschia cf. pusilla	saline pond	La Trinitat salt works, Ebro Delta, Catalonia, Spain	40° 35′ 19.65″ N	0° 41′ 21.69″ E	D.G. Mann
NIT1004CAT [DM1004]	Nitzschia cf. aequorea	saline pond	La Trinitat salt works, Ebro Delta, Catalonia, Spain	40° 35′ 19.65″ N	0° 41′ 21.69″ E	D.G. Mann
NIT1008KEL [DM1008MK]	Nitzschia soratensis	periphyton	Houselop Beck, Co. Durham, England, UK	54° 44′ 22.53″ N	1° 51′ 5.80″ W	D.G. Mann
NIT1009KEL [DM1009MK]	Nitzschia soratensis	periphyton	Houselop Beck, Co. Durham, England, UK	54° 44′ 22.53″ N	1° 51′ 5.80″ W	D.G. Mann
NIT1011KEL [DM1011]	Nitzschia palea	stream	Houselop Beck, Co. Durham, England, UK	54° 44′ 22.53″ N	1° 51′ 5.80″ W	D.G. Mann
NIT1012CAT [DM1012]	Nitzschia sp.	salt marsh sediment	Punta de la Banya, by the SET, Ebro	ND	ND	D.G. Mann

			Delta, Catalonia, Spain			
NIT1013ABR [DM1013]	Nitzschia cf. sigma	estuarine sediment	Aberlady Bay, East Lothian, Scotland, UK	56° 00′ 54.14″ N	2° 51′ 0.29″ W	D.G. Mann
NIT145D	Nitzschia supralitorea	sediment	Dunsapie Loch, Edinburgh, Scotland, UK	55° 56′ 43.41″ N	3° 09′ 11.56″ W	D.G. Mann
Nit24	Nitzschia frustulum	periphyton	Es Mercadal stream, Menorca, Spain	39° 52′ 19.26″ N	4° 8′ 0.48″ E	R. Trobajo
Nit25	Nitzschia frustulum	periphyton	Es Mercadal stream, Menorca, Spain	39° 52′ 19.26″ N	4° 8′ 0.48″ E	R. Trobajo
NIT327TM	Nitzschia umbonata	sediment	Threipmuir Reservoir, near Edinburgh, Scotland, UK	55° 51′ 31″ N	3° 19′ 42″ W	D.G. Mann
NIT329TM	Nitzschia palea	sediment	Threipmuir Reservoir, near Edinburgh, Scotland, UK	55° 51′ 31″ N	3° 19′ 42″ W	D.G. Mann
NIT330TM	Nitzschia sp.	sediment	Threipmuir Reservoir, near Edinburgh, Scotland, UK	55° 51′ 31″ N	3° 19′ 42″ W	D.G. Mann
NIT337TM	Nitzschia cf. hantzschiana	sediment	Threipmuir Reservoir, near Edinburgh,	55° 51′ 31″ N	3° 19′ 42″ W	D.G. Mann

			Scotland, UK			
Nit44	Nitzschia cf. pusilla	sediment	Threipmuir Reservoir, near Edinburgh, Scotland, UK	55° 51′ 27″ N	3° 20′ 17″ W	R. Trobajo
Nit50	Nitzschia draveillensis	sediment	Threipmuir Reservoir, near Edinburgh, Scotland, UK	55° 51′ 27″ N	3° 20′ 17″ W	R. Trobajo
Nit51	Nitzschia cf. gracilis	sediment	Threipmuir Reservoir, near Edinburgh, Scotland, UK	55° 51′ 27″ N	3° 20′ 17″ W	R. Trobajo
Nit53	Nitzschia linearis	sediment	Threipmuir Reservoir, near Edinburgh, Scotland, UK	55° 51′ 27″ N	3° 20′ 17″ W	R. Trobajo
Nit56	Nitzschia acicularis	sediment	Threipmuir Reservoir, near Edinburgh, Scotland, UK	55° 51′ 27″ N	3° 20′ 17″ W	R. Trobajo
Nit57	Nitzschia cf. pumila	sediment	Threipmuir Reservoir, near Edinburgh, Scotland, UK	55° 51′ 27″ N	3° 20′ 17″ W	R. Trobajo
NIT945CAT [DM945]	Nitzschia cf. pusilla	sediment	Brackish pool, Garxal, Ebro Delta, Catalonia, Spain	40° 43′ 23.7″ N	0° 51′ 18.8″ E	D.G. Mann
NIT952CAT	Nitzschia varelae	periphyton	Clot Lagoon, Ebro	40° 39′ 20.8″ N	0° 40′ 58.9″ E	D.G. Mann

[DM952]			Delta, Catalonia, Spain			
R10	Nitzschia microcephala	periphyton	Drainage channel of Encanyissada lagoon, Ebro Delta, Catalonia, Spain	ND	ND	R. Trobajo
R12	Nitzschia palea	periphyton	Drainage channel of Encanyissada lagoon, Ebro Delta, Catalonia, Spain	ND	ND	R. Trobajo
R2	Nitzschia lembiformis	sediment	La Trinitat salt works, Ebro Delta, Catalonia, Spain	40° 35′ 19.65″ N	0° 41′ 21.69″ E	R. Trobajo
R20	Nitzschia acicularis	periphyton	Houselop Beck, Co. Durham, England, UK	54° 44′ 22.53″ N	1° 51′ 5.80″ W	R. Trobajo
R8	Nitzschia palea	periphyton	Drainage channel of Encanyissada lagoon, Ebro Delta, Catalonia, Spain	ND	ND	R. Trobajo
RT5 [Nit 239]	Nitzschia amphibia	periphyton	artificial stream, Royal Botanic Garden Edinburgh, Edinburgh, Scotland, UK	55° 57′ 51.62″ N	03° 12′ 19.04 W	R. Trobajo
s0819	Nitzschia sp.	sediment	Trabucador Beach, Ebro Delta, Catalonia, Spain)	40° 38′ 50.15″ N	0° 46′ 12.56″ E	S. Sato
s0826	Nitzschia sp.	sediment	Trabucador Beach,	40° 38′ 50.15″ N	0° 46′ 12.56″ E	S. Sato

			Ebro Delta, Catalonia, Spain)			
s0863	Tryblionella sp.	lagoon sediment	Buda Island, Ebro Delta, Catalonia, Spain	40° 41′ 60.00″ N	0° 52′ 0.00″ E	S. Sato
Spain A2 [Nit B2=238]	Nitzschia palea	sand	Pond, Cala Castell, Girona, Spain	ND	ND	R. Trobajo
Spain A3 [Nit B4=205]	Nitzschia palea	sand	Pond, Cala Castell, Girona, Spain	ND	ND	R. Trobajo
Spain A4 [Nit C=206]	Nitzschia palea	sand	Pond, Cala Castell, Girona, Spain	ND	ND	R. Trobajo
Spain C [Aitor 5=261]	Nitzschia palea	periphyton	Reservoir, Letutxe dam, Bilbao, Spain	ND	ND	R. Trobajo
Sri Lanka1 [SLA=219]	Nitzschia palea	periphyton	Puddle, Dambulla Rock Temple, Dambulla, Central Province, Sri Lanka	ND	ND	R. Trobajo
Sri Lanka2 [SLB=234])	Nitzschia palea	periphyton	Lotus pond, Dambulla, Central Province, Sri Lanka	ND	ND	R. Trobajo
TRY1006CAT [DM1006]	Tryblionella cf. compressa	salt marsh sediment	Alfacs, by the SET, Ebro Delta, Catalonia, Spain	ND	ND	D.G. Mann
TRY1007CAT [DM1007]	Tryblionella cf. compressa	salt marsh sediment	Alfacs, by the SET, Ebro Delta, Catalonia, Spain	ND	ND	D.G. Mann
TRY946CAT [DM946]	Tryblionella apiculata	lagoon sediment	IRTA aquaculture lagoon, Ebro Delta,	40° 37′ 38.88″ N	0° 39′ 39.26″ E	D.G. Mann

			Catalonia, Spain			
TRY947CAT [DM947]	Tryblionella apiculata	lagoon sediment	IRTA aquaculture lagoon, Ebro Delta, Catalonia, Spain	40° 37′ 38.88″ N	0° 39′ 39.26″ E	D.G. Mann
TRY951CAT [DM951]	Tryblionella hungarica	lagoon sediment	IRTA aquaculture lagoon, Ebro Delta, Catalonia, Spain	40° 37′ 38.88″ N	0° 39′ 39.26″ E	D.G. Mann
TRY981CAT [DM981]	Tryblionella hungarica	lagoon sediment	IRTA aquaculture lagoon, Ebro Delta, Catalonia, Spain	40° 37′ 38.88″ N	0° 39′ 39.26″ E	D.G. Mann
TRY986CAT [DM986]	Tryblionella hungarica	lagoon sediment	IRTA aquaculture lagoon, Ebro Delta, Catalonia, Spain	40° 37′ 38.88″ N	0° 39′ 39.26″ E	D.G. Mann
UK [Nit7=BB2b=287]	Nitzschia palea	periphyton	Puddle, Burnham Beeches, Buckinghamshore, UK	ND	ND	R. Trobajo
Thonon Culture Collection (TCC) clones						
TCC139-2	Nitzschia palea	lake water	Lac Léman, France	46.4005342	6.56538714	A. Berard
TCC375	Nitzschia acicularis	periphyton	Alzette river, Ettelbruck, Luxembourg	49.8483921	6.11001875	F. Rimet
TCC378	Nitzschia dissipata	periphyton	Saone river, Parcieux city, France	45.9164281	4.81014387	F. Rimet
TCC380	Nitzschia fonticola	periphyton	Saone river, Parcieux city,	45.9164281	4.81014387	F. Rimet

			France			
TCC382	Nitzschia paleaeformis	periphyton	Saone river, Parcieux city, France	45.9164281	4.81014387	F. Rimet
TCC384	Nitzschia pusilla	periphyton	Rollingerbaach river, Rollingen, Luxembourg	49.7420135	6.11036207	F. Rimet
TCC385	Nitzschia pusilla	periphyton	Rollingerbaach river, Rollingen, Luxembourg	49.7420135	6.11036207	F. Rimet
TCC386	Nitzschia linearis	periphyton	Sûre river, Wasserbilig, Luxembourg	49.7136064	6.50380994	F. Rimet
TCC387	Nitzschia linearis	periphyton	Rollingerbaach river, Rollingen, Luxembourg	49.7420135	6.11036207	F. Rimet
TCC394	Nitzschia palea	periphyton	Dniepr river, Obolon, Kiev, Ukraine	50.4296152	30.5757185	T. Darienko
TCC395	Nitzschia palea	periphyton	Golosejevo Lake, Kiev, Ukraine	50.433333	30.516667	F. Rimet
TCC396	Nitzschia cf. pusilla	periphyton	Rollingerbaach river, Rollingen, Luxembourg	49.7420135	6.11036207	F. Rimet
TCC397	Nitzschia palea	periphyton	Schlennerbaach river, Hoscheid, Luxembourg	49.9472472	6.08152296	F. Rimet
TCC403	Nitzschia palea	periphyton	Attert river, Colmar Berg, Luxembourg	49.8145071	6.09982834	F. Rimet

TCC404	Nitzschia supralitorea	periphyton	Alzette river, Ettelbruck, Luxembourg	49.8483921	6.11001875	F. Rimet
TCC425	Nitzschia palea	periphyton	downstream site, rivière de Djalimou, Ile de Mayotte, France	-12.710833	45.055	L. Kermarrec
TCC468	Nitzschia palea	periphyton	downstream site, rivière de Dembeni, Ile de Mayotte, France	-12.735556	45.138333	L. Kermarrec
TCC474	Nitzschia inconspicua	periphyton	intermediate site, rivière de Coconi, Ile de Mayotte, France	-12.833056	45.134722	L. Kermarrec
TCC486	Nitzschia palea	periphyton	downstream site, rivière de Coconi, Ile de Mayotte, France	-12.833056	45.134722	L. Kermarrec
TCC487	Nitzschia inconspicua	periphyton	downstream site, rivière de Coconi, Ile de Mayotte, France	-12.833056	45.134722	L. Kermarrec
TCC488	Nitzschia inconspicua	periphyton	downstream site, rivière de Coconi, Ile de Mayotte, France	-12.833056	45.134722	L. Kermarrec
TCC498	Nitzschia inconspicua	periphyton	upstream site rivière de Kwalé, Ile	-12.8008977	45.2037549	L. Kermarrec

			de Mayotte, France			
TCC510	Nitzschia inconspicua	periphyton	downstream site, rivière de Longoni, France	-12.7289593	45.1667261	L. Kermarrec
TCC512	Nitzschia linearis	periphyton	Upstream site, rivière de Bouyouni, Ile de Mayotte, France	-12.735556	45.138333	L. Kermarrec
TCC521	Nitzschia costei	periphyton	Marla, rivière de des Galets, Ile de La Réunion, France	-20.9561077	55.2986267	L. Kermarrec
TCC533	Nitzschia fonticola	periphyton	rivière de Bras des étangs site, Ile de La Réunion, France	-21.1365223	55.4539641	L. Kermarrec
TCC537	Nitzschia acidoclinata	periphyton	rivière de Bras Caverne, Ile de La Réunion, France	-21.0025689	55.5857986	L. Kermarrec
TCC538	Nitzschia acidoclinata	periphyton	rivière de Bras Caverne, Ile de La Réunion, France	-21.0025689	55.5857986	L. Kermarrec
TCC550	Nitzschia costei	periphyton	grand Galet, rivière de Langevin, Ile de La Réunion, France	-21.2830131	55.6123903	L. Kermarrec
TCC560	Nitzschia acidoclinata	periphyton	rivière de Sainte Suzanne, Ile de La Réunion, France	-20.9070214	55.6058061	L. Kermarrec
TCC563	Nitzschia palea	periphyton	rivière de Sainte Suzanne, Ile de La Réunion, France	-20.9070214	55.6058061	L. Kermarrec

TCC571	Nitzschia inconspicua	periphyton	Cascade Niagara, rivière de Sainte Suzanne, Ile de La Réunion, France	-20.9095871	55.6009996	L. Kermarrec
TCC575	Nitzschia tubicola	periphyton	Cascade Niagara, rivière de Sainte Suzanne, Ile de La Réunion, France	-20.9095871	55.6009996	L. Kermarrec
TCC576	Nitzschia gracilis	periphyton	site Solvay (Usine), rivière Le Sanon Dombasle-sur-Meurthe, France	48.6283411	6.36750946	L. Kermarrec
TCC577	Nitzschia palea	periphyton	site Solvay (Usine), rivière Le Sanon Dombasle-sur-Meurthe, France	48.6283411	6.36750946	L. Kermarrec
TCC586	Nitzschia cf. pusilla	periphyton	Canal de Nantes à Brest, Nort-sur-Erdre, France	47.4349587	-1.49485016	L. Kermarrec
TCC600	Nitzschia palea	periphyton	rivière Isac, Guenrouet, France	47.5178263	-1.9455368	L. Kermarrec
TCC606	Nitzschia supralitorea	periphyton	rivière Le Gier, La Valla, France	46.4814418	-1.29413282	L. Kermarrec
TCC619	Nitzschia acidoclinata	periphyton	rivière Le Gier, La Valla, France	45.7534736	3.84982834	L. Kermarrec
TCC620	Nitzschia palea	periphyton	rivière Le Gier, La Valla, France	45.7534736	3.84982834	L. Kermarrec
TCC632	Nitzschia dissipata	periphyton	rivière La Saone, Fleurville, France	46.433333	4.88851453	L. Kermarrec

TCC665	Nitzschia cf. pusilla	periphyton	rivière Schlirbech downstream of Esch/Sûre, France	49.9093991	5.93432906	L. Kermarrec
TCC700	Nitzschia draveillensis	periphyton	Pisuerga river, Melgar de Fernamental, Spain	42.4	-4.25514984	L. Kermarrec
TCC707	Nitzschia dissipata	periphyton	Valdavia river, Osorno, Spain	42.417491	-4.3697569	F. Rimet
TCC767	Nitzschia palea	periphyton	estuaire de la Venoge, Lac Léman, Switzerland			A. Rimet
TCC853	Nitzschia communis	lake water	Azores, Portugal	37.732136	-25.474937	S. Almeida
TCC854	Nitzschia palea	river water	Miranda, Portugal	41.8342	-8.504449	S. Almeida
TCC876	Nitzschia dissipata var. media	periphyton	Norrtäljeån river near Norrtälje city, Sweden	59.75728	18.72059	S. Lacroix
TCC885	Nitzschia perminuta	periphyton	Siggeforasjön lake near Norrtälje city, Sweden	59.757282	18.720598	S. Lacroix
TCC886	Nitzschia cf. palea	periphyton	Siggeforasjön lake near Norrtälje city, Sweden	59.757282	18.720598	S. Lacroix
TCC900	Nitzschia cf. pusilla	soil	field (organic), France	48.800745	2.090712	F. Rimet
TCC901	Hantzschia amphioxys	soil	field (organic), France	48.800745	2.090712	F. Rimet
TCC940	Hantzschia vivax	roots	Nyéki-szállás lake, Fertőújlak village,	47.6771	16.8328	Edina Lengyel

			Fertőd, Hungary			
TCC944	Nitzschia supralitorea	sediments	Sós-ér lake, Dunatetétlen village, Solt, Hungary	46.7888.	19.1466	Edina Lengyel
TCC945	Nitzschia palea	sediments	Borsodi-dűlő lake, Fertőújlak village, Fertőd, Hungary	47.6815	16.8400	Edina Lengyel
TCC946	Nitzschia supralitorea	sediments	Böddi-szék lake, Dunatetétlen village, Solt, Hungary	46.7608	19.1437	Edina Lengyel
TCC949	Nitzschia reskoi	sediments	Borsodi-dűlő lake, Fertőújlak village, Fertőd, Hungary	47.6815	16.8400	Edina Lengyel
TCC950	Nitzschia supralitorea	roots	Borsodi-dűlő lake, Fertőújlak village, Fertőd, Hungary	47.6815	16.8400	Edina Lengyel

[1] see Witkowski et al. (2016)

Table 2. Primers for sequencing in Szczecin.

Primer name	Primer Sequences (5′–3′)	References
nSSU rDNA		
SSU1+[a, c]	AACCTGGTTGATCCTGCCAGT	Medlin et al. 1988
SSU11+[b, c]	TGATCCTGCCAGTAGTCATACGCT	Alverson et al. 2007
SSU515+[c]	TGGAATGAGAACAATTTAA	Alverson et al. 2007
SSU1004+[c]	CGAAGATGATTAGATACCATCG	Alverson et al. 2007
SSUB–[a]	CCTTCTGCAGGTTCACCTAC	Medlin et al. 1988
SSU568–[c]	CAGACTTGCCCTCCAATTGA	Alverson et al. 2007
SSU1672–[b, c]	TAGGTGCGACGGGCGGTGT	Ruck & Theriot 2011
rbcL		
rbcL40+[a, b, c]	GGACTCGAATYAAAAGTGACCG	Ruck & Theriot 2011
rbcL527+[c]	AAAACATTCCAAGGTCCTGC	Alverson et al. 2007
rbcL587–[c]	GTCTAAACCACCTTTTAAMCCTTC	Alverson et al. 2007
rbcL1255–[b, c]	TTGGTGCATTTGACCACAGT	Alverson et al. 2007
rbcL1444–[ac]	GCGAAATCAGCTGTATCTGTWG	Ruck & Theriot 2011
psbC		
psb*C*+[a, c]	CACGACCWGAATGCCACCAAT	Alverson et al. 2007
psbC22+[b, c]	CGTGGTGATACATAGTTA	Ruck & Theriot 2011
psbC221+[c]	ACGCATTGTTTCACCACC	Alverson et al. 2007
psbC–[a, c]	ACAGGMTTYGCTTGGTGGAGTGG	Alverson et al. 2007
psbC857–[c]	CTTTGGTTATGACTGGCGTG	Alverson et al. 2007
psbC1154–[b, c]	GCDCAYGCTGGYTTAATGG	Ruck & Theriot 2011
nLSU rDNA (D1, D2)		
D1R[ac]	ACCCGCTGAATTTAAGCATA	Scholin *et al*. 1994
D2C[ac]	CCTTGGTCCGTGTTTCAAGA	Scholin *et al*. 1994

[a] Forward and reverse primers for the first PCR amplification

[b] Forward and reverse primers for the second PCR amplification when the first PCR amplification fail

[c] Primers for sequencing

Table 3. The primers for sequencing in Edinburgh.

Primer name	Primers Sequences (5′–3′)	References
rbcL		
DPrbcL1+[a]	AAGGAGAAATHAATGTCT	Jones et al. 2005
DPrbcL7–[a]	AARCAACCTTGTGTAAGTCTC	Jones et al. 2005
DPrbcL5	CTCAACCATTYATGCG	Daugbjerg & Andersen 1997
DPrbcL11	CTGTGTAACCCATWAC	Daugbjerg & Andersen 1997
16F	TTAGAAGATATGCGTATT	Jones et al. 2005
14R	GAATACGCATATCTTCTAAACG	Jones et al. 2005
nLSU rDNA (D1, D2 or D1–D3)		
D1R+[a]	ACCCGCTGAATTTAAGCATA	Scholin et al. 1994
D3R–[a]	TCGGAGGGAACCAGCTACTA	Nunn et al. 1996
D2C–[a, b]	CCTTGGTCCGTGTTTCAAGA	Scholin et al. 1994

[a] Forward and reverse primers for PCR amplification

[b] Primers for sequencing. For later D1–D3 LSU sequences, the D2C sequencing primer was not necessary

Table 4. The primers for sequencing in Thonon. Genes and primers used for the molecular approaches (PCR and sequencing).

	Genes	Name	Primer Sequence (5′–3′)	References
PCR	nLSU	D1R	ACC CGC TGA ATT TAA GCA TA	Scholin et al. 1997
		D2C	CCT TGG TCC GTG TTT CAA GA	Scholin et al. 1997
	rbcL	DPrbcL1-F	AAG GAG GAA DHH ATG TCT	Daugbjerg and Andersen 1997
		DPrbcL7-R	AAA SHD CCT TGT GTW AGT YTC	Daugbjerg and Andersen 1997
	cox1	GazF2	CAA CCA YAA AGA TAT WGG TAC	Saunders 2005
		KEdtmR	AAA CTT CWG GRT GAC CAA AAA	Evans et al. 2007
	nSSU	1-F	AAC CTG GTT GAT CCT GCC AGT A	Medlin et al. 1988
		1528-R	CTT CTG CAG GTT CAC CTA C	Medlin et al. 1988
Sequencing	*rbcL*	NDrbcL6	GTA AAT GGA TGC GTA	Daugbjerg and Andersen 1997
		15R	ACA CCA GAC ATA CGC ATC CA	Jones et al. 2005
		16F	TTA GAA GAT ATG CGT ATT	Elwood et al. 1985
	nSSU	1-F	AAC CTG GTT GAT CCT GCC AGT A	Elwood et al. 1985
		528-F	GCG GTA ATT CCA GCT CCA A	Elwood et al. 1985
		1055-F	GGT GGT GCA TGG CCG TTC TT	Elwood et al. 1985
		536-R	AAT TAC CGC GGC KGC TGG CA	Elwood et al. 1985
		1055-R	ACG GCC ATG CAC CAC CAC CCA T	Elwood et al. 1985
		1528-R	CTT CTG CAG GTT CAC CTA C	Elwood et al. 1985

Supplementary File 10. Analysis of some apparently misidentified species.

*'***Bacillaria***' clones outside clade 1 (including 'Bacillaria II' and 'cf.* **Bacillaria***' clones*

The '*Bacillaria* cf. *paxillifera*' clone BA14c has been discussed in the main text. The two other clones of 'Bacillaria II' in the SSU tree (Supplementary Fig. 4) are Xmm24S4 (GenBank KU561172) and RVSN23 (GenBank KX575709). The GenBank data accompanying the Xmm24S4 sequence do not refer to a published paper documenting the clone, but a paper containing photographs of many Xmm clones was published by Huang et al. (2017), postdating the submission of the Xmm24S4 sequence on 15 January 2016. In the 2017 paper there are no photographs labelled as being of clone Xmm24S4, but there is one of "Xmm28S4" (Huang et al. 2017, p. 41) labelled "*Bacillaria* cf. *paxillifer*". In contrast, in the SSU phylogeny of their clones (Huang et al. 2017, fig. 2), Xmm28S4 is not mentioned and the only "*Bacillaria* cf. *paxillifer*" included is Xmm24S4. We therefore assume that one of the names given may be wrong. The photograph of Xmm 28S4/24S4 shows no feature that would identify the clone as a *Bacillaria*: two recently divided cells are illustrated, both far too small to be any described *Bacillaria* species and neither having the colonial morphology characteristic of the genus. A BLAST search (megablast, default settings) with KU561172 (clone Xmm24S4) as the query returns the SSU sequences of three "*Bacillaria*" sequences as close relatives – RVSN23, another Xmm clone (Xmm27S2), and clone BA14c – together with two strains attributed to *Nitzschia epithemioides* (Xmm24S1 and CCAP/1052/18, both incorrectly named as '*N. epithemoides*').

BLAST of the SSU sequence of clone RVSN23 (KX575709), identified as '*Bacillaria paxillifer*', not surprisingly returns the two Xmm '*Bacillaria*' clones Xmm27S2 (KY054943) and Xmm24S4 (KU561172) as the most similar sequences, followed by the Xmm24S1 *Nitzschia epithemioides* clone and *Bacillaria* cf. *paxillifer* BA14c (HM805020). No published information is available concerning the characteristics of clone RVSN23. GenBank records that the sequence was submitted by K. Renugadevi, C. Valli Nachiyar and G. Narendakumar, as part of unpublished bioprospecting research ("Extraction of potential compound from Bacillaria sp."). We wrote to the authors, who informed us (K. Renugadevi, email to D.G. Mann, 4 September 2019) that the clone was identified as *Bacillaria* from the BLAST similarity to sequences in GenBank of clones identified there as *Bacillaria*.

The submission and publication dates of the Xmm24S4 sequence KU561172 (15 January 2016 and 31 January 2017) and the RVSN23 sequence KX575709 (15 July 2016 and 30 January 2017) mean that neither can have influenced the other with respect to identification. However, both postdate the availability in GenBank of the BA14c *Bacillaria* cf. *paxillifer* (submitted 20 July 2010, published 13 July 2011) and this could therefore have influenced both identifications. As we have noted in the main text, however, BA14c does not have the special type of motile colony generally considered characteristic of *Bacillaria*; nor does its valve and girdle structure conform to true *Bacillaria* (e.g. our clone BAC901CAT. Altogether, therefore, there is no compelling evidence to believe that the 'Bacillaria II' clones belong to *Bacillaria*.

A further clone (SH349, "*Bacillaria* sp."), whose SSU sequence (GenBank KY320377) is subtended by the same basal node as other *Bacillaria* species but lies outside clade I (Supplementary Fig. 4; see also the *rbcL* and *rbcL*–LSU trees, Fig. 4, Supplementary Fig. 2). Though being identified as '*Bacillaria* sp.' and having a near-central raphe (An et al. 2017, fig. 3g), it lacks motile colonies (Prof. J.H. Noh, personal communication). Clone EW234 ("*Bacillaria paxillifera*"), on the other hand, is placed in clade 1 in the *rbcL*–LSU tree with 81% support. However, its morphology does not agree with that published for three species with motile colonies (*Bacillaria paxillifera, B. urve-millerae* and *B. kuseliae*) by Schmid & Jahn (2007), being more attenuated and rostrate at the poles and having denser striation (c. 27 in 10 µm, rather than a maximum of 24 in 10 µm in the other three species). It probably represents a new species.

It seems likely, therefore, that the non-monophyly of *Bacillaria* in the SSU tree reflects an implicit change in the definition of *Bacillaria*, from the 20th century definition that emphasized a unique type of motile colony (Karsten 1928, Hustedt 1930, Krammer & Lange-Bertalot 1988) to one that relies principally on sequence similarity (e.g. via BLAST) to whatever *Bacillaria* sequences are already in GenBank, coupled in at least some cases (BA14c and SH349) with the possession of a more or less central raphe (the position of the raphe in the other clones mentioned – Xmm24S4 and RVSN23 – is unknown).

Examples of other misidentified clones: further Xmm clones and clone A2ni ('*Pseudo-nitzschia* sp.')

Further dubious identifications include several others of the Xmm clones studied by Huang et al. (2017). Although it is safe to conclude that the Xmm clones they identified as *Cylindrotheca*, *Nitzschia* or *Psammodictyon* species do indeed belong to the Bacillariaceae, in several cases their positions in the SSU tree conflict markedly with those expected from other data. For example, the sequences given for Xmm clones of *N. epithemioides*, *N. dubiiformis, N. capitellata* and *N. palea* all belong to different major clades than the sequences of the same species provided by other workers, and Huang et al.'s photographs of these clones give no confidence that they have been correctly identified (see also the discussion of Xmm and other *Cymbella* clones discussed below). The same is true of some Xmm clones assigned to other diatom genera, such as three assigned to *Epithemia*: the photographs of these clones do not show *Epithemia* morphology and the sequences themselves clearly identify the clones as related to *Entomoneis*. In contrast, both the photographs provided and the sequences themselves confirm Huang et al.'s (2017) identification of clones Xmm21W1 and Xmm23S3 as species of *Psammodictyon* (Supplementary Fig. 4).

Clone A2ni was identified by Guo et al. (2015) as "*Pseudo-nitzschia* sp." but its *cox1* sequence (KJ671739) is distant from all other *Pseudo-nitzschia* species, which group together in a single clade in the *cox1* tree (Supplementary figure 7), as they do also in the 4-gene, SSU, *rbcL*, *rbcL*–SSU, and *rbcL*–LSU trees (the exception is the LSU tree, where *Pseudo-nitzschia* is paraphyletic with respect to *Fragilariopsis* and *Neodenticula*, though without support). Guo et al.'s SSU and *rbcL* sequences of A2ni were too short to meet our criteria for inclusion in the SSU, SSU-*rbcL* and *rbcL* datasets, but BLAST searches using the SSU and *rbcL* sequences of clone A2ni indicate that they are both most similar to sequences from clones identified as *Bacillaria* species. Guo et al. (2015) wrote that the species they studied "were identified to the species or genus level by using morphological characters based on observations under light and electron microscopy". Nevertheless, we wonder whether the identification of clone A2ni was influenced by *cox1* BLAST results, which do indeed give *Pseudo-nitzschia hasleana* (GenBank JN050311) as the highest scoring 'hit' (though with only 85% identity). Unfortunately, we received no reply from two emails to the corresponding author of Guo et al. (2015), in which we asked if voucher material from their study was available.

Other striking errors include "*Thalassiosira antarctica*" (AF374482), revealed as a *Fragilariopsis* (SSU tree: Supplementary Fig. 4) and "*Cymbella cistuliformis*" 1113 and 1120 (JF790980 and JF790983), nested among *Nitzschia* species in clade 8A-II (SSU tree: Supplementary Fig. 4). "*Thalassiosira antarctica*" AF374482 is annotated in GenBank (in version AF374482.2, dating from 2002) as "unverified". The sequence was obtained as part of a study of sexually induced genes (*Sig*) in Thalassiosirales, which are thought to be involved in oogamous sexual reproduction (Armbrust & Galindo 2001). Not surprisingly, given that *Fragilariopsis* species are not oogamous, no *Sig* genes could be amplified from the "*T. antarctica*" clone, unlike four out of the five other *Thalassiosira* species studied; also not surprisingly, the nSSU sequence of "*T. antarctica*" (AF374482) was very dissimilar to those of the five true *Thalassiosira* species (*op. cit.*, fig. 3).

For the two "*Cymbella cistuliformis*" SSU sequences (JF790980 and JF790983), it is hard to find an explanation. By the time these sequences were obtained (from cloned DNA: Rocke et al., 2013), the diversity of pennate diatoms was already quite well sampled and it should have been possible to assign sequences to the Bacillariaceae, rather than *Cymbella*. Furthermore, the community from which the clones were obtained – marine picoplankton – is entirely wrong for *Cymbella* but wholly plausible for *Nitzschia*. Unfortunately, the errors associated with JF790980 and JF790983 have proliferated further, with other Bacillariaceae sequences being wrongly assigned to *Cymbella*, presumably on the basis of BLAST returns indicating a similarity to the "*Cymbella cistuliformis*" clones. These further erroneously labelled sequences are two more Xmm clones (Xmm17W3 and Xmm32W3, with SSU sequences KY054947 and KU561171, respectively) and *Cymbella* sp. SMS45 (MT489362). An illustration of Xmm17W3 by Huang et al. (2017, p. 41) does not show any characteristics supporting its classification in *Cymbella*.

Nitzschia palea

Many *Nitzschia palea* clones have been sequenced and most form a well-defined, robustly supported clade, sister to sequences of *N. capitellata*. Discussion of the few clones identified as *N. palea* but lying outside the main clade is included in the main text.

Nitzschia pusilla

Clones identified as *N. pusilla* or *N. cf. pusilla* are scattered across the *rbcL* (Fig. 4) and SSU trees (Supplementary Fig. 4), in 8A-II and several different places in clade 6B. Reinvestigation of this species is needed, to determine which of the clones and sequences are really *N. pusilla*, i.e. are related to the type, which was studied in LM and TEM by Lange-Bertalot (1976). Several other species (*N. kuetzingiana* and *N. indistincta*, possibly also *N. parvula*, *N. obtusangula* and *N. retusa*) have been synonymized with *pusilla* by Lange-Bertalot (1976) and Krammer & Lange-Bertalot (1988) and these will also need further study, to see if any of them correspond to any of the other, different *pusilla*-like diatoms that have been sequenced. Unfortunately, valve morphology offers even less help in "*N. pusilla*" than in other *Nitzschia* species, because the valves are extremely simple and because of the fineness of the striation, which can be studied (and its density determined) only using electron microscopy. There appears to be no information about the girdle bands or the structure of the raphe canal in the type material of *N. pusilla* or any of the putative synonyms, despite the work of Lange-Bertalot (1976), Mikhailov (1984) and others.

Extra references

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