



Editorial

The molecular life of diatoms



Diatoms are unicellular photosynthetic eukaryotes that are arguably the most species-rich group of algae, having conquered most aquatic habitats since their major diversification around 65 million years ago (Bowler et al., 2010). They play a major role in the functioning of the global ecosystem, e.g., in silica and carbon biogeochemical cycles (Tréguer and De La Rocha, 2013; Field et al., 1998). They have a complex evolutionary history, and like other chromalveolates are believed to be derived from a serial secondary endosymbiosis involving both green and red algae combining with a eukaryotic heterotrophic host cell (Moustafa et al., 2009). Their rigid cell wall has constrained them to acquire an unusual mode of cell division, with mitotically-derived daughter cells becoming progressively smaller until they reach a critical size threshold, following which they must undergo sexual reproduction for size restoration (Lewis, 1984; Chepurinov et al., 2004). While many species are planktonic, the majority are benthic and can stick to virtually any surface. Many of these can move by gliding, a process mediated by the extrusion of polysaccharides from a slit in the cell wall known as the raphe (Edgar and Pickett-Heaps, 1984).

The most spectacular feature of most species of diatoms is their intricately structured silica-based cell wall known as the frustule. These cell walls exhibit an amazing variety of species-specific shapes and patterns. Diatom silica has very interesting physical properties, and is the envy of nanotechnologists as a 3D nano-patterned material produced from the bottom-up through self-assembly (Kröger and Poulsen, 2008). Ancient diatom biomass was a major contributor to fossil fuels, and today's diatoms are investigated as a source for renewable, carbon-neutral fuels for the future, as well as other applications in bio-, nano- and environmental technology (Gordon et al., 2009; Nassif and Livage, 2010; Fields et al., 2014). Despite the global importance of diatoms and their extraordinary metabolic and cellular capabilities, they have received little attention from molecular biologists. Recently, this has begun to change due to emerging insights from diatom genome projects (Armbrust et al., 2004; Bowler et al., 2008; Lommer et al., 2012) and substantial advances in genetic manipulation on selected model species (De Riso et al., 2009; Trentacoste et al., 2013; Daboussi et al., 2014). This rapid progress, together with the novel resources derived from metagenomics and oceanographic research, are providing completely novel opportunities to understand diatom biology and to elucidate their roles in marine ecosystems. In parallel, progress in diatom-based technologies has made these organisms an emerging source of novel substances (e.g., silica containing composite materials) with widespread relevance.

The diatom research community is currently experiencing a step change in exploration of this globally important group of organisms, learning to apply cross-disciplinary research approaches to studying the molecular foundations of many aspects of diatom biology, ecology and biotechnology. The tractability of diatoms for molecular biology

techniques is also attracting new scientists from other disciplines, and diatom molecular research is now being performed by both academic researchers and industry (e.g., for nanotechnology, biofuel, food industry, and waste-water management). The champions of such research are currently *Thalassiosira pseudonana* and *Phaeodactylum tricornutum*, due to the availability of high quality genome sequences and techniques for reverse genetics. These two organisms have also become a major focus with respect to other phytoplankton 'model' species (Fig. 1A). Notwithstanding, the number of publications based on these organisms pales in comparison with research efforts on the more conventional model organisms like the plant *Arabidopsis thaliana* (Fig. 1B). The total number of publications about diatoms is nonetheless considerably higher than for *T. pseudonana* and *P. tricornutum* alone, although molecular methods have yet to penetrate all areas of diatom research. To encourage the integration of such methods, Nils Kroeger, Thomas Mock, Peter Kroth, Mark Hildebrand, Ginger Armbrust and Nicole Poulsen organized the first conference dedicated to the Molecular Life of Diatoms in Atlanta, Georgia (USA) in 2011, which was followed by a second meeting held in Paris (France) in 2013 organized by ourselves together with Jacques Livage and Thomas Mock. In recognition of the current excitement in the field, we have assembled this Special Issue of Marine Genomics, consisting of one review, five full-length research articles and two method papers.

Wilhelm et al. (2014, p. 5–15) provide an up-to-date view of light acclimation in diatoms, and focus on current understanding of the underlying molecular mechanisms. The chloroplast genome of *Seminavis robusta* reported by Brembu et al. (2014, p. 17–27) provides further information about the genetic components of photosynthetic processes in diatoms, and also highlights the presence of an autonomously replicating plasmid within the chloroplasts of this species resembling those previously described in *Cylindrotheca fusiformis*.

Xu et al. (2014, p. 29–38) and Nemoto et al. (2014, p. 39–44) have both focused on the use of omics technologies to elucidate the processes underlying cell wall formation, the former in *Pseudo-nitzschia multiseries* and the latter in the oleaginous diatom *Fistulifera solaris*. Xu et al. used a proteomics approach to identify proteins whose concentrations increased in response to silicate starvation and found evidence for the importance of intracellular vesicle trafficking in the process, whereas Nemoto et al. performed an in silico mining of *Fistulifera* genome information to identify putative cell wall components. One gene was subsequently confirmed using reverse genetics technologies in *Fistulifera* to encode a protein localized to cell walls. The transcriptome of another diatom, *Ceratoneis closterium*, is reported by Hook et al. (2014, p. 45–53). This diatom is of interest because of its use in ecotoxicological studies and so the generation of a transcriptome is an important step forward.

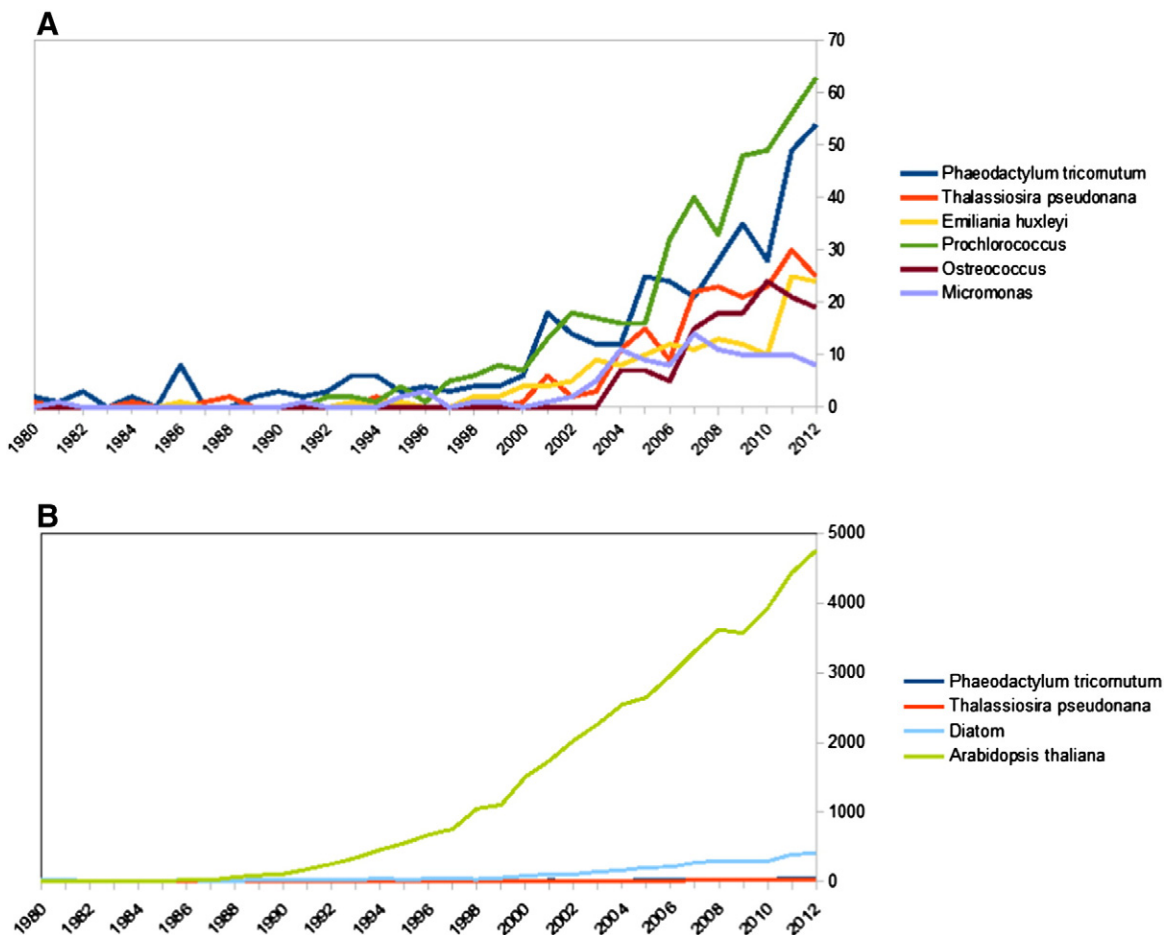


Fig. 1. Publication trends. A) Publications citing the major marine plankton model organisms; B) publications citing *Arabidopsis thaliana* and diatoms as comparison. Source of information: medline trend website using the indicated keywords (see <http://mltrends.org/ca/>). Figure kindly provided by Henri Abida (IBENS Paris, France).

The final three articles focus on the workhorses of diatom genomics, *T. pseudonana* and *P. tricornutum*. Yoshinaga et al. (2014, p. 55–62) describe the characterization of iron-responsive promoters in *P. tricornutum*, and Zhang and Hu (2014, p. 63–66) report the high efficiency nuclear transformation of this diatom by electroporation. Finally, Tirichine et al. (2014, p. 67–71) describe protocols for the extraction of histones from both these diatoms, techniques that are likely to become of significant utility in light of current interest in exploring epigenetics-based phenomena in diatoms.

This Special Issue of Marine Genomics therefore provides an interesting panorama of current molecular research on diatoms. The field is certain to grow further with the public release of hundreds of diatom transcriptomes as part of the Marine Microbial Eukaryote Transcriptome Sequencing Program (MMETSP) from the Gordon and Betty Moore Foundation (<http://marinemicroeukaryotes.org/>). The future looks bright for diatom research and the Molecular Life of Diatoms conference looks set to continue for the foreseeable future. See you at the third meeting of the series scheduled for Seattle in 2015!

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