Eukaryotic Microalgae Genomics. The Essence of Being a Plant

Steven G. Ball*

Unite´ de Glycobiologie Structurale et Fonctionnelle, Unite´ Mixte de Recherche 8576 du Centre National
de la Recherche Scientifique/Universite´ des Sciences et Technologies de Lille, 59655 Villeneuve
d’Ascq cedex, France

More than 1.5 billion years ago, a flagellated eukaryote entered into symbiosis with a photosynthetic bacterium that was clearly related to present-day cyanobacteria (Yoon et al., 2004). After the endosymbiosis of mitochondria, this second major event, now thought to have occurred only once (McFadden and van Dooren, 2004), had far-reaching consequences, as it gave rise to all photosynthetic eukaryotes, including the land plants. The organism carrying the primary endosymbiont subsequently diversified into three primary endosymbiotic lineages: the glaucophytes (a group of freshwater algae carrying primitive plastids), the rhodophytes (the red algae), and the viridiplantae (the true plants consisting of green algae and land plants). Upon sequencing the Arabidopsis genome and unraveling the secrets of the true plants, it became clear that 18% of the nuclear genome of plant biologists’ favorite model system could be traced back to the endosymbiont (Martin et al., 2002). It is thus particularly fitting that the kingdom plantae now be considered as the sum of all organisms descending directly from this ancient primary endosymbiotic event (Cavalier-Smith, 1998). Plant biologists were quick to recognize that green algae witnessed the evolution of many of the pathways that they were interested in studying. For this reason, the unicellular green alga Chlamydomonas reinhardtii was developed as a powerful genetic model. The major contribution of Chlamydomonas to the understanding of chloroplast biogenesis and function is now universally recognized (Rochaix, 2004). However, the usefulness of Chlamydomonas to the understanding of plant biology is not restricted to photosynthesis, and many other pathways have been or should be studied in this model organism. This is highlighted in this focus issue by a number of research articles or Updates concerned with analyzing the Chlamydomonas nuclear genome with respect to circadian rhythms (Mittag et al., 2005), cell cycle control (Bisova et al., 2005), plant respiration (Cardol et al., 2005), and metal transporters (Hanikenne et al., 2005). We believe the study of these topics would greatly benefit from the genetic and genomic approaches now accessible in a unicellular plant model system. In addition to research articles dealing with photosynthesis or related topics (Cohen et al., 2005; Forti and Caldiroli, 2005; Lemaire et al., 2005), several contributions to this issue deal with establishing a number of indispensable genomic tools for Chlamydomonas research. These include functional genomics tools, such as the generation of large-scale mutant banks for the selection of strains defective for either photosynthesis or nitrogen metabolism (Dent et al., 2005; González-Ballester et al., 2005). Equally relevant are reports concerning the use of microarrays (Erickson et al., 2005) and, most importantly, the development of routine and fast techniques for map-based cloning (Rymarquis et al., 2005). Indeed, hundreds of untagged mutants displaying interesting phenotypes have been selected over the years and are accessible through the Chlamydomonas genetic center (http://www.chlamy.org/strains.html) awaiting further molecular investigations. This issue of plant physiology was initially planned to celebrate the completion of the C. reinhardtii nuclear genome sequencing effort. As we go to press, the genome is not yet entirely completed but is accessible to all and sufficiently advanced for large-scale genomic investigations (http://genome.jgi-psf.org/chlre2/chlre2.home.html). Upon planning the issue, other smaller but highly relevant genomes became accessible, such as that of the red alga Cyanidioschyzon merolae (http://merolae.biols.u-tokyo.ac.jp) and that of the centric diatom Thalassiosira pseudonana (http://genome.jgi-psf.org/thaps1/thaps1.home.html), while the sequence of the another unicellular green alga, Ostreococcus tauri, approached completion. These developments have been reviewed by Arthur Grossman, who takes us in his introductory review on the path toward algal genomics (Grossman, 2005). He makes it clear that the stage is now set for molecular investigations dealing with other unicellular eukaryotic algae.

Diatoms are important contributors to global photosynthesis and the carbon cycle and are thus bound to become the focus of increasing attention and research efforts in the coming years. Surprisingly, they are not part of the plant kingdom but rather of the kingdom chromista, which is known to be derived from red algae by secondary endosymbiosis (a eukaryote that acquired a red alga endosymbiont by phagocytosis). It will be of interest to understand how these organisms
and their impressive multicellular brown algae cousins have reinvented the plant way of life through the use of typically hybrid (animal-plant) molecular toolkits. In this issue, Montsant et al. (2005) report on the comparative genomics of the two major subgroups of marine diatoms. The red algae are also of interest and more directly relevant to plant biologists as an ancestral sister plant lineage. Several contributors to this focus issue have systematically included the C. merolae genome together with that of Chlamydomonas in their genome-wide explorations. One Update and one research article pay tribute to their importance. In particular, a detailed comparative genomic analysis is reported between C. merolae and Caldariera sulphuraria, two very different members of the cyanidiales, a group of unicellular red algae living in extreme hot and acid environments (Barbier et al., 2005). Some have argued that because of their unusual environments, these algae would never become functional genomic models. It must be stressed, however, that a recent report reviewed in this issue (Misumi et al., 2005) describes the easy culture of C. merolae on solid media, its successful transformation, and the integration of genes through homologous recombination (Minoda et al., 2004). This would make this tiny red algal system the first plant system for which both transformation followed by homologous recombination and full genome sequence are accessible.

This issue and an issue of Eukaryotic Cell (http://ec.asmol.org/content/vol4/issue2/) convey the enthusiasm that most of us feel upon the development eukaryotic microalgal genomics. We hope that this will prompt more plant biologists to adopt a unicellular plant model in addition to their favorite vascular plant system to study the evolution of their pathways, as suggested by Gutman and Niyogi (2004). It is our belief that comparative functional biology is a powerful way to probe the unknown because it highlights the history on which these pathways have emerged and aids to perceive the logic of the processes involved. The essence of being a plant is indeed not confined to being terrestrial and having roots, stems, and leaves. It consists rather of being descendants of a tremendously successful partnership that was established more than 1.5 billion years ago.

LITERATURE CITED


