

PREFACE

Algae range in size from 1- μ m single-celled organisms to 60-m long giant kelps and have colonized virtually every single aquatic habitat on Earth. Algae comprise diverse and numerous oxygenic photosynthetic eukaryotes with representatives all over the eukaryotic tree of life, with the exception of the non-photosynthetic Unikont superphylum that includes all animals and fungi. Cellular and molecular studies of the last century provided the evidence that all algae derive from a major transition in the evolution of life, the endosymbiosis between one eukaryotic host cell and a photosynthetic bacterium, that subsequently evolved into an organelle, the plastid. Thus, despite their phylogenetic diversity, all algae are 'bound by plastids' (Delwiche, 2007).

In the last decades, the use of sequence data from a handful of genes has shed light on the huge diversity and the complex evolutionary history of algae. The recent development of large-scale sequencing studies provides unprecedented access to both the metabolic potential and the ultimate record of the evolution of a cell, its genome. Genomics, defined here in its broad sense as large-scale DNA sequencing projects, has revolutionized the study of algae in several ways. These data enable us to scale up our knowledge on algal diversity and evolution and open the book to reading about the underlying molecular mechanisms; the rise and fall of gene families, the transfer of genes from the endosymbiont to the nuclear genomes, as well as the hallmark of selection on gene content, gene amino acid structure and non-coding regions.

In this volume, we address some of the genomic insights gained into the ecology, the evolution and the biology of algae.

The first chapter (Not et al., 2012) provides an overview of the diversity and ecology of algae in the largest ecosystem on Earth: the ocean's surface. A bucket of seawater may contain hundreds of algal species invisible to the eye, marine phytoplankton, and the authors report how early morphological studies and DNA sequences from environmental samples, metagenomics, fostered the discovery of their diversity.

The following chapters review the evolutionary scenarios leading to this highly diverse group of eukaryotes. Chapter 2 (De Clerck, Bogaret, &

Leliaert 2012) reviews the diversity of the descendants of the primary endosymbiosis event, the Archaeplastida, that comprise the green algae, the red algae and the glaucophytes. Chapter 3 (Archibald, 2012) summarizes the complex history of algae that have evolved from the engulfment of some Archaeplastida algae by a eukaryote. These secondary endosymbioses of green or red algae have occurred several times independently in the course of evolution. Some algal groups are descendants of tertiary endosymbiosis; the engulfment of an algae that acquired its photosynthetic metabolism from a secondary endosymbiotic event. This complex evolutionary story of serial cell capture and enslavement was unveiled by the comparative analysis of the genome sequences of both the chloroplast, the nuclear and the nucleomorph genomes of these algae.

Chapter 4 (Weber & Medina 2012) gives an overview of the genomics of one of the many symbioses between algae and non-algae – the corals and anemones with their dinoflagellate *Symbiodinium* algal partners.

The following chapters are dedicated to case studies of genome projects within the green algae *Volvox* and *Chlamydomonas* (chapter 6 (Umen & Olson 2012)), the brown alga *Ectocarpus* (chapter 5 (The Ectocarpus Genome Consortium 2012)) and the Diatoms (chapter 7 (Mock & Medlin 2012)). Chapter 8 (Cadoret, Garnier, & Saint-Jean 2012) reports some of the genomic insights gained into the physiology of algae and their biotechnological potentials as nutritional complements, medicines or biofuels.

The last two chapters review how genomics enables a glimpse into the molecular basis of the interactions between algae and their environment. Chapter 9 (Grimsley et al. 2012) concerns recent genomic insights of algal viruses, providing clues about host-viral evolutionary and functional relationships. Chapter 10 (Toulza et al. 2012) reviews the power and challenges of metagenomics, the scaling up of genomes to the community level, for the microbial algae.

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