Diversity and ecology of green microalgae in marine systems: an overview based on 18S rRNA gene sequences

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With 5 figures in the text and an electronic supplement

Abstract: Green algae (Chlorophyta) are an important group of microalgae whose diversity and ecological importance in marine systems has been little studied. In this review, we first present an overview of Chlorophyta taxonomy and detail the most important groups from the marine environment. Then, using public 18S rRNA Chlorophyta sequences from culture and natural samples retrieved from the annotated Protist Ribosomal Reference (PR²) database, we illustrate the distribution of different green algal lineages in the oceans. The largest group of sequences belongs to the class Mamiellophyceae and in particular to the three genera *Micromonas*, *Bathycoccus* and *Ostreococcus*. These sequences originate mostly from coastal regions. Other groups with a large number of sequences include the Trebouxiophyceae, Chlorophyceae, Chlorodendrophyceae and Pyramimonadales. Some groups, such as the undescribed prasinophytes clades VII and IX, are mostly composed of environmental sequences. The 18S rRNA sequence database we assembled and validated should be useful for the analysis of metabarcode datasets acquired using next generation sequencing.

Keywords: Chlorophyta; Prasinophytes; diversity; distribution; 18S rRNA gene; phylogeny; ecology; marine systems

Introduction

Throughout history, the Earth has witnessed the appearance and disappearance of organisms adapted to their contemporary environments and sometimes these organisms have deeply modified the environment (Kopp et al. 2005, Scott et al. 2008). The best example is provided by the oxygenation of the ocean and the atmosphere by photosynthetic bacteria that first began about 3,500 million years ago (Yoon et al. 2004). Eukaryotic phytoplankton subsequently acquired a chloroplast, a membrane-bound organelle resulting from the phagocytosis without degradation of a cyanobacterium by a heterotrophic host cell (Margulis 1975), 1,500–1,600 million years ago (Hedges et al. 2004, Yoon et al. 2004). This event marked the origin of oxygenic photosynthesis in eukaryotes. During the course of evolution, endosymbiosis has been repeated several times, new hosts engulfing a eukaryote with an existing plastid, leading to secondary and tertiary endosymbioses (McFadden 2001). Early in their evolutionary history photosynthetic eukaryotes separated into two major lineages: the green lineage (which includes green algae and land plants) and the red lineage (including diatoms and dinoflagellates) (Falkowski et al. 2004). These two lineages diverged approximately 1,100 million years ago according to molecular clock estimates (Yoon et al. 2004), marking the beginning of algal diversification in the ocean. A number of fundamental differences exist between the members of these two lineages (Falkowski et al. 2004), in particular with respect to pigment content, cellular trace-element composition and plastid gene composition. Green algae possess chlorophyll *b* as the main accessory chlorophyll, while algae from the red lineage mainly harbour chlorophyll *c* (i.e. their chloroplast evolved from a Rhodophyta algae after secondary endosymbiosis), influencing their respective light absorption properties and ultimately their distribution in aquatic environments. Algae from the red lineage are often derived from secondary or tertiary endosymbioses and have a chloroplast surrounded by three or four membranes, while algae from the green lineage originate mostly from primary endosymbiosis and have a chloroplast surrounded by only two membranes. The evolutionary history of these lineages is probably much more complex than originally...