

Algal Genomics

7A.1

NATURE, NURTURE AND THE STRUCTURE OF MACROALGAL GENOMES

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The recent acquisition and analysis of complete genome sequences for two macroalgal species has provided unparalleled insights into the biology and evolutionary history of these important organisms. The recently published genome sequence of the filamentous brown alga *Ectocarpus siliculosus* (Cock *et al.*, Nature 2010) has not only provided clues as to how brown algae have adapted to the harsh conditions of the intertidal, but has also allowed the generation of hypotheses about the molecular events underlying the evolution of complex multicellular development in this group of organisms. The more recently completed genome sequence of the red alga *Chondrus crispus* (Collén *et al.*, unpublished) has similarly provided important information about the origins and the biology of the red algae. Both *Ectocarpus* and *Chondrus* are found in the intertidal zone, but they have had very different evolutionary histories and have been evolving independently for more than a billion years. Interestingly, they also exhibit very marked differences in terms of genome structure and organisation, suggesting that their evolutionary histories have played a more important role in shaping their genomes than their adaptation to the intertidal environment.

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DIVERSITY OF MARINE PRASINOPHYCEAE AND ASSOCIATED VIRUSES

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The order Mamiellales (Prasinophyceae) comprises freshwater and marine “green” unicellular photosynthetic eukaryotes. Many of these have very small cell sizes and are named ‘picoeukaryotes’ (cell diameter < 2 µm). The ecological importance of marine Mamiellales in coastal waters, their easy manipulation and their small genome sizes have fostered genome projects in several different species. In this presentation, recent analyses of the 6 available genomes from the *Bathycoccus*, *Micromonas* and *Ostreococcus* genera are presented and the insights gained into the species