

Chapter 29

Evolutionary Aside 29.1--Evolution of Multicellularity in Brown Algae

Five major groups of eukaryotes have independently evolved multicellularity: brown algae, green algae, land plants, fungi, and the metazoan animals. Did these different groups find common or unique ways to become multicellular? Comparative genomics may hold some clues. The genome of the brown alga *Ectocarpus* was sequenced with the goal of identifying genes needed for multicellularity. A total of 16,526 protein-coding genes were identified and compared with the closely related diatom branch in which multicellularity is absent, as well as sequenced plant, animal, green algal, and fungal genomes. No common trend emerged in terms of specific gene families that were added in lineages with multicellularity.

Comparisons with diatoms, however, did reveal an interesting trend. The number of transmembrane receptor kinases increased in the *Ectocarpus* genome. The kinases form a monophyletic clade that was distinct from those found in plants and animals. Transmembrane kinase receptors are important in signaling between cells, which is essential for coordinating cell growth and differentiation in a multicellular organism. It is plausible that transmembrane receptor evolution was a key to evolving multicellularity.