

J. Craig Bailey, Ph.D., Louisiana State University, 1996. (910) 962-2371 baileyc@uncwil.edu

My research focuses on the cell biology, evolution, and systematics of marine and freshwater algae. Recent initiatives also include structural genomics studies of organellar genomes (i.e., plastids and mitochondria).

Evolutionary studies in my laboratory involve determining DNA sequences for particular plastid- and/or nuclear-encoded genes. For example, we are examining plastid-encoded *rbcL* and *sufB* genes, nuclear 18S rRNA and glutamine synthetase (type II) genes, as well as a number of faster evolving noncoding DNAs. These molecular data are combined with morphological and biochemical data to infer relationships among species or higher taxa. Phylogenetic reconstructions are then used to trace the evolution of key characters that define taxa and to reevaluate their classification. Current systematics projects emphasize relationships among the chlorophyll *a + c*-containing algae. This lineage, often referred to as chromophytes or heterokont algae, includes chrysophytes, diatoms, pelagophytes, raphidophytes and silicoflagellates among others. Although some are macroscopic and/or benthic, most species within this morphologically diverse group are microscopic phytoplankton. On-going studies focus on the relationships among species placed in the Chrysophyceae, Chrysomeridales, Phaeothamniophyceae, Pinguiphyceae, Prymnesiophyceae, and Xanthophyceae. This work has resulted in the description of several new chromophyte taxa from freshwater, coastal or open-ocean habitats. In addition, I maintain an active interest in the evolution of the Rhodophyta. I am particularly interested in the systematics of calcified red seaweeds classified in the order Corallinales. These algae are widely distributed and play especially important ecological and geological roles in reef ecosystems. For example, coralline algae and coral animals are the major builders of coral reefs, which are home to one-quarter of all described marine species.

Ongoing cell biological studies focus on the evolution of the glutamine synthetase gene family among eucaryotes, the distribution of *sufB* genes among photoautotrophs, the regulation and function of the *sufB* gene product in plastids, and characterization of genes encoding transport proteins located on the plastid envelope.

Our genomics research focuses on the organellar genomes of microalgal species. For example, we are using high-throughput DNA sequencing technology to assemble physical and genetic maps (structure, coding capacity, gene content) for the mitochondrial genome of a marine flagellate. These data can then be used to accumulate functional data for gene products and to increase our understanding of the evolutionary pathways that have led to the tremendous diversity that characterizes mitochondrial genomes found in protists and other eucaryotes.

Other funded projects seek to 1) determine the level of genetic variability within populations of harmful bloom-forming algae responsible for "red tides" and "brown tides", 2) assess the biodiversity of coccoid microalgae in natural waters, and 3) develop molecular markers for studying the population dynamics of picoplanktonic microalgae at various temporal and spatial scales.