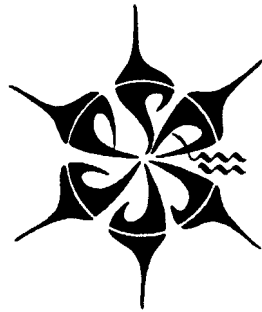
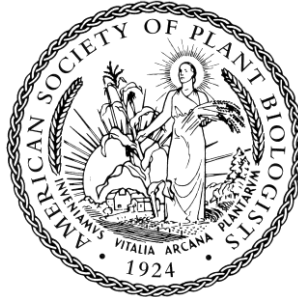


Plant Biology 2009 Final Program



Phycological
Society of America

***Final program and abstracts of symposia, plenaries,
minisymposia, talks, and poster presentations at
Plant Biology 2009***

**Joint Annual Meetings of the
American Society of Plant Biologists
and the Phycological Society of America**

***Hawaii Convention Center, Honolulu, Hawaii
Saturday July 18 thru Wednesday July 22, 2009***

P05047 New insights in the systematics of the Dumontiaceae-complex (Rhodophyta)

Fredericq, Suzanne-presenter slf9209@louisiana.edu(a) Kravesky, David (a) Freshwater, Wilson (c) Lopez-Bautista, Juan M. (d) Cho, Tae Oh (e) Norris, James N. (f) Hommersand, Max H. (b)
<http://youtube.com/nemastoma2>

"Two newly reported genera for the Gulf of Mexico that are currently placed in the marine red algal family Peyssonneliaceae, *Polystrata* and *Metapeyssonnelia*, are instead nested inside the Rhizophyllidaceae of the Dumontiaceae-complex as inferred from chloroplast-encoded *rbcL* and nuclear LSU rDNA sequence analyses. The Rhizophyllidaceae is a newly reported family for the Gulf of Mexico, with six species occurring in the region. The basis for interpreting morphological evolution in the Dumontiaceae-complex will be illustrated and discussed within a phylogenetic framework."

(a) University of Louisiana at Lafayette (b) University of North Carolina at Chapel Hill (c) Center for Marine Science, UNCW (d) The University of Alabama (e) Chosun University (f) Smithsonian Institution

P05048 "Preliminary assessment of macroalgal diversity in Bocas del Toro, Caribbean Panama"

Norris, James N-presenter norrisj@si.edu(a) Wysor, Brian (b) Freshwater, D. Wilson (c) Fredericq, Suzanne (d)
"A PRELIMINARY ASSESSMENT OF MACROALGAL DIVERSITY IN BOCAS DEL TORO, CARIBBEAN PANAMA >Brian Wysor, D. Wilson Freshwater, Suzanne Fredericq & James N. Norris > The Bocas del Toro province, Republic of Panama, hosts a complex of diverse habitats, from coral and sponge reefs, to seagrass meadows and mangrove cays that yield a species rich marine flora and fauna. Recent investigations have uncovered a biota, although similar to Caribbean Islands, may be more speciose than other, better-studied areas. Based on our preliminary recent collecting efforts, we estimate macroalgal species richness for Bocas del Toro region to be very high. The high diversity is not surprising given the short history of marine botanical investigations in the region. > Currently a conservative estimate indicates there are 151 red, 76 green and 32 brown algal species. Our initial studies of Bocas del Toro intertidal and subtidal algae have resulted in one published new species (Gavio & Fredericq 2003), many new distribution records for Panama, numerous tentative new species, and revealed that much of the marine floristic diversity for Caribbean Panama is represented by species throughout this unique region. φ"

(a) Smithsonian Institution (b) Roger Williams University (c) University North Carolina Wilmington (d) University Louisiana Lafayette

P05049 "New insights in the systematics of *Peyssonnelia* and the Peyssonneliaceae (Rhodophyta), with emphasis on taxa from the Gulf of Mexico and Panama"

Kravesky, David M-presenter dkravesky@yahoo.com(a) Norris, James N (b) Paul, Gabrielson W (c) Gabriel, Daniela (a) Fredericq, Suzanne (a)
<http://youtube.com/nemastoma2>

"*Peyssonnelia* Decaisne comprises a worldwide group of non-calcified or calcified, crust-forming red algae of great ecological significance, with some species involved in the establishment of rhodoliths. Of the eight genera currently recognized in the family, *Peyssonnelia*, is widely viewed to contain the largest number of species. The number of distinct species of Peyssonneliaceae present in the Gulf of Mexico has increased from 6 to 21. Comparative morphology, chloroplast-encoded *rbcL* and nuclear LSU rDNA sequence data suggest that species of *Peyssonnelia* do not occur in the Gulf of Mexico, and that previously reported *Peyssonnelia* species for the region actually belong to other genera of the Peyssonneliales."

(a) University of Louisiana at Lafayette (b) Smithsonian Institution (c) University of North Carolina

P05050 Comparative genomics of photosynthetic Heterokonts

phillips, naomi-presenter phillipsn@arcadia.edu(a) Braun, Ed (b) Moustafa, Ahmed (d) Bhattacharya, Debashish (d) Kapraun, Don (c) calhoun, sam (a) coaxum, teresa (a)

"Heterokonts (also called stramenopiles) comprise a monophyletic assemblage united by a shared endosymbiotic history that either exhibit a biflagellate heterokont condition (have distinct anterior and posterior flagella) or have heterokont ancestors. The group contains an enormous amount of biodiversity, with millions of species that can be divided into approximately 14 major lineages. The majority of these lineages are small unicells or simple filaments, but there is one lineage (the brown algae; Phaeophyceae) characterized by large multicellular thalli rivaling green plants in size and complexity. Despite the diversity of the heterokonts only a small number of genome sequences are currently available, especially for the photosynthetic heterokonts. We are interested in expanding the current dataset as efficiently as possible, so we are using relatively inexpensive methods (454 pyrosequencing and EST acquisition) to illuminate relationships among heterokont lineages and examine changes to genomic content that occurred during the shift to complex morphological and life histories in the brown algae. We present data on genome sizes as well as ESTs and 454 data from various heterokont lineages with an emphasis on the brown algae and its closest sister groups. "

(a) Arcadia University (b) University of Florida (c) University of North Carolina (d) University of Iowa

P05051 Detecting marine aliens: applying herbarium collections to investigate the genera *Ulva* and *Codium*

Maggs, Christine A-presenter c.maggs@qub.ac.uk(a) Mineur, Frederic (a)

"We show how using herbarium specimens both for morphological and molecular investigations can elucidate invasions by cryptogenic aliens, cryptic species and other algae responsible for taxonomic nightmares. DNA has been amplified from herbarium specimens up to 150 years old, in various herbaria. In *Codium fragile*, different subspecies are native to particular areas of the world and there is a single invasive subspecies. In *Ulva*, several clades are seen to be invasive, with some haplotypes becoming globally distributed and forming green tides. Some invasive clades are also associated with hull fouling, perhaps explaining how these have become global in extent. Morphological characters are misleading for identification and there seems little alternative but to use molecular data to identify taxa, especially those constituting green tides. "

(a) School of Biological Sciences, Queen's University Belfast, Belfast BT9 7BL, Northern Ireland

P05052 "Study of a cyanobacterium from thermal, saline waters with relatives from unexpected habitats"

Banerjee, Meenakshi-presenter meenakshi.banerjee@rediffmail.com(a) Castenholz, Richard (b)

"Thermophilic cyanobacteria (i.e. growth > 45 °C) that also grow at and above seawater salinity (i.e. >30-33 g L⁻¹ TDS) have rarely been reported and studied. In the present study, a cyanobacterium that constitute this rare type of extremophile were isolated from a submerged siliceous crust at 40-45 °C in a geothermal lagoon of altered seawater in southwest Iceland. Iceland Clone 2e, a *Leptolyngbya* morphotype, that barely survived in freshwater medium at 23 °C or in saline medium at 23 °C. At 45 °C-50 °C, in medium ranging from 28 to 94 g L⁻¹ TDS, it grew with a maximum rate of over 3 doublings 24 h⁻¹ under continuous illumination. This rate decreased by about one third at 54 °C, and death occurred at 58 °C. A comparison of the partial 16S rDNA sequence with others in the database revealed two apparent relatives in culture (>99% similarity) from slightly saline Greenland hot springs (1.3-1.6 g L⁻¹ TDS). Three other similar sequences (93-98% similarity) were from periodically dry, endolithic habitats in Yellowstone National Park. All six formed a distinct phylogenetic clade, suggesting their common ancestry. In a search for phenotypic