

to highly eutrophic. Twenty-six species have been identified to date: three from the Subgenus *Euglena*, thirteen from the Subgenus *Calliglena*, and ten from the Subgenus *Discoglana*. Taxa from field collections are identified in the lab, videotaped, photographed and logged into the database for the appropriate collecting site. Morphological features, cell measurements, habitat, photomicrographs, video clips and identification notes are then recorded on a cd-rom which can be used as a visual key to the species.

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A WEB-BASED DIGITAL KEY TO EUGLENOIDS

Uzwiak, D. J. & Triemer, R. E.
Division of Life Sciences, Rutgers University,
Piscataway, NJ 08554 USA

We are using Lucid Professional software to construct digital keys for the identification of Euglenoids. Digital keys offer a number of unique advantages over traditional paper keys, including: 1) users can describe characters in any sequence, and may skip uncertain characters, 2) the key program, by scoring as the user progresses, can "guess" what the result will be, and direct the user to the most informative characters, or narrow the field of likely taxa, 3) terms, characters, or taxa may be linked to descriptive pages that can include video clips, animations, microscopic images, and diagrammatic illustrations, as well as text. In addition to the advantages that a digital key offers over a traditional paper key, the Lucid key format includes html support, and this internet capability provides additional advantages over stand-alone digital keys. For example, the key becomes as accessible as the internet, allowing distribution to users with a broad range of interests. When run on-line, the key can hyperlink to related pages in the home site or in remote sites, allowing users to customize their experiences. While novice biologists may be directed to pages that illustrate and explain biological terms, experts will move quickly to species descriptions, which will include images, original species diagnoses, and a summary of taxonomic debate, where applicable. Our key will be housed in the Euglenoid project website (www.bio.rutgers.edu/euglena). In collaboration with others, we hope to link our keys to other similar keys so that any protistan taxa may be identified from one web address.

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ARE BLOOM-FORMING GREEN ALGAE CHEMICALLY DEFENDED?

Van Alstyne, K. L.

Shannon Point Marine Center, Western Washington University, 1900 Shannon Point Road, Anacortes, WA 98221 USA

Ulvoid green macroalgae, such as *Enteromorpha* and *Ulva*, can form large blooms that have deleterious impacts on the local biota. These algae are often assumed to be very palatable for most invertebrate and vertebrate herbivores because they lack obvious physical defenses, and because there have been few reports of their producing chemical defenses. However, in laboratory feeding preference assays, the ulvoid macroalgae *Enteromorpha linza* and *Ulva fenestrata* were low preference foods for green sea urchins, *Strongylocentrotus droebachiensis*. Both these algae and several other species of green algae produce large quantities of dimethylsulphoniopropionate (DMSP), which is enzymatically converted to dimethyl sulfide (DMS) and acrylic acid when the algae are physically damaged. In laboratory bioassays, both DMS and acrylic acid were potent feeding deterrents towards urchins at concentrations that the urchins would be likely to encounter in the field. The precursor in this system, DMSP, was a feeding attractant. Our data provide evidence that DMSP functions as a precursor in an activated defense system in marine macroalgae and suggests a similar function in phytoplankton. The presence of this activated defense system may contribute to the persistence of macroalgal blooms by making these algae unpalatable to some species of herbivores.

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DIVERSITY OF EUKARYOTIC PICOPLANKTON IN COASTAL WATERS

Vaulot D.¹, Romari K.¹, Valentin K.², Not F.¹, Simon N.¹, Biegala I.¹, Le Gall F.¹, Medlin L.K.² & Eikrem W.³

¹*CNRS et Université Pierre et Marie Curie, Station Biologique BP 74 296982 Roscoff, France;* ²*Alfred Wegener Institute for Polar Research, Bremerhaven, Germany;* ³*Department of Biology, University of Oslo, Oslo, Norway*

In comparison to prokaryotic picoplankton, our knowledge of the diversity of eukaryotic picoplankton is still very limited. Recently, clone libraries from the small sub-unit ribosomal RNA gene (rDNA) from oceanic samples have revealed the presence of many new eukaryotic groups, not represented in cultures (Lopez-Garcia et al. 2001. Unexpected diversity of small eukaryotes in deep-sea Antarctic plankton. *Nature* 409: 603-607; Moon-van der Staay et al. 2001. Oceanic 18S rDNA sequences from picoplankton reveal new eukaryotic lineages. *Nature* 409: 607-610). In the framework of the European program PICODIV, we are us-

ing the same approach to characterize picoplankton in coastal waters. In addition to clone libraries, we are also attempting to isolate novel strains in culture and to quantify key groups with oligonucleotide probes detected by fluorescence *in situ* hybridization (FISH). Some of the novel groups already observed in the Pacific Ocean are found in coastal waters pointing out their ubiquity. One such group, probably heterotrophic, occupies a basal position within the stramenopiles. Two other major novel groups are part of the alveolates and appear to be intermediate between dinoflagellates and apicomplexa. Among the photosynthetic groups, Mamiellales (Prasinophyceae), cryptophytes, chrysophytes and dinoflagellates dominate coastal clone libraries. Some sequences can be relegated to the novel class Bolidophyceae, previously known only from offshore waters. Among heterotrophic groups, ciliates are particularly abundant. Finally, coastal waters seem to harbor some novel eukaryotic groups, not observed previously such as one that appears close to the Rhodophyta.

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PATTERNS OF ALGAL ASSEMBLAGES FROM COAL MINE IMPACTED STREAMS WITHIN THE UNGLACIATED WESTERN ALLEGHENY PLATEAU

Verb, R. G.¹, Keiper, J. B.² & Vis, M. L.¹

¹Department of Environmental and Plant Biology, Ohio University, Athens, OH 45701 USA; ²Cleveland Museum of Natural History, 1 Wade Oval, University Circle, Cleveland, OH 44106 USA

Macroalgae and periphyton assemblages from abandoned coal mines, reclaimed sites, and reference streams within the unglaciated Western Allegheny Plateau were examined in order to determine if sites could be classified by community structure. Fifty-six streams were visited in May and June 1999. To assess the impacts of coal mining on the lotic system the periphyton and macroinvertebrates (to ascertain herbivory influence) from riffles and macroalgae from a 20-meter stream segment were collected. In addition, 29 environmental parameters (e.g. pH, metals, sulfate) and habitat conditions were examined at each stream site. A total of 594 infrageneric algal taxa and 40 macroinvertebrate taxa were recorded from these stream sites. Diatoms were the most abundant and diverse algal organisms (359 taxa), followed by chlorophytes (121), Cyanobacteria (42), euglenophytes (31), xanthophytes (14), chrysophytes (12), rhodophytes (6), dinophytes (6), and cryptophytes (3). Based on canonical correspondence analyses (CCA), the first axis was strongly correlated with pH for both periphyton ($r=0.93$) and macroalgal assemblages ($r=0.85$). The second axis was

influenced by specific conductance for both data sets ($r=0.64$ and 0.36). Multivariate techniques typically showed five major groupings of stream reaches that were defined by certain shared environmental and biotic attributes. For example, highly acidic sites were characterized by a dominant flora of *Euglena mutabilis*, *Eunotia exigua*, *Frustulia rhomboides*, *Klebsormidium rivulare*, and *Microspora tumidula*. Predictable relationships were observed between the water quality from abandoned and reclaimed mines and the biotic assemblages present, which may prove useful in the assessment and management of reclamation efforts.

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SYNTHESIS OF MOLECULAR RESEARCH ON BATRACHOSPERMUM HELMINTHOSUM (RHODOPHYTA) FROM STREAM REACHES IN EASTERN NORTH AMERICA

Vis, M. L., Hall, M. M., Machesky, N. J. & Miller, E. J.

Department of Environmental and Plant Biology, Ohio University, Athens, OH 45701 USA

The freshwater red alga *Batrachospermum helminthosum* was collected from eleven streams throughout the species range in eastern North America as follows: three stream reaches from Ohio, and one each from Michigan, Indiana, Tennessee, Louisiana, North Carolina, Connecticut, Rhode Island and Massachusetts. The molecular marker technique of inter-simple sequence repeats (ISSR) and sequence data from the plastid encoded rubisco large subunit gene (*rbL*), the mitochondrial COX2-COX3 gene spacer region, and the nuclear region of ITS1-5.8S rDNA-ITS2 were employed to examine biogeographic trends in this alga. Analysis of the *rbL* sequence revealed 5 genotypes with one genotype representing individuals from seven stream reaches. Data from the ISSR molecular markers gave a distinct banding pattern for each of 165 individuals examined. ISSR results showed all individuals within a reach clustered together but did not provide well-defined groupings based on stream reach. The sequence data for the COX2-COX3 gene spacer was invariant among individuals from a stream reach. The individuals from Connecticut, Rhode Island and 2 Ohio stream reaches were identical and similarly the individuals from the North Carolina and another Ohio location did not vary in sequence so that seven genotypes were recorded among the individuals from the eleven stream reaches. Analysis of the ITS1-5.8S rDNA-ITS2 region showed sequence variation not only among individuals from different streams but also among individuals from the same reach. The utility and congruency of these data sets to answer biogeographic questions will be discussed.