

## International Census of Marine Microbes:

### Microbial Eukaryotes Working Group (MEWG) Meeting Final Report

July 9-10<sup>th</sup>, 2007

Bigelow Laboratory for Ocean Sciences,  
West Boothbay Harbor, Maine, USA

#### Major Recommendations

- 1) *Elevate the importance of microbial eukaryotic diversity in ICoMM.* Eukaryotic species have received limited attention from ICoMM. ICoMM could play a key role as a central clearing house for information on these species and in bringing together the relevant scientific community.
- 2) *Collect the names of every marine protist by the end 2008.* This goal could be readily attained via a thorough inspection and aggregation of information available through the extant literature. Establish a mechanism to provide ‘species-pages’ for all known, described marine protistan taxa.
- 3) *Facilitate the transfer of biogeographical data to the ICoMM database.* Several of the taxonomic groups of protists have extensive biogeographical information (e.g. foraminifera, radiolaria, some diatoms, dinoflagellates). These data are often highly dispersed in the literature. ICoMM should lead the effort to collect and collate these data.
- 4) *Capture legacy data for all marine protists.* Many studies of protistan diversity include environmental and biogeographical information. ICoMM should capture this information.
- 5) *Engage a broad spectrum of taxonomic specialists to capture existing information on protistan diversity.* As goal (2) above is realized, taxonomic specialists (traditional morphology-based taxonomists and molecular taxonomists) should be engaged in a communal process that will identify cryptic species, synonyms species, to work towards developing reliable methods for identification (e.g. DNA sequencing).|
- 6) *ICoMM should partner with culture collections to foster culturing, cryopreservation methods for unispecies cultures or entire microbial communities in order to maintain voucher material for future studies.* The difficulty of voucher specimens is a crucial one for microbial taxa. ICoMM should establish a culture collection working group to improve resources for taxonomic, molecular vouchers, or other work.

## Summary of Workshop

This newly formed ICoMM working group met with the broad objective of assessing the status of what is *known*, what is *unknown* and perhaps *unknowable* regarding the diversity of marine microbial eukaryotes. The microbial eukaryotes considered by this working group are specifically marine protists (single-celled, eukaryotic organisms). This complements and overlaps with the research objectives of the Census of Marine Zooplankton (CMarZ). ICoMM encompasses both benthic and planktonic marine systems.

Protists constitute an important component of the microbial biodiversity of the world ocean. As the dominant primary producers (the microscopic algae) and important consumers in microbial food chains (heterotrophic protists, also referred to as protozoa, that consume bacteria, phytoplankton, other protozoa and occasionally metazoa), protists play fundamental ecological roles in the production and utilization of organic matter, nutrient uptake/release, and elemental cycling. They are key elements in all aspects of ocean ecology and biogeochemistry ranging from fisheries to global climate control. There is over 100 years of data on marine protists, inclusive of long term data series. More recently a rapidly expanding, complementary database of DNA sequence information is emerging. To date, these species have received very limited attention within the goals and activities of ICoMM.

A central theme for discussions among attendees at the workshop was how ICoMM was perceived within the scientific community, and the role of studies of microbial eukaryotes within the initiative. There was general agreement within the group that much of the scientific community perceives ICoMM as a project that is not yet a true community development effort. Further, there is a perception by many in the community that ICoMM is now primarily concerned with the pursuit of new technology (specifically the 454 tag sequencing approach), rather than cataloging the huge volume of information that presently exists on microbial diversity. New technologies will always capture our interest, but there was a clear agreement within the working group that progress on capturing existing information on microbial diversity and making it useful has lagged.

ICoMM can and should be aggressive about involving a broader scientific community. ICoMM should have a representative at every meeting, presenting posters, organizing meetings and holding dinners to bring the community together. There should be connections to the various marine Microbial Observatories that exist. Specifically, with regards to the charge of this working group, there was complete agreement that existing information regarding marine microbial eukaryotic diversity has been underexploited by ICoMM. There was concordance among the members that the situation could be rectified, and that much progress could be made towards documenting the *known* information regarding protistan diversity and distribution.

Due to the wealth of historical data on protistan species, some of these taxa could serve as excellent 'poster children' for how the community can be mobilized and united to assess and organize our knowledge of marine microbial diversity, and how to employ that collected knowledge to design plans for future investigations that might plumb the depths

of marine microbial diversity. In addition to great ecological/biogeochemical significance, protistan species and activities impact human economies (both positively and negatively) and human health. Much could be done to use that importance as a selling point to foster the efforts of ICoMM and garner additional resources to maintain its activities into the future.

Specific objectives of this first meeting of the MEWG included identifying datasets that might contain information on marine microbial eukaryote diversity, to outline goals for linking molecular and morphological data on these species, to discuss strategies for further identifying and compiling legacy data (both published and unpublished), to discuss how the ICoMM's assessment of microbial eukaryotic diversity might complement and interact with the barcoding for microbial eukaryotes, and to begin to identify mechanisms for mobilizing funds to accelerate a census of marine microbial eukaryotes.

### **Short Invited Presentations:**

**Linda Amaral Zettler** provided an overview of the ICoMM initiative and its complementarity to the Barcode of Life project. She described the inception of the ICoMM in late 2004, its relationship to the Census of Marine Life (CoML), and the overarching scientific questions being addressed within the ICoMM program. Linda stressed the international flavor of ICoMM as an organizational framework for exploring microbial diversity, and described the general missions of the other working groups within ICoMM (Open Ocean and Coastal Systems; Benthic Systems; Technology; Informatics and Data Management).

**David J. Patterson** provided an overview of the emerging Encyclopedia of Life, and its relationship to some existing informatics and repository projects encompassed by, or intersecting with, the ICoMM. These included Plankton\*net, MICROBIS and Micro\*scope. Micro\*scope (<http://microscope.mbl.edu>) is a communal repository of images of microorganisms in an editable multi-classification environment). MICROBIS (<http://icomm.mbl.edu/microbis/>) is a communal repository of information on all marine microbes including identifiers, information on time and location and was designed to hold environmental attributes. Plankton\*net (<http://planktonnet.awi.de/>) is a collection of distributed databases on marine microbes curated by individual laboratories worldwide. Paddy described EOL (<http://www.eol.org>) as a communal enterprise to create a web site that will provide information for every living species on the planet.

**Jan Pawlowski** discussed the diversity of benthic foraminifera and amoebae in the context of the known, unknown, unknowable. Jan noted the present disparity in taxonomic information based on morphology and that based on DNA sequences. He stressed the need for taxonomic revisions coupling molecular and morphological data. Studies in his laboratory attempt to bridge this divide by combining images and DNA sequencing of individual specimens. To date, his laboratory has produced some 8,000 benthic foraminiferan DNA extracts, and more than 1,000 partial 18S sequences among

300 genetically different species. Partial sequences of ITS rDNA, LSU, actin and beta-tubulin also exist for some specimens. There are approximately 5,000 modern (60,000 fossil species) described species of foraminifera (the vast majority are benthic species). Assessments of species diversity are based on micropaleontological-type studies based on dead or Rose Bengal-stained 'live' assemblages. Virtually all types of marine environments have been explored. Important databases for these species include John Murray's database (2006) which catalogs some 2061 species in 198 studies. Also, Jan noted the tremendous diversity of deep-sea foraminiferan assemblages, and the great potential of the ODP database as a source of information. Jan provided the view that there is little evidence for a cosmopolitan distribution of benthic foraminifera. Jan also noted that there are approximately 67 described species of marine Amoebozoa (plus acanthamoebids in brackish water; information from Alexey Smirnov). Thirty-eight of these species are in culture, and molecular information is available for two dozen of them. No review or book on the biogeography of marine amoebae has been produced. Jan noted that important 'unknown' aspects of the diversity of benthic foraminifera and amoebae include: How should we define foraminiferan species? How many cryptic/synonymous species are there? How many foraminiferan species have global/endemic distributions? Among the perhaps 'unknowable' aspects, he noted: How many naked microforaminifera are there? What is the life cycle, ultrastructure and cell biology of most of the species?

**Colomban de Vargas** spoke of the diversity and biogeography of pelagic calcareous protists (planktonic foraminifera and to a lesser extent, coccolithophorids). These organisms play an important role in the global carbon cycle, and occasionally (in the case of coccolithophorids) form massive blooms that are visible via remote sensing capabilities. For planktonic foraminifera, only 50-60 morphospecies are known, and their biogeography is extremely well known from plankton tows, sediment traps and sediment cores because of the paleoclimatological significance of these specimens. The CLIMAP database (top cores) may represent a huge database for these species. The morphospecies concept may mask a significant biological diversity of planktonic foraminifera (cryptic species). DNA sequence information may also be problematic as foraminifera may possess multiple (divergent) rDNAs. For coccolithophorids, there are approximately 280 morphospecies, but half of these species may be haploid/diploid stages of the same species. The 18S gene may not be useful for species-level distinctions because it apparently has very little sequence divergence in coccolithophorids.

**Bob Andersen** presented information on microbial eukaryotes (i.e. protistan) culture collections and their role in ICoMM, and the importance of picoeukaryotes (usually defined as eukaryotes <2-3  $\mu\text{m}$  in size). There are approximately 200 culture collections that specialize in microscopic algae, and they are very active. In contrast, relatively few culture collections maintain protozoa and specialize in them, and they tend to be less active. Bob noted that for minute protists, their relatively simple morphologies mask a lot of diversity. There are  $\approx$ 100 described species of picoplanktonic protists (mostly described from sequence) but probably thousands have not yet been described. Sequencing (followed by culture and chemical/physiological studies) have established the existence of several new lineages of picoplankton, particularly among the photosynthetic

forms. The overall diversity of these species, their ecologies and biogeographical distributions are not known. Sequence information is expanding more rapidly than culture and classical descriptions, and molecular studies of picoplanktonic microbial eukaryotes have revealed a tremendous diversity of presently-undescribed taxa. There is a potentially important role of ICoMM as a mechanism for bringing together descriptions, photographs, drawings, electron micrographs, physiological and environmental information for these species. Bob also provided a short summary of the status of the Barcode of Life project, based on his participation at the June, 2007 meeting in Guelph, Canada.

**Seshagiri Raghukumar** spoke on the diversity of Labyrinthulomycetes and microbial eukaryotes in India. He noted the importance of mangroves as sites for fungal growth, and the dramatic impact of the southeast monsoons on the salinity of the estuaries on the west coast of India. Seshagiri recounted regional information on foraminifera (Rao), and ciliates (Kalvathi). He noted the potential importance of the permanent oxygen minimum zone in the Arabian Sea (150-700 m) as an environmental determinant in assessing regional diversity among microbial eukaryotes. Among the Labyrinthulomycetes, a major consideration for assessing diversity is that morphospecies descriptions require an examination of specific life cycle stages. There are approximately 50 known species, although the possibility of cryptic species is strong. There are 52 references that include most of the described species. They use a direct staining (acriflavine) technique for counting them in water samples. Staining approach yields about three orders of magnitude more than the culture approach ( $\approx 100/\text{liter}$  by culture,  $\approx 100/\text{ml}$  by acriflavine).

**John Dolan** discussed the extent and nature of information on the diversity of marine ciliates. Clearly, planktonic forms are dominated by 'naked' oligotrichous ciliates and tintinnids, but benthic ecosystems hold a tremendous diversity of ciliate forms and functions. John presented three large data sets describing tintinnid diversity in the South Pacific going back as far as 1929 and as recently as 2004. He demonstrated substantial differences in the diameter of the oral opening of the tintinnid assemblages sampled at these three times. John made the point that these morphometric features may provide valuable tools for interpreting climatic/ecological changes in ecosystems. Other microbial eukaryotes that form rigid structural features provide similar tools for examining climate-related changes (e.g. the extensive use of foraminifera, radiolaria, diatoms, chrysophyte scales, etc.).

**Demetrio Boltovskoy** provided an overview of radiolarian diversity, the status of our knowledge, and some of the problems associated with these species. He noted the problem of synonymous species among the described species, going back all the way to Haeckel's work. Identifying the developmental stages of a single species as multiple species has been a problem with these long-lived specimens. Demetrio described the work of the World Radiolarian Distributional Database (WoRaDD), a database being constructed in conjunction with the CMarZ group of CoML. Its goals include establishing the extent of radiolarian diversity and their distributions vis-à-vis water patterns in the global ocean. This enterprise includes an analysis of species diversity with latitude, coastal-oceanic distributions, water-sediment assemblages, and their

correlations. A summary of 1000 plankton tows (100,000 data points), 500 sediment traps (50,000 data points) and 2000 surface sediment samples (70,000 data points) contribute to this analysis. Demetrio noted the existence of some 100 publications that constitute sources of data, and about 900 species names (including conditional identifications). Demetrio (and Colombari de Vargis) noted that there has been very little molecular work on radiolaria, and no sequences of CO I presently exist.

### **Major Conclusions/Recommendations of the Working Group**

#### **1) Elevate the importance of microbial eukaryotic diversity in the ICoMM.**

The group spent considerable time discussing the role that eukaryote microbiology presently plays in ICoMM. This role was perceived by the working group to be minimal to none, but they noted that protists could and should constitute a major effort for the ICoMM. There was a strong consensus that the ICoMM has not moved forward on microbial eukaryotes in a way that it could have by this time, and it should now take substantive steps to elevate the visibility of microbial eukaryotes within the census' efforts. Microbial eukaryotes (specifically protists) represent a huge, presently untapped source of information on microbial biodiversity in the ocean. *There was very strong desire to see this situation rectified, and to see protistan species brought into the mainstream of ICoMM activities.* As a group, protists represent rich sources of information on microbial morphology, physiology and molecular (DNA sequence) information. Much of this information is readily available in the scientific literature, and some of it has already been summarized for some major taxa (e.g. radiolaria; see Boltovskoy presentation summary). Moreover, environmental information (legacy data) is rich for some of these species.

There was also discussion of the practical usefulness of showcasing microbial eukaryotes in the ICoMM initiative. Many of these species are morphologically complex and physically beautiful. They constitute excellent 'poster children' for describing the goals of the census and as an aid in facilitating support for the program. There are strong aspects of discovery, human and ecosystem health, and global climate change in the study and cataloging of microbial eukaryotes. For example, protists are a visible component of studies reporting the recent discovery of many uncultured/undescribed species in oceanic realms throughout the world, at hydrothermal vents and in anoxic ocean basins. In addition, many of these species have immediate value as tangible examples of the threats to humans and ecosystems posed by ballast water transport and occurrence of harmful alga blooms (e.g. red tides). Finally, these species play central roles in global climate change studies vis-à-vis the fate of polar ecosystems and proposed schemes for ocean fertilization and carbon sequestration. The ICoMM should make use of these taxa as illustrative material when explaining its mission.

#### **2) Catalog all named marine protists by 2008**

*A significant initial near-term goal for the ICoMM would be the collection of all protistan names across all of the many protistan lineages that inhabit the ocean.* This cataloging effort will not resolve some issues of protistan taxonomy (i.e. cryptic and synonymous species), and it will not address the identity of many newly discovered

uncultured/undescribed species being detected through sequence studies. However, if made available in a suitable on-line environment, it would facilitate those developments, and it would provide a tremendous amount of information to begin a census of marine microbial eukaryotes. Following (or during) the collection of all protistan names, biogeographical information and legacy data collection should be captured. This latter component of the census of marine microbial eukaryotes could produce a notable product for the ICoMM by 2010. This effort should be co-ordinated with the WoRMS (world Catalog of Marine Species) project being led by Mark Costello and Edward vanden Berghe.

Taxonomic information for protists is varied in characters. It includes morphology (the traditional taxonomy), molecular (mostly rDNA sequences, but also other genes), pigment composition and physiological abilities (particularly for picoplanktonic algae). A major goal within the census should be linking morphology-based taxonomies to molecular and physiological taxonomies. Construction and coordination of this massive database would be an overwhelming undertaking for any single lab, although small contributions from many individual laboratories could play a huge role in identifying sources of material for the database. *The ICoMM could and should play a pivotal role in facilitating the population of a microbial eukaryote database.* For example, developing and advertising a mechanism for coordinating the collection and deposition of protistan data into MICROBIS and Micro\*scope would provide a vehicle for entraining numerous investigators as informal collaborators. Such a structure would then be available to inform the Encyclopedia of Life.

The working group members noted that the development of a 'skeleton' database for the microbial eukaryote component of the ICoMM might be focused around protists presently contained in formal culture collections. These collections are numerous enough (see presentation by Andersen) to provide a reasonable diversity of taxa to begin the census, and represent some of the most intensively studied species. Therefore, these species would allow the development of a format for the database that would encompass the disparate types of information. Finally, the existence of a 'template' for the database would provide a useful example of the type of information for which the census is looking.

### **3) Facilitate the transfer of biogeographical data to the ICoMM database**

The working group concluded that some of the difficulty with soliciting participation in ICoMM probably relates to the fact that the community really does not understand what kind of information is desired from them, nor can they afford to spend large amounts of time collecting and entering information into an ICoMM database. Both may be significant impediments to participation in the ICoMM. Resources should be earmarked for the technical assistance that will be required to put together the skeleton website/database noted above, and to put in place a mechanism and the physical support (i.e. people and a pipeline) to aid the acquisition of information into the ICoMM database. A physical template, or skeleton database, would address the issue of 'what' is needed. The presence of a way of supporting data acquisition (e.g. via a search engine that might aid in identifying and downloading information on particular protists) would

lessen the time commitment of collaborators and thereby hopefully improve participation in the census. Therefore, the working group strongly recommends that significant resources be designated for these tasks.

#### **4) Capture legacy data for all protists**

There was also clear agreement on the importance of capturing legacy data ('What is known') for microbial eukaryotes. ICoMM has a mandate to capture that information for marine protists. Nonetheless, the working group noted that for many well-described species, this information is widely dispersed in the literature. This situation further indicates the importance of an automated or semi-automated means of searching and acquiring information on protistan species by electronic means. ICoMM should work with the Biodiversity Heritage Library to ensure that the relevant literature is digitized and made available on line for scrutiny.

#### **5) Engage a broad spectrum of taxonomic specialists to capture existing information on protistan diversity**

The MEWG recognized a dire need to develop a global consortium of microbial taxonomists in order to meet the goals of the census. Taxonomic specialists are vital for assessing the diversity of any group of species, but the situation is unique and critical for protists. First and foremost, expertise in morphology-based taxonomy is waning within the community. Most new information that is being acquired is DNA sequence information, and there is a critical need to relate that information back to morphospecies before that expertise disappears. ICoMM/EoL might play a vital role in addressing this issue. Second, protists are an incredibly diverse collection of microbes, and each group employs unique morphological features as taxonomic criteria, which in turn require unique collection, processing and observation to assess those characters. Therefore, protistan taxonomists are many, and possess unique bases of taxonomic knowledge. It is necessary to access virtually all of this expertise to properly construct a census of marine protists. A very brief summary of some of these taxonomic specialists was produced by the working group (see Appendix I), but a much more complete list will need to be developed.

Effectively utilizing this expertise in the development of a protistan database will present logistical challenges. One possible scenario that was discussed would be a three-step process. A group of experts for each protistan group could be brought together to compile information on each taxon. That information would then be entered in the ICoMM database by ICoMM staff and made available through the internet. The taxonomic authority(s) could then enter the database and validate the information. This process would minimize the level of effort required by the experts. It was unanimously agreed by members of the working group that an electronic database of protists developed around 'species-pages' would be of tremendous value and a truly unique accomplishment that the ICoMM can provide to the scientific community.

#### **6) ICoMM should partner with culture collections to foster cultures, cryopreservation methods for unispecies cultures or perhaps entire microbial communities in order to maintain voucher material for future studies.**



Microbial species present unique problems with respect to the establishment, preservation and maintenance of voucher specimens. Formal, well-supported protistan culture collections represent both a source of species, as well as a source of knowledge on the most appropriate methods for long-term maintenance of voucher material. Several types of analyses might be required of voucher material in the future to address morphological, physiological or molecular (DNA sequence) aspects of a species. Optimally, frozen viable protistan cells would be the best source of material, but not all protistan cells survive present freezing procedures. Support for and collaboration with culture collections to foster research on new protocols for cryopreservation would greatly help the overall census initiative.

**Other Questions/Issues Raised and Discussed by the Working Group:**

A variety of issues and questions related to the recommendations detailed above were raised during discussions within the MEWG meeting. These issues were not resolved, but some of them provide insight into the thinking of the working group.

*454 tag sequencing.* The diversities of marine microbial assemblages (bacterial, archaeal and eukaryotic) are immense. For eukaryotes, the assessment of marine microbial eukaryotic diversity presents unique issues that relate to the immense variety of protistan forms and the consequent need for several different taxonomies for the various groups. As a result (and analogous to the situation for bacteria/archaea) investigators have turned to DNA sequences as a tool for assessing protistan diversity.

ICoMM has aggressively promoted the use of 454-based tag sequencing for assessing microbial diversity. This is understandable given the enormous diversity revealed by the initial applications of this tool to natural samples. The 454 approach is perhaps the only extant approach that offers the potential to estimate the total diversity of microbial assemblages in nature. The information it yields will be vital to developing scientific research agendas. Moreover, the use of 454 (and other sequencing approaches) will facilitate the establishment of molecular identifications for protistan taxa. This will ultimately allow more automation in the analysis of natural samples and therefore is highly desirable. Nonetheless, there was a perception expressed by members of the MEWG that the diversity of marine microbes is now embodied solely by the 454 and what it can do. This is not the case for microbial eukaryotes. While 454 may constitute the cutting edge of microbial diversity analyses for the foreseeable future, for protists, visual information (drawings, light micrographs, electron micrographs), cultures and physiological information also need to become a part of the ICoMM effort.

*'Big' questions that remain.* The working group identified a number of important questions that should be the focus of discussion in future meetings, and that will be the focus of future studies of microbial eukaryotes, either within ICoMM or other initiatives. Some of these questions represent long-standing questions in ecology, geochemistry and other fields, but the existence of the ICoMM brings some of these questions into focus and perhaps within reach of being answered in the not-so-distant future. These questions included: How does the choice of a gene for studying microbial diversity affect our understanding of the diversity of that assemblage? How does diversity of a microbial

community relate to function? What are the appropriate scales of measurement for assessing microbial diversity? How do vastly different spatial/temporal scales in the ocean relate to species diversity and biogeography?

## **Appendix I.**

**List of taxonomic specialists.** A discussion was conducted near the conclusion of the workshop to provide a (very) preliminary list of taxonomic experts that might be enlisted to reconcile information collected from the literature on various protistan taxonomic groups. These specialists, and others as they are identified, might be consulted for vetting species names obtained during the aggregation of all protistan species names.

<u>Taxonomic Group</u>	<u>Taxonomic Experts</u>
Ciliates	Agatha, Dolan, Montagnes, Lynn, Foissner, McManus
Forams	Pawlowski, De Vargas, Habura, Bernhard, Bowser
Acantharia	Amaral-Zettler
Radiolaria	Boltovskoy, Takahashi, Dolven
Amoebae	Smirnov, Andersen, Patterson, Amaral-Zettler
Dinoflagellates	Montresor, Moestrup, Hallegraeff, Tomas, Larsen, Gomez
Diatoms	Koistra, Mann, Kociolek, Moestrup
Other Algae	Moestrup, Andersen, Young, Inoyue, Kawachi, Hoef-Emben, Simon, Edvardsen
Parasites	Leander, Guillou, Coats
Microfungi	Raghu, Honda, Coats, Fell
Heterotrophic flagellates	Leadbeater, Smirnov, Won-Je Lee, Patterson
Culture Collections	ATCC, CCMP, CCAP, many others

### **Meeting Participants:**

**David Caron** (Chair), University of Southern California, USA (dcaron@usc.edu)  
**Demetrio Boltovskoy\***, Universidad de Buenos Aires, Argentina  
(demetrio@bg.fcen.uba.ar) (attended by phone)  
**Jan Pawlowski**, University of Geneva, Switzerland (jan.pawlowski@zoo.unige.ch)  
**John Dolan**, Station Zoologique Villefranche-Sur-Mer, France (dolan@obs-vlfr.fr):  
**Colomban de Vargas\***, Station Biologique Roscoff, France (vargas@sb-roscoff.fr)  
**Seshagiri Raghukumar**, Myko Tech Pvt. Ltd., India (s\_raghukumar@mykotech.com)  
**Robert Andersen**, Bigelow Laboratory, USA (randersen@bigelow.org)  
**Linda Amaral-Zettler**, ICoMM Secretariat, MBL, USA (amaral@mbl.edu)  
**David Patterson**, ICoMM Scientific Organizing Committee Member, MBL, USA  
(dpatterson@mbl.edu)

\*Demetrio Boltovskoy and Colomban de Vargas are Census of Marine Zooplankton (CMarZ) representatives to the MEWG. John Dolan and Jan Pawlowski are also members of the CMarZ project.

### **Members not in attendance:**

Daniel Vaultot, (vaultot@sb-roscoff.fr); picoeukaryotes  
Tomoko Yuasa, (r046003n@u-gakugei.ac.jp): Radiolaria/Acantharia and general  
microbial eukaryote surveys in Japan  
Alex Worden, (aworden@rsmas.miami.edu): picoeukaryotes  
Thorsten Stoeck, (stoeck@rhrk.uni-kl.de): anaerobic eukaryotes

### **Meeting Agenda:**

#### **Monday, July 9<sup>th</sup>, 2007**

Breakfast on your own at the Comfort Inn

0800: Transport to Bigelow Laboratory

0930: Linda Amaral-Zettler: ICoMM: Unveiling the Ocean's Hidden Majority

1000: David Patterson: micro\*scope, MICROBIS, and EOL

1030-1100: Break

1100-1115: David Caron: Charge to ICoMM Working Group: What do we currently  
know about Marine Microbial Eukaryotic Diversity?

1115-1145: Jan Pawlowski (Benthic Foraminifera/Amoebae)

1145-1215: Colomban de Vargas (Calcareous Protists including Haptophytes)

1215-1330: Lunch

1330-1400: Robert Andersen (Culture Collections and picoeukaryotes)

1400-1430: S. Raghukumar (Thraustochytrids and Micro Euk surveys in India)

1430-1500: John Dolan (Ciliates)

1500-1600: Coffee Break – Open to Bigelow colleagues

1600-1700 Dave Caron – Summary

Transport to the Tugboat Inn

1830-2000: Dinner at the Fisherman's Wharf Restaurant

#### **Tuesday, July 10<sup>th</sup>, 2007**

Breakfast on your own at the Tugboat Inn

0830: Transport to Bigelow Laboratory  
0930-1000: Demetrio Boltovskoy: Radiolaria (via teleconference)  
1000-1030: David Caron: Review/ Identifying gaps: The Unknown and Unknowable  
1030-1045: Break  
1045-1200: Usefulness of data to the community  
12:00-1300: Lunch  
1300-1500: Short term, Midterm and Long-term goals for Microeuks in ICoMM  
1500-1700: Tour of Bigelow Culture Facility  
Meeting ENDS  
Dinner provided at the Tugboat Inn