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Improving genomic resources for copepods - a key requirement for the advancement of copepodology in the 21st century

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MONOCULUS Copepod Newsletter

The Newsletter of the World Association of Copepodologists

Number 52

November 2006

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Message from the President

Dear copepodologist:

Why and how did you become a copepodologist? Did you aim to be a copepodologist from your university days or earlier? My career as a copepodologist comes from many accidental happenings. I deeply thank God for these unexpected things to guide me presently to a president of the WAC. It is my happiness to interact with all WAC members who may have had a variety of stepladders to become a copepodologist.

The failure of spawning of the red spotted groupers in my undergraduate thesis work obliged me to work with planktonic copepods. The Inland Sea of Japan, where my university is facing, was a Mecca of fish aquaculture in the late 60s and early 70s, when aquaculture techniques rapidly advanced, primarily thanks to success of rotifer (*Brachionus*) mass culture and artificial fertilization of commercially important fish species. I dreamed to be a fish farming specialist. I built a bed above the fish tank, and kept watching the spawning behavior the whole day over the summer. Poor fish! They did not spawn. Then, my advisor, a marine cladoceran specialist, advised me, "Why don't you study copepods?" If the fish had spawned, I would never have become a copepodologist.

The next important thing to direct me to a copepodologist or biological oceanographer was my one-year stay at the Scripps Institution of Oceanography. Although my paper exam score was very low, I was fortunate to be selected as an exchange student. My brain was just like a sponge to absorb new knowledge in biological oceanography and English. Professors and students around me were so wonderful that I was eager to meet them again after I left from Scripps. Then, I decided to aim to be a university professor, when I was 25 years old.

Life is always full of unexpected things and meetings with new people. There is a Buddhism term of 'en', which means a relation, or a function to make a cause and consequence relation stronger. My previous 'en's have made me what I am today as a copepodologist. I now enjoy the wonderful 'en' to interact with WAC members.

— Shin-ichi Uye, President
Hiroshima University, Japan



WAC members and spouses assembled during the dinner in honor of Kurt Schminke. Left to right: Gritta Veit-Köhler, Setsuko Uye, Shin-ichi Uye, Kai-Horst George, Pedro Martínez Arbizu, Thomas Glatzel, Gisela Schminke, Sybille Seifried, Claudia Halsband-Lenk, Janet Reid, Gisela Moura, Jutta Glatzel, and Horst Kurt Schminke. Not shown: Hildegard Juhl. (Photo from Claudia Halsband-Lenk.)

Kurt Schminke Retires

Prof. Dr. Horst Kurt Schminke, zoologist at the Institute for Biology and Environmental Sciences at *Carl von Ossietzky* University Oldenburg, retired on 29 September 2006. On that day a Biodiversity Symposium was held in his honor. The meeting was arranged by his wife, the closest colleagues of his research group *Zoosystematics & Morphology*, present students, former doctoral and diploma students and candidates for the state examination, as well as by numerous academic companions at home and abroad, who have accompanied him throughout his studies and active years. With this surprise we honoured Prof. Schminke, who celebrated also his 65th birthday on 29 September.

“You are one of the first professors at Oldenburg University whom we biology students contacted”, said Tim Migawski and Sebastian Rakers in their laudatory speech on 29 September 2006. “During our first semester you gave us beginners, who had just left school, an understanding of zoology. In your introductory lecture *Phyla of the Animal*



Some of the participants in the Biodiversity Symposium honoring Kurt. First row, from left: Janet Reid, Virginia Museum of Natural History, Martinsville, U.S.A.; Horst Kurt Schminke, University of Oldenburg; Wilko Ahlrichs, University of Oldenburg. Second row, from left: Shin-ichi Uye, Hiroshima University, Japan; Prof. Wolfgang Wägele, Forschungsmuseum Alexander König, Bonn; Michael von Tschirnhaus, University of Bielefeld; Thomas Glatzel, University of Oldenburg. (Photo by Wilfried Golletz.)

Kingdom we were fascinated from the very beginning by your ability to describe all animals, from tiny protists up to big mammals, without notes and with a multitude of Latin names that were still unfamiliar to us, in order to make us understand them better. For this purpose, you used manifold media: tables, blackboards, films and foils. We have been recalling especially the films about the common housefly or the English version *Colourful Cuttle*. They gave us the opportunity to casually check our English, which proved very beneficial later on” ...



Thomas Glatzel and Hilde Juhl, long-time volunteer for the Monoculus Copepod Library, at the dinner. (Photo by Jan Reid.)

Prof. Schminke studied biology, Romance and Slavic languages and literature in Kiel and Tübingen. After the state examination for the secondary teaching profession he took his doctor's degree with his thesis entitled „Evolution, System und Verbreitungsgeschichte der Familie Parabathynellidae (Bathynellacea, Malacostraca)“ [Evolution, system and history of dispersal in the family Parabathynellidae (Bathynellacea, Malacostraca)] and habilitated in Kiel in 1979 with his thesis entitled „Die „Zoea-Theorie“ der Entstehung der Bathynellacea (Crustacea, Syncarida)“ [The “Zoea theory” of the development of Bathynellacea (Crustacea, Syncarida)]. In the very same year (winter semester) he accepted a call to Oldenburg University for the chair of Zoology with a focus on Zoomorphology, which he had taken over already in spring (summer semester) as a deputy. He was dean of the Biology Department from 1980 to 1982 and vice-president of Oldenburg University from 1982 to 1984.

His main fields of research are phylogenetic systematics, functional morphology, evolution and biogeography of crustaceans (Bathynellacea) and copepods (Copepoda).

In particular, he clearly and vehemently represented the interests of systematics and biodiversity in the realms of science and politics in Germany. In collaboration with his companions he achieved the following results:

- The World Association of Copepodologists (WAC) including the Monoculus Copepod Library and the newsletter MONOCULUS; he was president of this society from 2002 to 2005.
- A cooperative agreement between the Alfred Wegener Institute (AWI) in Bremerhaven and *Carl von Ossietzky* University of Oldenburg since 1986.
- The Osnabrück/Oldenburg summer school for Systematic Zoology since 1989; for many years, one-week intensive laboratory courses were performed to impart systematic-ecological knowledge and working methods several times per year. Each course was devoted to a certain group of animals and was carried out by a recognized expert.
- The Association of Biological Systematics (GfBS); he was the founder president of this society from 1997 to 2000.
- The study group *Zoologische Systematik* within the Deutsche Zoologische Gesellschaft (DZG) (German Zoological Society).
- The journal *Organisms, Diversity and Evolution*.
- The German Centre for Marine Biodiversity Research [Deutsches Zentrum für Marine Biodiversitätsforschung (DZMB)] in Wilhelmshaven since 2000, in association with the federal states Niedersachsen (Lower Saxony), Hessen (Hesse) and Hamburg, with a cooperative agreement between the research institute Senckenberg, Frankfurt, and *C.v.O.* University of Oldenburg; in collaboration with teachers of the AWI, Senckenberg am Meer, and the DZMB this led to the major field of study *Marine Biodiversitätsforschung (Marine Biodiversity Research)*, which was established at *C.v.O.* University of Oldenburg in the winter semester 2003/04.

All of these initiatives are still crowned with success, because they fill the thirst for knowledge and the fundamental requirement of communication between established scientists and students.

Meanwhile, eight species from various animal groups: Isopoda, Coleoptera, Amphipoda, Acari, Copepoda, and Bathynellacea bear Prof. Schminke's name. The first species of crustaceans (Bathynellacea) found in India in groundwater recently, *Habrobathynella schminkei* sp. nov., has also been dedicated to him and has been named after him in recognition of his academic merits.

— Thomas Glatzel
Carl von Ossietzky Universität Oldenburg, Germany
and
Jan Reid

Monoculus Library Moved to Wilhelmshaven

Dear Copepodologists:

The Monoculus Library moved in 2006 from the University of Oldenburg to the Senckenberg Research Institute, Department German Center for Marine Biodiversity Research, in Wilhelmshaven.

Please keep sending your reprints to the Monoculus Library at the new address below. Electronic formats like PDF are becoming the format of choice of many journals instead of reprints. Therefore we would be happy to get reprints in PDF format also.

You can submit your electronic reprints and your queries for copepod literature to pmartinez@senckenberg.de. Please write in the subject the word "monoculus." This will help for automatic sorting of the mail.

Thank you!

— Pedro
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9th International Conference on Copepoda Status of Proceedings Volumes

Dear colleagues,

Hope that you are fine since our last meeting in Tunisia. It was great to meet you in Tunisia and hope seeing you soon. I started 2006 with some health problems, but now everything is fine and we wish to keep our preliminary schedule to have at least the first proceedings in the *Journal of Plankton Research* printed out during 2006 (1 year after the conference).

It is now time to finalise both proceedings and have them published this year (at least one of them). The first proceeding in the *Journal of Plankton Research* is almost done. Many thanks again to Kevin and Aditee for their great help, to all contributors and of course to my co-guest editors

for this issue, Néjib and Jiang. About the second issue, many thanks to Geoff Boxshall who is now working hard to get it ready for *Hydrobiologia*. Sorry to many colleagues that I have not answered about the second proceedings; you will receive an email from Geoff Boxshall very soon.

We are trying to help as much as possible all colleagues to get their manuscript published or improved. It is logical to delay a little the second special issue, so some manuscripts can have another chance to be published in our proceedings. Thank you for your understanding,

If you have a more personal question, please feel free to send an email to my regular email box: Sami.Souissi@univ-lille1.fr

Many thanks for your participation in the 9th ICOC. The web site will be updated during the next weeks.

Best wishes

— Sami Souissi

There have been significant delays in the preparation of the second volume of our conference proceedings – which will be published in the journal *Hydrobiologia* – but we do now have a timetable for the final stages of editing and production of this volume. All authors who submitted manuscripts should have been contacted during October to explain the situation.

The editor in chief, Professor Koen Martens, has confirmed that *Hydrobiologia* is still interested in publishing this volume. However, he emphasised that papers must conform to the newly defined scope of the journal. Specifically, the editorial board has determined that *Hydrobiologia* no longer accepts descriptive taxonomy papers unless they contain a significant component of biogeography or phylogenetic analysis. All conference proceedings published by *Hydrobiologia*, including ours, are subject to this restriction. This is non-negotiable. The proceedings editors are guest editors and we are only able to provisionally accept papers “subject to final acceptance by the editor in chief”.

The deadline for final submission of all reviewed and revised manuscripts will be 15th December 2006. I request all authors to pay particular attention to formatting the text and the references into the correct journal style. *Hydrobiologia* has a very efficient electronic proofing system and we expect publication in mid 2007.

— Geoff Boxshall,
Mohammed Néjib Daly Yahia & Sami Soussi
(guest editors)

A Copepod Genome Project: Opening Discussion

At the Tunisia meeting in 2004, Stewart Johnson and James Bron assembled a group of WAC members who were interested in working toward a common goal of sequencing a genome and/or expressed sequence tags of a copepod's genome. James delivered a presentation in which he introduced many of the issues that we copepodologists would have to consider to make such an endeavor a success. The two letters below describe different parts of this problem. Both letters have among their goals educating the copepod community about how genomics can further study of copepods, sharing ideas and perspectives, and soliciting input.

Improving Genomic Resources for Copepods – A Key Requirement for the Advancement of Copepodology in the 21st Century

James E. Bron, Grace A. Wyngaard
and Stewart C. Johnson

Introduction

With more than 11,500 species (Humes, 1994), and arguably the most numerous of the world's metazoans, copepods carry a global biological importance that is belied by their generally small size. Copepods are key components of food webs, major food sources for important fishery species, and conduits of global energy transfer pathways. In addition, copepods may pose ecological threats as invasive species, are important as major parasites of wild and cultured organisms, and may act as carriers of disease organisms of medical and veterinary importance. Because of their diversity and global representation, copepods may also serve as key environmental indicators of anthropogenic pollution and climatic change.

Rationale for a Copepod Genome Project

Genomics is broadly defined as the comprehensive study of the interactions and functions of whole sets of genes and their products. The development of genomics resources for copepods is of interest not only to molecular biologists and geneticists, but is also of concern to all researchers whose work touches on copepod biology and ecology (reader – this means you!). By this we mean that the existence of genomic resources, *i.e.*, gene / protein sequences, informs the broadest possible spectrum of research disciplines. Areas that will benefit from the development of copepod genomic resources are those that involve the study of: 1) biosystematics / biodiversity, 2) phylogeny, 3) population genetics, 4) key biological processes, *e.g.*, respiration,

reproduction, excretion, detoxification, energetics, nutrition, environmental adaptation, immune function, host-parasite interactions, *etc.*, 5) bioactive compounds from copepods for medical and other uses, 6) copepods as bioindicators of, *e.g.*, climate change / pollution / pathogen exposure and 7) a wide variety of other disciplines (enter your particular discipline here...).

One example of the utility of genomic resources involves DNA microarray technology. This technology allows for the simultaneous study of the expression levels (transcription profiling) of very large numbers of genes (up to hundreds of thousands), providing information concerning which genes are up-regulated and down-regulated at any particular moment in an organism's life-cycle. This approach, for example, allows one to probe the physiological responses of organisms to variables such as temperature, salinity, pollution, predation, *etc.* Sequencing and identifying large numbers of genes would greatly facilitate the use of microarray technology. Genes related to the biological processes of interest would be printed onto glass slides (arrays). Samples would then be taken from a copepod (population, individual, tissue or individual cells), sampled at a specific point in time or under a particular physiological or behavioural state. Complementary DNA (cDNA) or amplified RNA, both copied from a template provided by the messenger RNA (mRNA) extracted from the samples, would then be labelled and hybridized onto the arrays to compare levels of expression. Microarray studies could be coupled with quantitative trait locus (QTL) mapping studies to link the genes with particular functions and traits. A number of groups working on copepods have successfully applied such a microarray approach to the exploration of physiological adaptation, speciation and host-parasite interactions.

Copepod genomics resources will also enable the application of other technologies to their study. The proteome can be defined as the full set of proteins encoded for by the genome. The field of proteomics allows for the qualitative and quantitative comparison of proteomes under selected conditions, with the goal of determining the biological processes at work. Because the identification of proteins requires sequence information, the development of copepod genomics resources is crucial for those wishing to apply proteomics to copepod studies.

The above notwithstanding, it is not desirable, efficient or logical to expect the development of whole genome sequences for all copepod species. It is clear from early genome sequencing examples, *e.g.*, the fruit fly *Drosophila melanogaster* and the nematode *Caenorhabditis elegans*, that the establishment of tractable model species, which possess supporting genomic and proteomic resources, helps to augment the scientific utility and therefore visibility of such organisms across the board. This is often accompanied

by an increase in general interest and funding across research disciplines. The latter observation with respect to funding follows from the increasing realisation that genomic and proteomic studies must eventually be rooted in classical biological disciplines, in order to draw sense from the overwhelming quantities of data generated by current technologies.

There are a number of strategies for establishing genomic resources for any organism or group of organisms. The most complete and expensive approach, is to sequence the full genomic DNA of the organism, which comprises both the coding (principally DNA that is transcribed into mRNA and translated into proteins) and non-coding regions (regions that do not contain instructions for proteins). Non-coding sequences contain regions of DNA involved in the regulation of coding regions as well as “junk DNA” (DNA with no currently understood function). Full genome sequencing provides: 1) a picture of the total genetic capabilities of an organism; 2) full-length sequences for genes; 3) information on the relationship of genes and the structural and control elements that are associated with them; 4) a template for interpreting sequences deriving from the same or different taxa; and 5) potentially unexpected discoveries on genomic architecture and molecular evolution. Alternatively, a second and substantially less expensive strategy is to sequence a large number of ESTs (Expressed Sequence Tags) from cDNA libraries. A cDNA library of an organism (or tissue thereof) contains the majority of the genomic information that is required for the production of all of its proteins under a defined set of conditions. Such a library is representative of the “transcriptome” of the organism, *i.e.*, those genes that are actively being transcribed into the proteins / peptides required under a given set of physiological / environmental conditions or at a particular moment in the organism’s life-cycle. In functional studies ESTs are often considered to be more targeted and therefore more efficient than the full genome approach. However, to ensure good representation of all of the genes within a genome, these studies must be conducted on cDNA libraries constructed for the widest possible range of biological states, *e.g.*, life-history stages, sexes, temperatures, nutritional states, *etc.* The disadvantages of this approach are: 1) that information on the structure and organization of the genome, genetic regions responsible for gene control and the full genetic capacity of the organism will be lacking; and 2) that the sequences obtained will be partial, so that a full-length sequence for any given gene must further be determined. The full genome strategy can perhaps be considered to be more generic than other approaches; however, such an approach is not only extremely expensive but also provides data from only a single or limited number of individuals of a single species. Whilst having a full genome sequence of any given copepod would greatly facilitate the genome sequencing of subsequent copepod species by providing a scaffold for

assembly, and a template for annotation, it is worth noting that assembly and annotation of a full genome itself relies upon the prior existence of extensive EST and other sequence resources (*e.g.*, cosmid and bacterial artificial chromosome (BAC) libraries).

The ideal approach probably comprises a combination of these two major strategies: sequencing the full genome of a single selected species, while building large EST libraries (>150,000 ESTs) for a variety of species of interest.

Current status of genomic resources

As can be seen from Table 1, only limited nucleotide and proteomic resources currently exist in the public domain for any species of copepod, and those nucleotides that do exist comprise principally 4-5 targets that are routinely used for phylogenetic studies, *e.g.*, 18S, ITS. Further sequences exist in private libraries; however, such collections do not directly benefit the larger community. The cost of full genome sequencing depends largely upon the actual genome size of the organism to be sequenced. For those copepods listed in publicly accessible databases, genome sizes range from an estimated 137 Mb (million base pairs) for *Cyclops kolensis* to 12,186 Mb for *Calanus hyperboreus*. These figures compare to the human genome, which is estimated at 3,423 Mb, and that of the fruit fly *D. melanogaster*, which is estimated at 180 Mb (Gregory 2006).

Table 1. Nucleotide and protein sequences for metazoan species in public-access databases, illustrating the poor representation of Copepoda relative to their importance as a group (data from NCBI Taxonomy Browser, 20/08/06).

	Nucleotide Sequences	Protein Sequences
Metazoa	55,865,421	1,561,653
Vertebrata	47,788,354	1,113,542
Arthropoda	3,890,583	285,984
Hexapoda	3,669,110	261,429
Crustacea	104,269	14,252
Malacostraca	82,565	8,363
Copepoda	2,677*	1,582

*Calanoida 853, Cyclopoida 258, Harpacticoida 522, Poecilostomatoida 145, Siphonostomatoida 867.

Selection of model species

For the full genome sequencing approach, the expense involved ensures that very few copepod species can be chosen for sequencing. When asked to suggest the ideal model species, most researchers will immediately make a good case for the species they work on (using the “my species is best” criterion); however, in order to provide a community-wide resource, it is essential to consider a wider range of criteria upon which to base such a critical decision.

Some of the characteristics of a candidate organism for genome sequencing that might be considered to be important are:

- Potential relevance of the chosen species to the maximum number of researchers, and its ability to contribute to key areas of research in copepod biology.
- Broad “real-world” relevance (*e.g.*, major constituents of plankton, benthos or having a high economic impact or involvement in the aetiology or transmission of disease in other organisms).
- A substantial existing knowledge-base in terms of, *e.g.*, basic biology, ecology, physiology, genetics, *etc.*
- The species should ideally be amenable to laboratory culture and manipulation.
- The species or close relatives should show a global distribution and be maximally available to interested research groups.

Other, more difficult questions can also be asked: *e.g.*, is it better to study a species with a smaller genome, which is cheaper to sequence and more tractable but which may lack key genes or gene groups; or to study a larger genome, as advocated by the comparative genome evolution working group (<http://www.genome.gov/12511814>). A larger genome may display a more complete gene set (or more “junk”?) but may be less easy to work with. Also should one target an ancient / less specialised group or a more modern, possibly more highly-specialised group? There are also features that might make a species more useful in terms of culture, portability or ease of observation, *e.g.*, robustness, a rapid life-cycle, an easy, well established culture system (freshwater vs. seawater, feeding requirements, temperature requirements), portability, *e.g.*, having diapause eggs, established cryopreservation techniques or broad geographic distribution. The size of adults affects such considerations as ease of physical manipulation (large=better) and ability to observe microscopically or process for antibody or *in situ* nucleic acid labelling techniques (small=better). Although not a necessity, the ability to produce inbred lines would also assist genome sequencing and gene mapping and association studies for ascribing functions to genes.

Finally, and perhaps a requirement that may sadly obviate all the others, is the ability to obtain funding for a full-scale sequencing project, which may often depend on the perceived “importance” of an organism, this in turn largely depending on the direct economic impact of the organism in the eyes of national governments, international funding consortia and other larger funding agencies. In these terms, aspects of copepods that may help to garner funding include: 1) the “insects of the sea” argument, 2) the fact that they are key components of the food chains that lead to commercially important species and similarly comprise a key component of global energy transfer pathways, 3) their potential as key

environmental indicators of such processes as anthropogenic pollution and climatic change, 4) biosecurity concerns for some invasive species, 5) their importance to global biodiversity studies, 6) their role as important pathogens of wild and cultured organisms, 7) their role in transmission of disease to other organisms, *e.g.*, humans, and 8) their potential to provide products of interest to biotechnology.

The Way Forward

The mechanism and source(s) of funding largely depend upon the type and scale of project proposed. Costs for a full genome sequencing project may run from several millions of pounds for a small genome to tens of millions of pounds for a large genome (dollars US), hence there are more limited possibilities for full / partial funding or undertaking the work, which include national institutions such as the Sanger Institute (U.K.), NCBI, TIGR and DOE-JGI (U.S.A.) and possibly other international funding bodies such as the European Union. More limited projects comprising the creation of large EST libraries for one or more species may be funded through national research funding councils such as BBSRC and NERC (U.K.), Genome Canada (Canada) and NRC (U.S.A.). Each of these will have its own interests and strictures for funding; however, a requirement for any community-based sequencing program must be that sequence data be publicly accessible as soon as possible. The structure of a project depends again upon the overall approach and the project objectives, such that a project could function under the auspices of an informal or structured consortium or might alternatively require a fully structured organisation with a formal project management team. In the case of a full genome sequence, the latter would be a necessity.

The way forward begins with members of the copepodology community having sufficient interest to lend support to the concept of a copepod genome project. A number of independent genome-sequencing initiatives have already been proposed (see below for a description of one such initiative); however, this should not dissuade members of the community from coming together for discussion and participation in wider, community-led initiatives. In order to undertake such a project, the community needs to complete a number of tasks, which include: 1) the identification of interested parties; 2) the development of a strategy for advancing the proposal, including the selection of individuals or organisations willing to champion the cause; 3) the identification of the principal copepod(s) of interest; 4) the identification of funding sources; 5) the production of an outline plan (white paper) that identifies the need for a genome, the approach to be taken, the organisations / individuals involved and the plans for dealing with such issues as public access, genome annotation, curation, bioinformatics support, database management, training considerations and web resource development; and 6) the

development of a communications strategy and associated network in order to keep interested parties informed of progress. One major hurdle in the process described above is the establishment of a consensus concerning the best initial copepod(s) species to be sequenced. Perhaps the best approach to such a problem is the establishment of an independent committee supported by experts from within and external to the copepodology community who may make a balanced and informed decision on the community's behalf.

Given the extended timescale of a full-genome sequencing project, no given copepod species can currently be considered to be substantially ahead of the field in terms of the availability of genomic resources or progress towards a funded genome project, although some species do possess genomic resources that may help to form the basis for prospective genome projects. For this reason the authors would be delighted to receive comments, suggestions or notes of interest from members of the community or to answer questions relating to the establishment of or use of genomics or proteomic resources (no hate-mail please).

— James Bron
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and
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Dear Colleagues,

In their letter, James Bron, Grace Wyngaard and Stewart Johnson advocate the need for a dialogue for building the genomics resources for copepod research. They also eloquently describe the criteria that should be used for selecting species for comprehensive genome and EST sequencing projects. These include factors such as genome size and complexity, wide geographic distributions to maximize accessibility to investigators worldwide, and ability to generate inbred lines. In addition to these criteria, we should also consider the specific questions or problems that we would like to address. Advances in functional

genomics are enabling us to move fairly quickly from descriptive genome sequencing to identifying the functions and interactions of genes, conferring the ability to address problems across a wide array of disciplines in biology at a mechanistic level.

In this letter, we would like to share with you our plans for sequencing the genome of the calanoid copepod *Eurytemora affinis*. We first discuss why we chose this species as a model organism, then we describe how this copepod genome project will facilitate future copepod genome sequencing projects, and finally, we make recommendations on how to build a community of researchers that could utilize genomic tools to address a variety of questions in copepodology. We highly encourage the copepod community to begin discussing what other genomic resources would benefit research in copepod biology. Insights into morphology, ecology, and evolution on copepods will be greatly enriched by having genomic resources for multiple copepod species.

The copepod *Eurytemora affinis* serves as an excellent model for addressing fundamental questions in ecology and evolutionary biology, including those regarding adaptation, speciation, morphological stasis, niche evolution, biological invasions, and host-pathogen coevolution. *Eurytemora affinis* is a key component of subtropical and temperate estuaries throughout the Northern Hemisphere. This copepod is a major grazer of algae and serves as a food source for many important fisheries. Within the past century, *E. affinis* has invaded freshwater lakes and reservoirs multiple times independently¹. For example, *E. affinis* entered the Great Lakes ca. 1958, probably through dumping of ship ballast water^{2, 3}. These invasions have serious implications for disease transmission, because *E. affinis* hosts a variety of potential disease agents, such as the pathogen *Vibrio cholerae*.

Because of the association between *E. affinis* and *V. cholerae*, The Institute for Genome Research (TIGR), a Division of the J. Craig Venter Institute, is interested in sequencing the genome of *E. affinis*. This sequencing project will probably begin in 2007. The copepod *E. affinis* is a main host of *Vibrio cholerae*⁴⁻⁶, but the nature of the association is not well understood. The riverine and estuarine bacterium *V. cholerae* causes cholera, an acute, diarrheal illness. In general, models of vector borne diseases have not been well developed in aquatic systems. Complex interactions between *E. affinis* and *V. cholerae* might affect virulence of *V. cholerae*. For example, chitin induces natural competence in *V. cholerae*, allowing the bacteria to take up DNA from their environment and acquire genes necessary for virulence⁷. In addition, growth on chitin induces the production of toxin-coregulated pilus (TCP) by *V. cholerae*⁸, which is critical for virulence. Also, the ability of *V. cholerae* to enter or exit dormancy might be related to the

association of *V. cholerae* with *E. affinis*, particularly when the copepods are in diapause. A comprehensive genome sequence and annotation of *E. affinis* would greatly facilitate identifying genes and pathways that encode the most relevant traits, such as those associated with copepod physiology and virulence. Because TIGR has already sequenced the genomes of several serovars of *V. cholerae*, we will be able to use entire genome sequences of both host and pathogen to understand genetic responses of host-pathogen interactions and the dynamics of this disease.

Aside from host-pathogen dynamics, there are other important questions that could be addressed using *E. affinis* as a model. For example, *E. affinis* provides an exceptional model for exploring mechanisms of niche evolution. Phylogenetic analyses have revealed that freshwater invasions have occurred multiple times independently from genetically distinct saline sources¹. Most notably, some clades have given rise to invasive populations, while others have not¹. Direct comparisons of source and invading populations have revealed evolutionary adaptations that are associated with habitat transitions^{9, 10}. Analysis of multiple independent invasions is beginning to offer insights into repeatability of evolutionary pathways and parallel evolution across independent invasion events^{1, 10}. Finally, comparing invasive and noninvasive populations is allowing us to determine properties that are exclusive to successful invaders^{10, 11}. The use of cDNA microarrays has allowed the Lee Lab to analyze functional categories of genes associated with freshwater invasions by *E. affinis*¹⁰. A comprehensive genome would allow us to determine the actual targets of natural selection during these invasions.

Finally, *E. affinis* provides an excellent model for exploring patterns of speciation in copepods. Species concepts are difficult to define among copepods, with many studies showing lack of correlation between morphological traits, genetic distance, and reproductive isolation¹²⁻¹⁶. Thus, the field could benefit greatly from integrating genetics and development underlying morphological traits with the genomics of reproductive isolation. Like many copepods, *E. affinis* forms a species complex that displays jagged and idiosyncratic patterns of speciation^{14, 15}. Patterns of molecular evolution, morphological evolution and reproductive isolation are completely uncorrelated and discordant¹⁵. Despite the extremely high levels of genetic divergence among clades (up to 20% at COI), there is a high degree of morphological stasis¹⁵. Moreover, there is reproductive isolation between genetically and morphologically proximate populations¹⁴. *Eurytemora affinis* offers an excellent model for the genomic study of speciation because they are easy to cross in the lab for studies of reproductive isolation and possess a well-defined clade structure.

From a practical standpoint, *E. affinis* is one of the best candidates with which to begin a copepod genome sequencing project. It is tractable as a genomic model, and has among the smallest copepod genomes (1C = 300 MB)¹⁷. The small genome greatly lowers sequencing costs and complexity of the assembly process, possibly allowing full closure and completion of the project to a 'gold standard' level. This species does not possess chromatin diminution¹⁷, a feature in some copepods where large fragments of the genome are discarded from the presomatic line during development. Extensive work has been devoted to developing culture techniques for this species, and as a consequence it is readily cultured in a laboratory setting. Inbred lines of *E. affinis* can easily be generated, avoiding problems associated with heterozygosity, which often plague the assembly phase of genome sequencing projects. Currently, inbred lines are being reared in the Lee Lab in preparation for the genome sequencing project.

In short, *E. affinis* provides an excellent candidate for a comprehensive genome project from multiple perspectives. However, if we want the entire field of copepodology to advance and take full advantage of genomic resources, we should not stop here. We describe the utility of choosing *E. affinis* as a model organism in order to illustrate the types of questions that we plan to address in a mechanistic fashion, using genomics tools. The availability of this genome sequence will make subsequent copepod genome projects much faster and cheaper by providing the template for assembly and annotation. We hope that this example inspires others in the field of copepodology to think about their questions and about the best species that could be used to address those questions.

As a community, we should begin discussing how genomic tools could be used to address the most vexing and interesting problems in copepod biology. For example, comparative genomics across multiple species could help us understand morphological evolution and elucidate problems in morphological taxonomy. It has been demonstrated multiple times that morphological characteristics are inadequate for defining many copepod species. In some cases, single gene phylogenies are inadequate, as well. We need to integrate our traditional methods with frameworks that more accurately reflect the evolutionary history of copepod groups.

The copepod community lags behind other communities (e.g., *Daphnia*, decapods) in employing genomics approaches. How do we train our community in this new area? The copepod community needs a plan. GAW would like to prepare a grant proposal to fund a training workshop and major symposium on a range of genomics topics to advance the field of copepodology to be held at the 10th ICOC in Thailand in 2008. We would like to hear from you about your interest in participating in or attending such a

workshop and symposium. What do you need to become a participant or supporting member of a copepod genomics project? In addition to educating our membership about genomics approaches, we could have a dialogue on a wide range of topics, including additional choices of candidate species for sequencing. One example of how we might approach a community wide discussion is described on a website (<http://www.biology.uiowa.edu/workshop/>) maintained by investigators of protists, who gathered together to choose candidate species for their first genome sequencing efforts.

We think that now is the time for copepodologists to take advantage of new technologies in genomics. As a community, we can benefit from the successes and mistakes of prior sequencing efforts on other taxa. The hardest work lies ahead: mobilizing the copepod community, preparing the grant proposals, ... and finally annotating the final sequences. We welcome input from investigators who are engaged in research that would benefit from a copepod genome sequencing project in the immediate future (e.g., QTL-mapping, resolving deep phylogenies, quantitative genetics, molecular genetics, molecular physiology, adaptation, gene expression analyses, etc.). To participate in the discussion, subscribe to a listserv created specifically for discussion by sending an email to COPEPODGENOME-L@listserv.jmu.edu. Grace Wyngaard will add your name to the subscriber list. We will begin this discussion group as an unmoderated one, so that messages are shared with all participants instantaneously. If problems arise, such as subscribers sending spam, James Bron and Grace Wyngaard will moderate. *Let the discussion begin!*

— Grace Wyngaard
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and
Carol Eunmi Lee
University of Wisconsin, Madison, U.S.A.
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Facts about Copepod and Branchiuran Research in the First Half-Decade of 2000

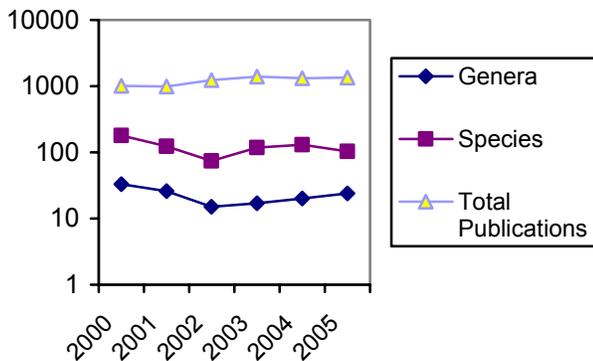
I thought it would be interesting to figure out the productivity of copepod and branchiuran researchers, and find out how many new genera and species were described for the first six years of the 21st century.

Since the beginning of this decade there have been 135 new genera and 728 new species described. During the years 2000-2005 sequentially, the numbers of new genera and new species were as follows: 33, 26, 15, 17, 20, 24 = 135 genera; and 179, 124, 74, 118, 130, 103 = 728 species. The numbers of species described per order were: Cyclopoida = 256, Harpacticoida = 186, Calanoida = 168, Siphonostomatoida = 92, Monstrilloida = 18, Arguloida = 3. There were 11 new families established during this period.

According to my calculations, there have been 48,270 publications dealing with copepods since 1600. There were 7,309 publications dealing with copepods from 2000 through 2005, with yearly totals of 1014, 993, 1237, 1392, 1326, and 1347, respectively. Just this year alone from January - September, 701 articles on copepods have appeared.

Curiously, the number of copepod papers being published yearly seems to be on the rise; however, the number of new taxa described appears to have a downward trend — could it be that there are not enough taxonomists out there?

— Chad Walter
National Museum of Natural History
Smithsonian Institution, Washington, DC, U.S.A.



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3) Financial support application:
December 16, 2006.

Notes: Since the organizer is raising the funds for financial support as much as possible, I encourage young scientists and scientists from developing countries to apply.

— Shin-ichi Uye
Hiroshima University, Japan



Robert Vivian Gotto
1921 – 2006

You just couldn't help but like Viv Gotto. He was a warm and open-hearted person, he liked people, and he was gifted with a wonderful sense of humour. Luckily for us, he was also a genuine enthusiast about copepods, particularly those living symbiotically with marine invertebrate hosts. Viv lived a rich life, experiencing great success and joy as a family man, as a scientist and as an international sportsman and we strongly suspect that the key to his happiness was achieving a good working balance between all the diverse areas of interest in his life. In addition to his distinguished career in zoology, Viv was a tennis player of international standing. He was a member of the Irish Davis Cup team from 1953-61, captaining it on thirteen occasions. He played in five Wimbledon Championships and, in 1953, he held both the Irish hardcourt singles and doubles championships. Here we will concentrate on Viv the scientist and copepod expert, but if you are interested in a fuller account of his life, we strongly recommend reading his recent book *Footprints in the Sea: Tales of a Marine Biologist* (Ballyhay Books 2004). This contains fascinating stories of his life, including his service during the war and his success as an international tennis player.

Viv Gotto was born and raised in the city of Belfast, Northern Ireland. He was the youngest of four siblings. His father ran a small business connected with the linen industry. At that time Belfast was a major industrial city of the United Kingdom, famed for its shipbuilding, most notably the construction of the Titanic. Viv showed an early interest in

natural history and the family home was on the outskirts of the city within easy reach of fields, meadows and the coast of Antrim. Like many boys of the time, Viv developed an interest in collecting beetles, moths, dragonflies, and bird's eggs. By the age of eleven he had already joined the Belfast naturalist's Field Club and was assisting Professor Gregg Wilson, from Queen's University (Belfast), with collecting mosquitoes from local marshes. His schooling was interrupted by a prolonged viral infection but despite this, at the age of 18, he entered Queen's University to study zoology at the outbreak of war in Europe in 1939. It was in the zoology department he met his future wife, Gwyneth.

In 1944, with the war in Europe and the Pacific still underway, both Viv and Gwyneth decided to join the Royal Air Force and elected to serve in the meteorological section. After some time in various camps in the UK and Sri Lanka, Viv was dispatched to the Cocos Keeling Islands in the East Pacific. These tropical islands were quite remote, 600 miles west of Java, but were an important cable and wireless link to Australia. Invasion by the Japanese army was a distinct possibility and Viv was issued with a Sten gun (but no ammunition) in order to defend the met station – a series of huts on the shore with corrugated metal roofs. The tropical islands had scant terrestrial life to interest a zoologist except for a few rats, geckos, and seabirds. However they were surrounded by beautiful pristine coral reefs and it was here that Charles Darwin, on his Beagle voyage, began to formulate his ideas about reef formation. Viv had the opportunity to savour these reefs long before such wonders were filmed for television by the SCUBA pioneer Jacques Cousteau. The reefs abounded with vibrant and colourful fish and corals, the pinnacle of evolution was arrayed before the eyes of a zoologist more used to cold grey waters of the United Kingdom. However, Viv's stay in "Shangri-La" was short lived and after only a few months the war ended and he returned to Queen's University to complete a first class honours degree and subsequently commenced as an assistant zoology lecturer along with Gwyneth, whom he married in 1947. Viv was destined to spend his entire scientific life at Queen's University. He was awarded a D.Sc. in 1964 and became reader in zoology in 1980. He retired in 1984 but maintained an active interest in copepod research until his death in April 2006.

As is often the case in science, the initiation of Viv's interest in copepods was rather serendipitous. The university ran marine biology field courses at Portaferry on Strangford Lough, south of Belfast and Viv and Gwyneth spent their honeymoon helping with students on the Easter vacation course. Viv's first serious research at Queen's was on the marine plankton sampled at the entrance to Strangford Lough. However, it was Gwyneth who inadvertently directed him towards associated copepods which were to become his life's obsession. In 1948, while examining live samples of colonial ascidians, she noticed a sluggish mobile

“red sausage” crawling within the ascidians. It took some time for the trained zoologists to identify the beast – by leafing through Sars’ Account of the Norwegian Crustacea. It turned out to be the first Irish record of the copepod *Mychophilus rosea*. It proved to be quite common in Strangford Lough and, as little was known of its life history, Viv began studies of the general biology of the females which he first published in 1954. (He was particularly delighted to report the eventual first discovery of the male of this species thirty years later in a joint paper with Holmes & Lowther.) Studies of other ascidicolous copepods followed. Viv devised an ingenious set-up of lenses and miniature aquaria to observe *Ascidicola rosea* through the transparent wall of its ascidian host. He may well have been the first scientist to make detailed observations of copepods going about their day to day business within their hosts.

Viv was soon fascinated by copepods living in association with marine invertebrates and his research focussed primarily on the British and Irish fauna. He had intimate familiarity with the Irish fauna in particular, gained both through his own studies and through running student practicals and marine vacation courses at Portaferry over many years. The collated records of Irish copepods were published in collaboration with Mark Holmes in 1992 and 2000. Viv’s survey work turned up a remarkable number of novelties. Viv was the first to record many European continental species from British and Irish waters and he was able to make live observations of several associated species: *Sabelliphilus elongatus* on the fan of the Peacock Worm, *Synaptiphilus tridens* on its sea cucumber host, and *Eunicicola insolens* on the polychaete *Eunice*. His primary interest was in the biology of these copepods and their interactions with the host. For some of these much-neglected copepod species Viv’s papers are still the only source of biological data. He studied their feeding, their host location biology, their reproduction behaviour and their distributions. Inevitably in the course of such work Viv came across species new to science. Taxonomy was not his main interest, nor did he enjoy the preparation of detailed scientific drawings. Nevertheless he described a total of 15 new species of copepods parasitic on marine invertebrate hosts, as well as three new genera (*Lichomolgoides*, *Anomoclausia* and *Paralobodelphys*). *Anomoclausia* remains the type species of a monotypic family, the Anomoclausidae, and has not been re-reported since its establishment in 1964.

Viv’s papers have generated insight into the biology of these peculiar parasites and have highlighted their marvellous suite of adaptations to symbiotic life. In 1979, his review, *The association of copepods with marine invertebrates*, brought together for the first time all that was known about the diverse range of copepod taxa affiliated with non-vertebrate marine fauna. Viv’s excellent Linnean Society synopsis, *Commensal and Parasitic Copepods Associated with Marine Invertebrates (and Whales)*,

published in 1993 (and updated in 2004) remains the best working guide for the identification of copepods associated with marine invertebrates in northern European seas.

Viv was an entertaining lecturer who enjoyed talking about his science. His fascination for the study of complex interrelationships of marine species was expounded in his book, *Marine Animals: Partnerships and Other Associations*, an excellent text, then and now, introducing students to the wonderful world of symbiosis. He was renowned for lacing his lectures with hilarious anecdotes and roars of laughter were frequently heard emanating from the lecture hall. Some stories we can’t resist repeating: Viv’s account, for example, of the capture of a wingless parasitic fly (Hippoboscidae) for the departmental slide collection on a holiday in Sardinia. The fly had been spotted lurking in the fur of the hotel cat but proved impossible to catch as it disappeared into the fur. Eventually three of the holiday makers climbed into a bath with the struggling cat holding it down until the parasite was finally cornered and transferred into a small bottle of gin! Viv was an all round naturalist competent to delve into many zoological areas. One unusual puzzle that came his way concerned the so called “Golden Salamander” – a beautiful gold relic recovered in 1967 from Spanish shipwreck off the Irish coast dating back to the time of the Spanish armada of 1588. Although the relic had been likened to a salamander, a creature probably familiar to Spanish artisans, Viv was the first zoologist to examine it and came up with a different theory. He noted its reptilian features and its peculiar side flaps and postulated convincingly that it may have been an early artistic representation of a flying lizard, perhaps based on dried specimens traded to early Spanish explorers to the far east.

Viv was a committed supporter of the WAC and its series of International Conferences on Copepoda: presenting papers at the meetings in Amsterdam, Ottawa, London, Karuizawa (Japan), Baltimore and Oldenburg. He always had an encouraging word for students and provided numerous points of constructive feedback in his reviews of manuscripts for his professional colleagues. His many contributions to the study of copepods have been honoured in the names of at least three copepod species: *Enterocola gottoi* Conradi, López-González & García-Gómez, 1992, *Acaenomolgus gottoi* Stock, 1995, and *Sphaeronella gottoi* O’Reilly, 2001.

Viv was a genuinely nice person, a real naturalist and an outstanding contributor to copepodology. We will all miss him.

— Myles O’Reilly
Scottish Environment Protection Agency,
Glasgow, Scotland
and
Geoff Boxshall
The Natural History Museum, London, U.K.

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New Books and Websites: Reviews

Marine Parasitology Edited by Klaus Rohde

CSIRO Publishing, Collingwood, Victoria, Australia,
2005. ISBN: 0643090258. AU \$135.00; CABI Publishing,
Wallingford, Oxon OX10 8DE, UK. Hardback, 592 pp.
£60. Details at WWW.publish.csiro.au

A new book on marine parasites has recently been published. It includes several chapters relevant to copepods, as well as chapters on general issues such as the nature of parasitism, life cycles of parasites, and the relationship between hosts and parasites. Considering that feeding off other organisms in an obligate symbiotic (ie. living together) relationship is the most common life style in the world, the ubiquitous copepods are naturally involved as both hosts and parasites.

The book covers all parasitic groups of organisms in the marine environment, from insects and mites to unicellular protists. Did you know that some 40 phyla have been identified in the latter group alone? Copepods are included in the extensive chapter on Crustacean parasites, which also deals with Isopods, Branchiurans, Tantulocarids, Ascothoracids, Cirripeds and Amphipods. All sections are written by recognised experts.

The importance of crustacean parasites is made clear in the introduction of the Crustacea chapters: "Of all the metazoan groups discussed in this book, the crustaceans are the most diverse and ubiquitous. Among them, the copepods are dominant". This statement is certainly backed up by Geoff Boxshall's section on copepods, where he states that of the 11,500 species of copepods, about half live in symbiotic associations. The section is logically laid out, and cover morphology, life cycles and effects on hosts. A useful list of copepod families parasitic on marine fishes is included. The main theme is the adaptation to the main host groups, viz. invertebrates and vertebrates, with the basic copepod body plan as a starting point. Figures of some of the known body forms of marine parasitic copepods are presented, and their morphological departures from the cyclopoid segmentation pattern is explained. The strong sexual dimorphism occurring in some genera is also discussed. In all, a fascinating review of all the incredible shapes our favorite animals can take.

Subsequently, the different life cycle patterns of parasitic copepods are reviewed, again with a basic pattern as the point of departure. We learn about modifications in the nauplius and copepodid phases, and how fit into the many life cycles. Attention is drawn to the abbreviation of the cycles in the case of fish parasites, but also to the fact that for most parasitic copepods the life cycle is not known. Finally, some of the effects on the host, both in terms of pathology and economic importance, are briefly discussed. Examples of the latter aspect are presented in chapter 10,

"Economic and environmental importance", in the sections "Effects of salmon lice on Atlantic salmon" and "Effects in finfish culture". Regrettably, the effects in mollusc culture are not mentioned in the section on this host group.

But there are other sections which are relevant to copepods in the book. They concern copepods as hosts for other parasites. Two of these are other crustaceans, the Tantulocaridae and Isopoda. Reading the section on isopods I was surprised to learn that a larval stage of the group Epcaridea are parasites of other crustaceans, including copepods. These large "microniscus" larvae are ectoparasitic, and feed on the copepod before leaving to find the final host, a decapod. Of the more exotic parasites are sponges, one of which uses copepods as hosts. These parasites are covered in their own chapter.

I'd say that the following chapters are directly relevant for us:

Chapter 1, The nature of parasitism, pp. 1-10

Ch. 4, Crustacean parasites, pp. 123-170

Ch. 6, Behavioural aspects of parasitism, pp. 259-278

Ch. 7, Ecology, pp. 279-325

Ch. 9, Zoogeography, pp. 347-369

Ch. 10, Economic and environmental importance, pp. 371-425

Then there are examples in other chapters of copepods as intermediate hosts, e.g. for cestodes. Finally, there is an extensive reference list, and index of important terms and taxa at the end.

This is a beautiful book, and I recommend it for everybody with an interest in marine ecology.

— Peter Heuch
National Veterinary Institute
Oslo, Norway



This photograph of *Lophoura* placed 18th (of 20 prizes awarded) in the 2006 Nikon Small World Competition. The photo was taken by Harold Taylor of Kensworth, U.K.

Amazon Fish Parasites
Second Edition
by Vernon E. Thatcher

Aquatic Biodiversity in Latin America /
Biodiversidad Acuática en América Latina
Volume 1. Series Editors: Joachim Adis, Jorge R. Arias,
Guillermo Rueda-Delgado & Karl Matthias Wantzen.
Scientific Reader to the Editors for this volume:
František Moravec
Pensoft Publishers, Sofia-Moscow, ISBN @@@.
165x240 mm, 500 pp., including 194 plates of figures in
line drawings and photos (15 plates in color);
publication date: February 2006. Pensoft Online
Bookshop: www.pensoft.net

From the series editors:

The book covers the following Phyla and Classes: Protozoa (Myxozoa, Sporozoa), Plathelminthes (Trematoda, Monogenoidea, Cestoda), Nematoda, Acanthocephala, Crustacea (Copepoda, Branchiura, Isopoda), Hirudinea and Pentastomida that are known to parasitize Amazonian fishes. In addition to the keys and checklists, each chapter gives information on the morphology, life cycles, pathology, prevention, treatment, collection and methodology, as well as general reference data on each taxon. An alphabetic table of host fishes with their respective parasites is provided. The book will prove to be useful for parasitologists, ichthyologists, aquaculturists, pisciculturists and all those interested in Neotropical fish parasites.

British Fresh-Water Copepoda,
Volumes I-III
By Robert Gurney

CD book for Windows and Mac, with fully searchable
text and navigation. 2005. Pisces Conservation. £65.80 or
approx. \$125/€97. ISBN 1904690335.

From the publishers:

The three volumes of Gurney's "Copepoda" were published by the Ray Society in 1931, 1932 and 1933 respectively. Vol. I covers the Calanoida, Vol. II the Harpacticoida, and Vol III the Cyclopoda & Caligoida. The greater part of Vol. I deals with habitat, life cycle and distribution, then the remainder of the 3 volumes cover the taxonomy and individual species in great detail, with over 2,000 illustrations. Like many other Ray Society monographs, "British Fresh-water Copepoda" remains one of the most important works on its subject, many years after its publication.

Pisces Conservation are delighted to release "British Fresh-water Copepoda" on CD, for Windows PCs and Macs, with fully searchable text and hyperlinks for ease of navigation.

As with all our e-books, the quality of reproduction of illustrations and text is excellent.

The books are in Adobe Acrobat pdf format (with free Reader software supplied), allowing high-quality printing of the text and plates.

CSA Discovery Guides:
Hydrothermal Vent Communities
by Carolyn Scearce

<http://www.csa.com/discoveryguides/vent/review.php?SID=aj285hm8mgaht448b3mubhau0>
Released May 2006.

This is a review of the discovery and exploration of hydrothermal vents and their associated flora and fauna. It includes a nicely illustrated general review, list of key citations, glossary, links to 26 websites on hydrothermal vents. Several of the citations focus on or refer to copepods.

Movement and Energy Metabolism of
Marine Planktonic Organisms
By E. V. Pavlova

Translated from Russian. 2006. Universities Press,
Hyderabad, India. 216 pp. ISBN 81 7371 495 9. Rs 510.00
<http://www.universitiespress.com/display.asp?categoryID=1&isbn=81-7371-495-9>

From the publisher's website: The monograph generalizes multi-year investigations on the energy metabolism and motility of marine planktonic organisms, from flagellated algae to salps, from different regions of the World Ocean. The effect of various factors changing activity and metabolism during experiments has been considered. Common features and differences in the character and speed of movement of organisms with different ecology have been demonstrated. Data on basal, standard, and total metabolism have been compared; current approaches have been taken into account, and new approaches and methods for the estimation of metabolism when approaching ecological problems are suggested.

This is an English translation of the 1987 monograph published by Akademia Nauk, Moscow.

**Philippine Freshwater Zooplankton
An illustrated list of freshwater
zooplankton in the Philippines
By Fl. Petersen, DANIDA Consultant
(Cand. Scient, University of Copenhagen)
SEAFDEC Binangonan**

3. edition (= 2. web-edition). December 30 2004.
(Rotifera updated. Small errors corrected)
<http://www.dafnier.dk/philippines/zooplanktonphilippines/index.htm>

WAC Affiliation with the ICZN

Dear WAC members:

I have recently received an invitation letter from the International Commission on Zoological Nomenclature (ICZN) to join the ICZN affiliates.

Because their activity is important in copepodology, I think that WAC should contribute some. I already signed the Moc and send it back to Dr. Polaszek. I ask your understanding.

With best wishes,
Shin

Here follows the text of the letter from Dr. Polaszek:

ICZN Affiliation - Memorandum of Cooperation

Dear Dr. Shin-ichi Uye,

I am writing to you as Executive Secretary of the International Commission on Zoological Nomenclature (ICZN). As you will be aware, ICZN produces the internationally recognised and accepted Code for naming animals (now in its 4th edition, and on the web at: www.iczn.org/iczn/index.jsp), as well as resolving problems that arise with the names of animals. ICZN provides these services through its Commissioners, up to 30 international specialists, and its secretariat based at the Natural History Museum in London.

ICZN's activities are mandated by the International Union of Biological Sciences, of which it is a member, and the Convention on Biological Diversity. ICZN is also an Associate Participant of GBIF, the Global Biodiversity Information Facility.

At ICZN we now see the emergence of a further, significant benefit to all taxonomists and other users of animal names through the development of ZooBank, a system of registration for the scientific names of animals.

The initial proposal appeared in *Nature* last September, and has received strong support from the zoological community. A copy of the *Nature* commentary is attached. It is also accessible through the ICZN website (www.iczn.org), where you will also find discussion of the proposal and related matters.

The work of ICZN will become increasingly important in the face of current global problems facing the environment, biosecurity, biodiversity, conservation, and other issues affecting animals, such as climate change and avian flu. It will become even more essential to ensure the correctness of the scientific names of animals in documentation relating to import and export, quarantine, medicine and veterinary science, and conservation, e.g. red data lists and CITES.

In previous messages we have asked associated organisations for direct financial assistance, however modest, to contribute towards the costs of carrying out the functions of ICZN. While we greatly value this support, we realise that this is an unsustainable fundraising strategy for keeping ICZN running in perpetuity. We are therefore currently seeking not a financial contribution but a statement of approval of ICZN's role and products, in the form of the attached Memorandum of Cooperation. We hope that by building up a critical mass of support from the users of ICZN's products and services we can lobby for financial help from other donors.

Your signature on the attached MoC could therefore be critical for the future of ICZN and consequently for the maintenance of standards, sense and stability in animal names.

Yours sincerely,



Andrew Polaszek
Executive Secretary, ICZN

ICZN Affiliates

Memorandum of Cooperation

As signatories to this Memorandum of Cooperation with the International Commission on Zoological Nomenclature, we support the overall aim of the Commission, that of promoting "Standards, Sense and Stability for animal names in science". We endorse the activities of the Commission in producing and periodically revising the *International Code of Zoological Nomenclature*, and ruling on cases where animal nomenclature requires resolution.

We recognise that the Commission is a unique body of specialist scientists, truly international in its composition, who freely donate their services to the work of ICZN. Without the existence of ICZN, and particularly without the Code, animal scientific nomenclature would rapidly become unstable.

Now more than ever, with information technology revolutionising the way that animal taxonomy is undertaken and the means by which the results of taxonomic research are disseminated, ICZN has a central and crucial role to play in maintaining stability of animal names.

We also support ICZN's Mission and Vision statements:

Mission:

The International Commission on Zoological Nomenclature is dedicated to achieving stability and sense in the scientific naming of animals.

Vision:

The International Commission on Zoological Nomenclature (ICZN), acting in the capacity of adviser and arbiter, assists the zoological community through generation and dissemination of information on the correct use of the scientific names of animals.

This includes the publication of the International Code of Zoological Nomenclature and the Bulletin of Zoological Nomenclature containing applications to, and rulings by, the Commission.

ICZN will distribute this information as widely as possible, working towards the provision of a free service.

By signing this Memorandum of Cooperation we are therefore pleased to become ICZN Affiliates forthwith.

Signed: Shin-ichi Uye
President, World Association of Copepodologists
19 September 2006

Brazilian Society of Limnology Publications Now Available Online

The three periodicals of the Sociedade Brasileira de Limnologia are now directly accessible via the following URLs. Contributions to the journals are welcome.

Acta Limnologica Brasiliensis

http://www.sblimno.org.br/acta/my_web_sites/acta_limnologica.htm

Limnotemas

http://www.sblimno.org.br/editorial/MontaHome.asp?qsTpl=lista_limnotemas.tpl&qsCaminhoTpl=../templates/

Boletim

http://www.sblimno.org.br/editorial/MontaHome.asp?qsTpl=lista_boletim.tpl&qsCaminhoTpl=../templates/

— Ricardo M.P. Coelho
Universidade Federal de Minas Gerais
Belo Horizonte, Brazil

English Version of "Biology of Inland Waters"

Beginning in 2007, an English version of the Journal "Biology of Inland Waters" is to be published. It will contribute to better information exchange between Russian and foreign scientists. The English version of the Journal "Biology of Inland Waters" will offer foreign investigators an opportunity obtain regular information about the scientific results of Russian colleagues.

The English version of the Journal will be published by "International Academic Publishing House Nauka/Interperiodicals." Contact:

Nauka-Export
e-mail: naukaexport@naukaran.ru
Fax: 8(495) 334-71-40 or 8(495) 334-74-79

— Nina A. Ziminova
Executive Secretary
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E-mail: isdat@ibiw.yaroslavl.ru

New Journal: Pan-American Journal of Aquatic Sciences

"The *Pan-American Journal of Aquatic Sciences*' aim is to be a fast and free of charge media for publication of original scientific articles in the Aquatic Sciences such as Biology and Ecology of aquatic organisms, Biological-, Physical-, Chemical- and Geological Oceanography, Limnology, Coastal Management, Fisheries Biology, Aquatic Ecosystem, Management, Aquaculture and related areas."

This is an open-access, electronic journal, initiated in 2006. Languages are English, Spanish, and Portuguese. See the website: <http://www.panamjas.org>

— Jan Reid

News from or about Members

Mark Grygier named ICZN Commissioner

Mark Grygier is one of the new members of the International Commission on Zoological Nomenclature. This body was founded in 1895 and currently comprises 19 members from 17 countries.

The ICZN website explains that the Commission operates in two main ways:

ICZN publishes the International Code of Zoological Nomenclature containing the rules universally accepted as governing the application of scientific names to all organisms which are treated as animals.

ICZN provides rulings on individual nomenclatural problems brought to its attention, in order to achieve internationally acceptable solutions and stability.

http://www.nhm.ac.uk/hosted_sites/iczn/

The recently revised ICZN website is well worth a visit! It is notable for its cleanly elegant design, and very informative, with a Mission and Vision statement, an explanation of "What We Do," the names of the members of the Secretariat and the Commissioners, and a summary of the ICZN's history. The *International Code of Zoological Nomenclature* is available online, and can also be ordered in book form. Abstracts from the *Bulletin of Zoological Nomenclature* from 2001-2006 are also posted on the site.

There is information about the *Official Lists and Indexes of Names and Works in Zoology*. Several useful links including one to ZooBank, now in a prototype version based on Thomson Zoological's "Index of Organism Names", which is the electronic archive of the *Zoological Record*, going back to 1978 (vol. 115). The entire list of names in the ZR will soon be available.

Many good wishes to Mark as he takes on his new responsibilities!

— Jan Reid

From Andrey Marchenkov:

I finished my scientific activities last year and now I am engaged in absolutely another field of interest - I have a job in the only Russian Marine Aquarium, in Saint Petersburg. The Aquarium is very young - we only started our job on 27 April 2006 and all work here is highly interesting. You can visit our web site:

<http://www.planeta-neptun.ru/oceanarium/index.html>

With best wishes,
Andrey Marchenkov

From Bruce Coull:

Dear All: Many of you know that I retired as Dean and Professor June 30, 2006, with a great party with USC colleagues, Columbia & SC friends AND many of my former students. I was overwhelmed with the nice things they said about me (I guess I fooled them all) and had a great time visiting.

This does not mean I have left the University. I have moved out of the Dean's office and will shut down my marine biology lab within the next 6 months. I am still on campus in the same building as the School of the Environment (I moved from the 7th to the 2nd floor) - so come see me if in the neighborhood. My telephone number has changed (see below) - all other contact information remains the same (easiest and preferred email is bccoull@sc.edu)

I will work part-time with the Center for Humans and Nature (New York and Chicago based non-profit) on a project educating local governments about conservation and environmental ethics as they relate to land use in the of SC low country. Who says life does not begin anew at 63!

Hope you will stay in touch.

Best, Bruce
Bruce C. Coull
Carolina Distinguished Professor & Dean Emeritus
School of the Environment, Univ. of South Carolina
Columbia, SC 29208 USA
803.777.8997(Voice); 803.777-5715 (Fax)
AND
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New Member

David Fields

Bigelow Laboratory for Ocean Sciences
180 McKown Point Road West
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U.S.A.
dfields@bigelow.org

Fields of interest: Small-scale bio-physical interactions in plankton. Zooplankton ecology – Sensory ecology.

WAC Treasurer's Report

Beginning balance January 1, 2005	\$28,127.31
Membership dues paid	3,656.92
Interest earned	275.21
(Postage for mailing <i>MONOCULUS</i>	14.27)
(Charge for wiring travel grants	80.00)
(Charge for tracing seed money sent to the 9th ICOC Organizing Committee	45.00)
(Travel grants	1,884.55)
(Student Awards at 9th ICOC	1,600.00)
Balance December 31, 2005	\$28,435.62

I am retiring from teaching at the end of this school year. Persons wishing to pay their dues by mail should now send them to this address:

John A. Fornshell, Ph.D.
6911 Quander Road
Alexandria, Virginia 22307
U.S.A.

— John Fornshell
Treasurer, WAC
Alexandria, U.S.A.

New Domain for Copepoda List

Dear Copepoda List members,

I have decided to move the Copepoda List to this new address under the USP domain. The previous address under the Oceanografia.org domain has been hard to manage because of excess of SPAM arriving at my mailbox, as the list moderator.

To post messages to the list, simply write to copepoda@listas.usp.br.

If you want to change your settings, please click on the second link of the subscription message, which starts with ... <https://listas.usp.br/mailman/options/copepoda/> followed by your email address.

I apologize for the trouble, and hope this will launch a new and more active phase in communication among list members.

— Best regards,
Rubens
Rubens M. Lopes
Instituto Oceanografico, Universidade de São Paulo
São Paulo, Brazil

Editor's Notes

For their contributions and assistance for this number, I am grateful to Annemarie Avenant-Oldewage, James Bron, Bruce Coull, Frank Ferrari, John Fornshell, Thomas Glatzel, Claudia Halsband-Lenk, Peter Heuch, Stewart Johnson, Simon Jones, Carol Lee, Rubens Lopes, Andrey Marchenkov, Pedro Martínez Arbizu, Iskandar Mirabdullayev, Paul Montagna, Juan Paggi, Vadim E. Panov, Ricardo M. Pinto-Coelho, Eduardo Suárez-Morales, Danny Tang, Shin-ichi Uye, Chad Walter, Grace Wyngaard, and Nina A. Ziminova.

Thanks to Mr. Jonathan Pocius of Keating & Co., media representative for Nikon, for granting permission to reproduce the photo of *Lophoura*.

— Jan Reid, Editor
Martinsville, U.S.A.

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Membership in the WAC: Any person interested in any aspect of the study of Copepoda is eligible for membership in the WAC. Contact the General Secretary for an application form and other information.

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Newsletter: All members receive the newsletter *MONOCULUS*, which appears at least once a year, in electronic or printed versions.

Copepod Libraries: Monoculus-Library: C/o Prof. Dr. Pedro Martínez Arbizu, Forschungsinstitut Senckenberg, DZMB-Forschungsinstitut Senckenberg, Monoculus-Library, Suedstrand 44, D-26382 Wilhelmshaven, Germany.

C. B. Wilson Library: C/o Mr. T. Chad Walter, Smithsonian Institution, PO Box 37012, NMNH, MRC-163, Washington DC 20013-7012, U.S.A.