

## Theme Session A

### **Biochemical, biogeochemical, and molecular approaches to the study of plankton ecology and species diversity**

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Marine biodiversity and ecology are being transformed by novel biochemical, biogeochemical, and molecular approaches and techniques. However, many scientists working with traditional approaches have yet to appreciate the power and potential of such methods, and many of those developing the new methods are not aware of their possible applications for marine ecology. Molecular approaches, including DNA barcoding and community metagenomics, can accurately assess species diversity, reveal cryptic and new species, and illuminate phylogeny. Analysis of gene expression by quantitative PCR and microarrays can reveal the influences of environmental variability on species. Biochemical and biogeochemical markers, including trace element and stable isotope compositions, allow tracking of material flow in food webs and trophic relationships. Also, dietary components and food quality can be correlated with species' vital rates, recruitment and productivity; and histochemical and enzyme kinetic assays can reveal physiological condition, growth rates, and impacts of biotoxins and pollutants. These and other advances are rapidly transforming marine research, bringing improved understanding of species diversity, distribution and abundance, as well as dynamic insights into species and community ecology, and interactions and adaptive responses of organisms to environmental conditions and change.

Theme Session A brought together scientists studying diverse applications of molecular and biochemical approaches in marine plankton ecology and ecosystem functioning. The focus was on: 1) characterization of plankton species diversity; 2) effects of environmental variability on physiological processes; and 3) trophic relationships, rates and adaptive capacities in pelagic food webs. The successful session attracted 27 contributions (15 oral and 7 poster presentations; 5 withdrawn) ranging from single species to phyla, and from genetics to ecosystem studies. Some highlights of the presentations include:

- 1) Species diversity and phylogeny: Multi-gene phylogenetic analysis including slow nuclear and fast mitochondrial genes improves insight into the evolution of calanoid copepods [A01]. DNA microarray technology allows rapid characterization of genome-wide patterns of metabolic gene expression in *Calanus finmarchicus* [A03]. This method has strong potential to reveal physiological condition and vital rates, as well as interactions between organisms and the environment. A promising application of this technology was shown for phytoplankton species monitoring, with an automated molecular microarray sensor to be installed in a Ferry-Box System [A06]. An overview on Census of Marine Life DNA-barcoding for marine monitoring and biodiversity studies

emphasised potential applications for ecosystem and fisheries research and management [A05].

- 2) Species's adaptations and functional roles: Ecological niches were identified for two families of deep sea copepods based upon fatty acid and stable isotopic patterns, with highest similarities in species with close phylogenetic relationships, emphasising that physiological adaptations must be evaluated with an evolutionary perspective [A10]. Clade-specific distribution and trophic role was shown for the *Eurytemora affinis* species complex, with special emphasis on spatial and temporal variation in predation pressure and trophic level [A07]. Phylogenetic, toxicological and regional comparisons of *Alexandrium* spp. proved that spatial differences in toxic algae blooms are related to species and strain-specific expression of toxin genes. [A12].
- 3) Trophic markers in food web analysis: In the sub-Arctic Iceland Sea, trophic relationships between key species were revealed using fatty acids and stable isotopes, with successful separation of trophic levels and resolving *Calanus* dependent and independent food web divisions [A08]. The importance of migrating *Calanus* for vertical carbon flow and as food for Arctic deep sea copepods was conclusively indicated by stable isotopes and fatty acid patterns [A10]. In contrast, partly inconclusive results were found in stable isotope signatures for pelagic and cryopelagic food web structure in the Antarctic, which may be attributed to high variation in POM baselines [A19]. Ground-truthing of trophic markers with stomach content in Australian brackish fish species showed conclusive results for niche separation, although only DHA:EPA ratios predicted the primacy of pelagic or benthic feeding habits of the species [A09].
- 4) Organism – environment interactions: Functional responses of enzymes enhance our understanding of how organisms, their physiology and vital rates are able to respond to changing environmental regimes. The digestive system of *Temora longicornis* reacts to dietary changes within hours, as shown by changes in expression of lipolytic enzymes [A15]. A comparison of metabolic enzymes, conditional states and vital rates of *Centropages typicus* in field and experimental approaches, indicated the potential of biochemical indicators as proxies for growth and productivity of zooplankton, and also highlighted the need for more experimental calibrations [A18].
- 5) Key processes in fish recruitment and ecosystem function: A synchronous application of various enzymatic assays during a field study mapped phytoplankton vital rates at high resolution, reflecting several scales and ecosystem characteristics, including the ratio between new and regenerated production [A11]. Spatial and temporal variations in fatty acid contents of Iberian sardine and their prey was related to sardine condition and reproduction, indicating their potential to improve understanding of larval survival and recruitment [A17]. Biochemical

indicators (composition and fatty acids) linked European sardine condition and recruitment potential to oceanographic conditions in the Western Iberia Upwelling Ecosystem, indicating control of sardine population dynamics by bottom-up effects in the region [A14].

The session discussion focussed on the current and future potential of molecular and biochemical approaches, present gaps in knowledge and future perspectives in taxonomic, physiological and ecosystem studies. This led to the following conclusions:

- Studies of functional responses that integrate different methods and time-scales (gene expression, enzyme activity, changes in vital rates) and those that reduce organism level responses to their basic processes (e.g., enzyme activity) will greatly improve our understanding of organisms' interactions within communities and with the environment.
- Further study is needed on adaptation and acclimation (e.g. common garden or sibling experiments) to understand the flexibility of species and population responses to environmental changes.
- Comprehensive energy budgets of organisms are needed to improve understanding of functional responses, key processes and energy flows in ecosystems. These are also needed to develop biophysical modelling at many scales.
- Analysis of intra- and inter-specific differences in behaviour, adaptation and response to environmental drivers and stresses must be interpreted in the context of evolution, with full consideration of phylogenetic constraints.
- Stable isotopes alone are not ideal or sufficient for identifying trophic structures within an ecosystem, particularly if variable POM composition does not reflect the basis of the food web. An ecosystem approach will require integration of diverse methods, data, and results.

#### **General conclusions:**

Theme Session A reflected a wide variety of molecular and biochemical techniques that are currently developing and available in marine ecology. Applications shown gave new insights into processes from genes to ecosystems. The potential for scientific integration - dissolving barriers between disciplines - is enormous and will lead to greatly enhanced understanding in coming years. These methods have proven their high potential to (1) determine the importance of species biodiversity in ecosystem functioning; (2) enhance understanding of organism - environment interactions and thereby strengthen prediction of species and community responses to environmental change; and (3) provide valuable tools for elucidating key processes in the population dynamics of plankton and fish, and monitoring ecosystem function and health.

We highly recommend that ICES continue to investigate, encourage and integrate molecular and biochemical techniques into broader scientific approaches, surveys and strategies. The promising perspectives and session discussions resulted in a strong recommendation for ICES Working Group on Zooplankton Ecology, in concert with other expert groups and individuals, to organize and hold a

workshop to bring together scientific and technical experts to foster training, development and integration of molecular and biochemical approaches to advance marine ecology and ecosystem management.