



THEME SECTION

Introducing genomics, proteomics and metabolomics in marine ecology

Idea and coordination: Stewart C. Johnson, Howard I. Browman

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Introduction

Stewart C. Johnson^{1,*}, Howard I. Browman²

¹Institute for Marine Biosciences, National Research Council, 1411 Oxford Street, Halifax, Nova Scotia B3H 3Z1, Canada

²Institute of Marine Research, Austevoll Research Station, 5392 Storebø, Norway

Genomics, proteomics and metabolomics, used alone, in combination with each other and/or with more traditional methods, are fields of study that are rapidly transforming many areas of biological and biomedical research. They have enabled the transition from sequential studies of single genes, proteins or metabolites to what might be considered a more 'ecological approach', involving the simultaneous study of many components and their interactions with the environment (from pathways, through cell tissues to whole organisms and communities) (Hollywood et al. 2006, Joyce & Pálsson 2006). The development of these fields has been supported by the concurrent development of many new technologies and methods such as quantitative PCR, RNA interference assays, and fourier-transform ion cyclotron resonance (FT-ICR) mass spectrometry. Many of these technologies and methods are now used to address

fundamental smaller-scale questions in areas such as ecology, biodiversity and evolution.

With the exception of the use of genomics to address questions about the diversity and ecology of marine microbial communities ('metagenomics', i.e. Venter et al. 2004, DeLong et al. 2006, Sogin et al. 2006 and references therein), these fields have as yet not been broadly applied in marine ecology. The goal of this Theme Section (TS) is to provide an introduction to these fields, including information on how they have been applied (or could be applied) to address questions in marine ecology. Contributors were invited to explore questions such as: Is knowledge gained by the application of such technologies in marine ecology worth the money? Will technologies such as DNA bar coding ever replace traditional taxonomic studies? Have research areas such as environmental genomics

*Email: stewart.johnson@nrc-cnrc.gc.ca

met research expectations? What is the scientific value of large-scale genomic sequencing of marine animals? What factors limit the application of these technologies in the marine sciences? How can marine scientists be better trained to take advantage of such technologies? How can scientists with genomics, proteomics and metabolomics skills be encouraged to address questions in marine ecology?

Several common themes unite the contributions to this TS:

(1) Improved genomics resources (i.e. gene/protein sequences) for marine organisms will greatly facilitate the application of these fields to questions in marine ecology. To date, the development of genomics resources for marine organisms has been primarily focussed on marine microbes (see Thomas et al., in this TS). However, genomics resources for other taxa are at present limited to the full genome sequence of the 'model species', the purple sea urchin *Strongylocentrotus purpuratus*. Genomics sequencing efforts for other model and non-model species, including the diatom *Thalassiosira pseudonana*, the surf clam *Spisula solidissima*, the sea squirts *Ciona intestinalis* and *Ciona savignyi*, the tunicate *Oikopleura dioica*, the little skate *Leucoraja erinacea*, and the mollusc parasite *Perkinsus marinus*, are in progress. As noted by Dupont et al. (in this TS), both small- and large-scale expressed sequence tag (EST) resources and other genomic tools are becoming more available for species from a wide range of taxa. However, taken together, all of these resources still cover only a small fraction of marine taxa. With time, these resources will become more numerous as increased sequencing speed and reduced cost make genomic studies of marine organisms feasible for more research groups.

(2) Multidisciplinary teams, and the sharing of source materials and information, will add value to marine ecological research. Contributors to this TS emphasize the importance and value of developing multidisciplinary teams to plan, conduct, analyze and interpret the large amounts of information generated by these fields of study. However, in order to realize their full potential, it will be necessary to integrate these data with classical ecological approaches and knowledge. Distel (in this TS) discusses the importance of the preservation and sharing of biological source materials, and the information obtained from them. Providing research groups with methods to access samples and information that they would not normally be able to obtain will help to promote the multidisciplinary culture that is necessary to take full advantage of these fields of study when applied to marine ecological research.

(3) Data management, data sharing, other bioinformatics resources and knowledge are needed to extract meaningful biological information from large

complex data sets. Contributors to this TS emphasize the fact that genomics, proteomics and metabolomics generate extremely large data sets that are difficult to interpret. The availability of bioinformatics resources, and personnel who are knowledgeable and skilled in their application, often limits the success of such studies. In fact, relatively simple processes such as data storage and data sharing often exceed the capacities of many research laboratories. Within each of these fields, the development of resources and tools with which to interpret data is evolving rapidly. In addition, new resources and tools to integrate 'omics' data sets, with the goal of understanding biology at the systems level, are also becoming more widely available (de Keersmaecker et al. 2006, Joyce & Palsson 2006). The ability to understand and appropriately utilize these bioinformatic resources and tools requires a great deal of training and is an area of expertise in itself. Future marine ecologists will need these skills and thus appropriate training at both the undergraduate and graduate level needs to be considered.

It is our hope that this TS will stimulate discussion within the marine ecological community, as well as encourage interactions between marine ecologists and other research groups that routinely use these fields of research. The goal is to develop the relationships and networks that would enable the formation of multidisciplinary teams that are so crucial for obtaining funding for large-scale marine ecological research programs that utilize and, more importantly, integrate these fields.

Acknowledgements. S.C.J.'s research is supported by the National Research Council of Canada and Genome Canada. H.I.B.'s research, and his editorial activity for MEPS, are supported by the Institute of Marine Research, Norway, The Research Council of Norway, and the Inter-Research Science Center.

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