



Volume 24, Part 1, December 2015

Marine Genomics

CONTENTS

(Abstracted/Indexed in: A.G.I.'s Bibliography and Index of Geology; Aquatic Sciences and Fisheries Abstracts; Bulletin Signalétique, Chemical Abstracts, Current Contents, Elsevier BIOBASE/Current Awareness in Biological Sciences, Geo Abstracts, Geoscience Contents, ISI Web of Science; Marine Science Contents Tables, Oceanic Abstracts and PASCAL/CNRS, Also covered in the abstract and citation database Scopus®, Full text available on ScienceDirect®, PubMed)

The marine genome: structure, regulation and evolution

Guest Editors: Roberto Danovaro, Maria Costantini and Cinzia Verde

Cover legend: The DNA as the main information storage in marine organisms.

As it appears in the cover image, marine organisms originate from and thrive in sediments, water and dissolved air. To understand marine life, knowledge of the structure of DNA is necessary for comparative purposes. The articles assembled in this Special Issue are aimed at characterising marine organisms by analysing their genome and transcriptome, and performing evolutionary comparison. The themes range from RNA and DNA extraction to analysis of various genes and proteins evolution, regulatory sequences, gene regulation and the search for new producers, as a source for bio-prospecting.

The concept of the cover image was devised by Dr. Rimantas Kodzius (KAUST) and graphically developed by the scientific illustrator Heno Hwang (KAUST Office of Academic Writing Services).

Editorial

The marine genome: structure, regulation and evolution
R. Danovaro, M. Costantini and C. Verde 1

Special issue Articles

An overview on genome organization of marine organisms
M. Costantini 3
Metagenetic tools for the census of marine meiofaunal biodiversity: An overview
L. Carugati, C. Corinaldesi, A. Dell'Anno and R. Danovaro 11
Marine metagenomics as a source for bioprospecting
R. Kodzius and T. Gojobori 21
Mitochondrial gene order variation in the brachiopod Lingula anatina and its implications for mitochondrial evolution in lophotrochozoans
Y.-J. Luo, N. Satoh and K. Endo 31
Transcriptomic analysis of Nodal- and BMP-associated genes during juvenile development of the sea urchin Heliocidaris erythrogramma
M. Byrne, D. Koop, P. Cisternas, D. Strbenac, J.Y.H. Yang and G.A. Wray 41
Evolutionary volatile Cysteines and protein disorder in the fast evolving tunicate Oikopleura dioica
L. Berná and F. Alvarez-Valin 47
New insights into evolution of IgT genes coming from Antarctic teleosts
S. Giacomelli, F. Buonocore, F. Albanese, G. Scapigliati, M. Gerdol, U. Oreste and M.R. Coscia 55
The upstream regulatory sequence of the light harvesting complex Lhcf2 gene of the marine diatom Phaeodactylum tricorutum enhances transcription in an orientation- and distance-independent fashion
M.T. Russo, R. Annunziata, R. Sanges, M.I. Ferrante and A. Falciatore 69
Insights into possible cell-death markers in the diatom Skeletonema marinoi in response to senescence and silica starvation
I. Orefice, C. Lauritano, G. Procaccini, A. Ianora and G. Romano 81
Effects of the oxylipin-producing diatom Skeletonema marinoi on gene expression levels of the calanoid copepod Calanus sinicus
C. Lauritano, Y. Carotenuto, V. Vitiello, I. Buttino, G. Romano, J.-S. Hwang and A. Ianora 89
The diatom molecular toolkit to handle nitrogen uptake
A. Rogato, A. Amato, D. Iudicone, M. Chiurazzi, M.I. Ferrante and M.R. d'Alcalà 95
Genome-wide comparison of ultraviolet and ethyl methanesulphonate mutagenesis methods for the brown alga Ectocarpus
O. Godfroy, A.F. Peters, S.M. Coelho and J.M. Cock 109
High-quality RNA extraction from copepods for Next Generation Sequencing: A comparative study
S. Asai, A. Ianora, C. Lauritano, P.K. Lindeque and Y. Carotenuto 115

http://ees.elsevier.com/margen

For a full and complete Guide for Authors, please go to: http://www.elsevier.com/locate/margen



1874-7787(201512)24P1;1-I

Available online at www.sciencedirect.com

ScienceDirect



Volume 24, Part 1, December 2015

ISSN 1874-7787

Marine Genomics

Special Issue

The marine genome: structure, regulation and evolution

Editor-in-Chief: Frank Oliver Glöckner

Guest Editors
Roberto Danovaro
Maria Costantini
Cinzia Verde

MARINE GENOMICS

Vol. 24, Part 1 (2015) 1-118

SPECIAL ISSUE STRUCTURE REGULATION EVOLUTION

ELSEVIER



Contents lists available at ScienceDirect

Marine Genomics



Editorial

The marine genome: structure, regulation and evolution

The genomes of all living organisms are under continuous changes over time, through both small- and large-scale events (genome rearrangements, duplications) ultimately leading to their evolution. By studying these changes, we are reaching a better understanding of the functional role of various genetic elements, as well as the regulatory hierarchy among these elements (Tang and Lyons, 2012).

The analysis of genomic information is having an impact on every area of life sciences and beyond. A genome sequence is a prerequisite to understand the molecular basis of the phenotype, how it evolves over time and how we can manipulate it to provide new solutions to critical problems. Such solutions include therapies and cures for disease, industrial products, approaches for biodegradation of xenobiotic compounds and renewable energy sources. Along with improvements in sequencing technologies, there is also a growing interest in metagenomics and in the power of comparative analysis of groups of related genomes.

Recent advances in sequencing technology offer improved tools to accurately sequence, decipher, assemble and reconstruct the genomes from a wide variety of organisms. The availability of full genome sequences and improved bioinformatics pipelines, are opening new perspectives for investigating marine organisms' genomes. In view of the exponentially growing availability of new genome sequences, stewardship of these data in the long term becomes a priority (Field et al., 2008).

Over the course of evolution, genes of certain types and families proliferate and expand in numbers, in many cases along with functional innovations and increasing complexity. Comparative analyses from model organisms allow us to understand the structure and function of regulatory systems. Recent studies have focused on topological properties and the evolution of regulatory networks and their components. Our understanding of natural networks is also paving the way to embedding synthetic regulatory systems into organisms, allowing us to expand the natural diversity of living systems to an extent we had never before anticipated.

Many sub-branches of genomics are emerging, including marine genomics and these demand new ways of data management. Marine environments are the cradle of life, containing 95% of the world's biomass and 38 (19 endemic) of the 39 known animal phyla (Titilade and Olalekan, 2015). Besides providing about half of the oxygen that we breathe and acting as moderators of global climatic change, by sequestering about 50% of the CO₂, they have a crucial influence on global biogeochemical cycles and on the human wellbeing.

Marine environments include many diverse pelagic and benthic habitats and although these environments support a rich abundance of life, marine biodiversity has received much less attention than its terrestrial counterpart. Although the genomic revolution is rooted in

medicine and biotechnology, marine genomics currently delivers a great quantity of data by its own.

In conclusion, the integration of high throughput data and adoption of genomic tools will permit to disclose new genomic data. With each new genome sequenced, studied and compared, more insight will be gained on how genomes work and retain their composition and structure, and on what changes are likely to occur over time under various environmental cues.

The international community of marine genomics is growing day by day thanks to great extent of information becoming increasingly available. In recognition of the current excitement in the field, we have assembled the Special Issue entitled "The marine genome: structure, function and regulation".

The aim of this Special Issue is to assess the impact of this knowledge on organism biodiversity and ecology, emphasising evolutionary adaptations in living systems. This Special Issue only scratches the surface of the immense value of the field of marine genomics.

An up-to-date view on the genome organisation of marine organisms, from vertebrates to invertebrates, is provided by Costantini (p. XX) highlighting compositional features and evolution. Carugati and co-authors (p. XX) focused their attention on a benthic component of marine organisms, the meiofauna, which includes the most abundant and ubiquitous metazoans of the world, the nematodes. These organisms are highly diversified and metagenomic approaches are being extensively used to study their biodiversity. In marine environments, nutrient concentrations affect growth, distribution and survival of phytoplankton, mainly diatoms (marine microalgae), due to significant spatial variability of some nutrients such as nitrogen. Marine metagenomics is also an excellent tool to have access to the abundance of novel genetic information and to unlock the width of metabolic diversity in microorganisms, as reviewed by Kodzius and Gojobori (p. XX). In fact, metagenomics is providing valuable information for uncultivable samples, novel genes, pathways and genomes. In particular, genome engineering and systems biology promote enhancement of biological and chemical producers and creation of novel bio-resources, becoming an effective way to efficiently produce known and novel foods, livestock feed, fuels, pharmaceuticals and fine or bulk chemicals.

Omic technologies are a useful tool to elucidate the processes underlying genome evolution and developmental processes, as reported the following contributions. By transcriptomic analysis, Luo and co-authors (p. XX) demonstrate that the mitochondrial gene order in the brachiopod *Amami lingula* is completely shuffled, and that mitochondrial genomes have limited value for inferring the phylogenetic position in lophotrochozoans because of their evolutionary rates in brachiopods and bivalves. Byrne and co-authors (p. XX) use the developmental transcriptome generated in *Helicoidaris erythrogramma*, a species of sea