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 characterizing marine organisms by analysing their genome and transcriptome, and performing evolutionary comparisons. 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).

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Special Issue: Structure, Regulation and Evolution

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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 biodiversity 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 sequencing 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 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 on un cultivable 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.

Omnis 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 *Ammonia 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 *Heliocidaris erythrogramma*, a species of sea