



Editorial: High Throughput Omics Technologies for Understanding Molecular Stress Response and Devising Mitigation Actions

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Editorial on the Research Topic

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Oceans play a significant role in the sustenance of human life on the planet. Approximately, 79.3 and 28.7 million tons of fish are produced from oceans annually through capture fisheries and aquaculture respectively, which contributes about 17% of global animal protein consumption (FAO, 2018; Bennett, 2019). Apart from contributing to food and nutritional security, oceans act as the largest carbon sink on earth and play an essential role in regulating atmospheric, material and energy cycles. About 60% of the total ecological services of the biosphere come from the oceans and over three billion people across the globe are reliant upon the oceans for livelihood (OECD, 2022). As agricultural land resources decline, the dependence on oceans for food production may increase.

However, with an increase in population, the oceans have fallen prey to a high level of anthropogenic activities. High quantities of pollutants such as microplastics, heavy metals, and persistent organic compounds have reached the oceans, affecting marine life. Apart from these pollutants, the global increase in temperature is another factor that has tremendously affected marine life.

For sustainable human well being, oceanic health needs to be preserved from further deterioration. Considering this, the United Nations has proclaimed the current decade (2021-2030) as “The Decade of Ocean Science for Sustainable Development”. This program intends to coordinate and promote science-based policy implementation across the globe to restore oceanic health. The physiological and molecular responses of marine life forms to stressors act as good indicators of oceanic health and could be useful in providing a scientific base to the policymaking process. Thus, it is vital to study the molecular stress responses of marine organisms.

High throughput OMICS technologies such as genomics, transcriptomics, proteomics and metabolomics provide valuable tools for biomarker discovery that could be used to assess the health of different oceanic life forms, thereby providing clues on the environmental health. These biomarkers are important from an environmental health assessment point of view and are also helpful in assessing the efficacy of any mitigation action applied.

With this backdrop, the present Research Topic was created to invite research and review articles from researchers across the globe working on molecular stress responses in marine life forms. It contains five research articles and one review article, as summarized below.

San et al. have used the Illumina HiSeq 6000 transcriptome sequencing platform to assess the response of marine fish *Trachinotus ovatus* to hypoxia and reoxygenation. They have observed significant downregulation of genes for chemokines, chemokine receptors, interleukins, complement factors, and other cytokines. However, upon reoxygenation of the fish, genes related to phagocytosis and protein degradation were upregulated, indicating that the fish body repaired the stress-induced damage by rapidly removing the misfolded proteins.

Wang et al. have used PacBio Isoform Sequencing and Illumina RNA Sequencing to assess *Apostichopus japonicus*' response to heat stress. They observed that the genes with altered expression in the heat-stressed *Apostichopus* fell into four in 4 classes; 1. genes related to folding, sorting, and degradation of proteins, 2. genes related to immune and infectious diseases, and genes related to signal transduction and post-transcriptional regulation.

Jalal et al. studied the rhizospheric microbiomes associated with coastal plants *Suaedamonoica* and *Delphinium glaucum*, which showed the presence of Proteobacteria, Actinobacteria, Firmicutes, Gemmatimonadota, Bacteroidota, Halobacterota, Cyanobacteria, Chloroflexi, Planctomycetota, and Myxococcota in the rhizosphere of the plants.

Patel et al. studied the overcrowding stress-induced proteomic changes in lumpfish (*Cyclopterus lumpus* L.), which showed signs of allostatic overload type 2 (chronic stress) due to oversensitivity to ACTH and a reduced negative feedback system with increased baseline levels of cortisol.

Sharma et al. evaluated the ameliorative effects of *Withania somnifera*, *Embllica officinalis* and *Achyranthes aspera* (L.) in UV-B ray exposed *Catla Catla* and found that all the three medicinal plants helped the fish to overcome the harmful effect of radiation.

Ghosh et al. have vividly reviewed the growing importance of marine bioactive components, including their origins, classification, possible health advantages, green extraction processes (both traditional and developing), biomedical applications, and food applications.

Indeed, this Research Topic is multifarious in its scope; it covers studies on both the stress response and amelioration strategies. The information generated in the studies has used some of the most contemporary techniques like transcriptomics, proteomics, and metagenomics. We are hopeful that the articles will be helpful to researchers and policymakers working in the field of marine environmental monitoring and management.

AUTHOR CONTRIBUTIONS

All authors listed have made a substantial, direct, and intellectual contribution to the work and approved it for publication.

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The remaining authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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