

## Genomics and Aquaculture Developments: An Overview

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### EDITORIAL

Genomics defines as sequencing and understanding the functionality of large set of DNA as well as RNA contained in organisms and an ability to manipulate them could function as plausible benefits that could be acquired from this field. The last decade is found to have exponential growth in sequencing technologies and bioinformatics tools, especially in extraction of genomic data from organisms which can be used in improving both fundamental knowledge and their application in aquaculture, ecology and fisheries. For development of sustainable food security towards the world's increasing demand for high protein food via aquaculture and fisheries, progress in genomics is absolutely essential. Despite of being overwhelmingly advantageous and beneficial, practical use of genomics application is not common in aquaculture production and fisheries management as expected. The need for greater communication among fishery scientists, geneticists, and fishery managers, as well as better communication of the potential of genomics approaches and results to stakeholders thru the adoption of a clear and understandable communication, are among the possible solutions to stimulate wider application of genomics knowledge.

Research shows that researchers used single nucleotide polymorphism markers (SNPs) to find quantitative trait loci (QTL) for the body form of the huge yellow croaker, demonstrating the potential of genome-wide correlations (*Larimichthys crocea*). Multiple genes in four QTL areas appear to be responsible for body form. The markers discovered can now be used to select for body shape in aquaculture breeding programmes, a trait that is desired.

Transcriptomics was used to identify transcripts exclusive to the testis (897) and ovary (13) and then explore their possible function in sex-related events using the same species.

Researchers examined the differential expression of genes in the brain, liver, and muscle of rapid and slow growing European sea bass (*Dicentrarchus labrax*) from a shared population using a distinct transcriptomics methodology. This research adds to our understanding of the molecular basis of growth variation in European sea bass, but it is likely to be applicable to other species as well. The findings imply that divergent growth may be caused by alterations in endocrine regulatory pathways including insulin-like growth factor, insulin, and the stress axis.

The regeneration potential of the retina of the ed-claw crayfish (*Cherax quadricarinatus*) complex eye was investigated using transcriptomics. The scientists discovered differently and uniquely transcribed retinal genes in regenerating and non-regenerative eyes, as well as processes that may regulate ocular regeneration in the crustacean compound eye, by comparing regenerating and non-regenerating eyes.

Finally, transcriptomics can be employed to discover the carpet-shell clam's immune repertoire (*Ruditapes decussatus*). C1q domain-containing proteins (63), tumour necrosis factors (15), and toll-like receptors (15) were the gene families with the largest representation in the immune system (10). Further phylogenetic research revealed a large diversity of toll-like receptors, as well as lineage-restricted expansions.

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**Received:** May 20, 2021, **Accepted:** May 25, 2021, **Published:** May 30, 2021

**Citation:** Sri Lakshmi A (2021) Plastic and its Effect on Marine Environment. J Aqua Res Dev 12: 638.

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