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Genomic Research in Fishery Sector: Current Status and Future Prospects

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Large scale efforts on genomics has resulted in greater understanding of the genomic architecture, their evolution and underlying biological mechanisms in fish. Although, significant achievements in fish genome sequencing initiatives have been undertaken globally, further targeted efforts are needed to realize its full potential. It is expected that the knowledge of structure and function of genomes and their interactions with non-genetic components of production systems will help to improve productivity, as well as in conservation and sustainable management of fisheries. In this direction, integrative multi-omics data intensive projects may be carried out in consortium mode research by pooling the expertise from different domains. These efforts will pave way for efficient resource use, to reduce production cost and increase farmers' income.

Introduction

Fish genetic resources (FGR) are vital for their role in food security, nutrition and livelihood generation. As per key UN Goal of 2030 for Sustainable Development, the capture fisheries and aquaculture, which form important components of fish genetic resources, shall have to play an essential role in meeting nutritional security and achieving sustainable development. For this purpose, an urgent need is felt for mainstreaming agrobiodiversity, which includes its characterization, conservation and sustainable utilization. With the limitation in increasing capture fishery production, aquaculture is the next best option for meeting the demand of growing population. The FGR offers its diversity for improving the production of domesticated species and provides new species for diversification of aquaculture. It also supports the country's foreign exchange, including seafood exports as well as ornamental fish trade. Traditionally, the genetic improvements in fisheries were achieved through the selective breeding programmes, however, with the advancements of modern genomic tools, it is now possible to address biological queries or alter phenotypes in the ways not previously imagined. Application of genomics in fisheries has resulted in a significant surge in bio-prospecting of genes and allele mining, whereby several novel genes and alleles have been discovered, which may have potential role in increasing production and planning conservation strategies. This article focusses on some of the strides made in fish genomic research in India along with future prospects.

Genome Sequencing

Whole genome information provides insights into structure and organisation of genes, which gives understanding into their function and roles in biological systems. The genome re-sequencing offers opportunity to unearth and understand the genomic variations, developing genome-wide markers to estimate genomic variability and for their associations with a particular trait, while comparative genomics helps to infer evolutionary processes and ancestry of the genes among the species. The completion of human genome project, at the turn of the century, followed by advancements in massive parallel high-throughput DNA sequencing technologies and strong computational tools, have transformed the genomics sector in a significant manner. Human genome sequencing initially employed Sanger sequencing, which even though produced high-quality DNA sequences, was time and cost intensive. Second (Next) generation sequencing (NGS) methods in early 2000s, like pyrosequencing (Roche 454), bridge amplification-based sequencing (Illumina) etc., heralded large scale genomics research in fisheries sector. It was followed by Third Generation Sequencing (3GS) technologies, like Pacific Biosciences Sequencing and Oxford Nanopore Technologies that can produce long reads, revolutionised the study of fish genomes at a high resolution. Genome sequencing projects in fish started in the early 2000s, with Japanese pufferfish, *Fugu rubripes*, to be the first to have its whole genome sequenced in 2002. In 2009, Genome 10K Project was launched by a consortium of scientists in Santa Cruz, California to sequence 10,000 vertebrate genomes, including 4000 fish species, with a mission to understand how complex animal life evolved through the changes in DNA. The project aimed to sequence at least one individual from each of the ~66,000 vertebrate species. The publication of zebrafish (*Danio rerio)* genome in 2013 started a new

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**Author for Correspondence: E-mail-Mohindra.Vindhya@icar.gov.in* chapter in fish genomics.

In 2020, Fish10K (The 10,000 Fish Genomes) Project was announced, as a sub-project of Earth BioGenome project, to exclusively sequence 10,000 fish species, with an aim to study the evolution and development of vertebrates, based on the big data of fish genomics. In contrast to the draft assemblies generated earlier, the focus is now to use combination of short-reads, long-reads and Hi-C technologies to construct chromosomal-level genome assemblies. Globally, around 867 fish genomes were sequenced and assembled at different levels (https://www.ncbi.nlm.nih.gov/ genome, accessed on August 22, 2022), which included genome sequences of over 86 aquaculture species. The smallest assembled genome is that of silver spinyfish, *Diretmus argenteus* (302.36 Mb), while the largest one cloudy catshark, *Scyliorhinus torazame* (4470.98 Mb) (https://www. ncbi. nlm.nih.gov/genome/?term=Scyliorhinus+torazame).

In India, several fish genomes have been sequenced and assembled under different schemes, includes magur (*Clarias magur*); rohu (*Labeo rohita*) by ICAR-NBFGR and ICAR-CIFA under DBT funding; hilsa shad (*Tenualosa ilisha*), and catla (*Catla catla*) by ICAR-CIFA and ICAR-NBFGR and White Shrimp (*Penaeus indicus*) by ICAR-CIBA under Consortium Research Project (CRP) on Genomics of ICAR led by ICAR-NBFGR; wild variant of zebrafish (*Danio rerio*) by CSIR-IGIB, New Delhi, pabda (*Ompok bimaculatus*) by AIIMS, New Delhi. An oomycete (*Aphanomyces invadens*), a fish pathogen, has also been sequenced at ICAR-NBFGR. Several gene variants and novel genes were identified for the first time in fish in these studies. ICAR-NBFGR has also developed a databases on AqGR such as AqGRISI (Aquatic Genetic Resource Information System of India), FBIS (DNA barcode information), FishMicrosat (microsatellite information), FMiR (mito-genome resource), Fish Karyome (chromosome information) and HRGFish (hypoxia responsive genes) focused on fisheries (Murali *et al.*, 2019). Mitochondrial genome is a valuable resource not only for species identification but also for understanding the evolution and phylogenetic distribution of the species. It has a small size (16-17 kb) and circular structure with maternal inheritance, rapid evolution, limited recombination and variable evolutionary rates across its genes. Globally at present, mitochondrial genomes of over 2900 fish species, representing about 426 families under 67 orders, have been sequenced (https://mail.nbfgr.res.in/fmir/).

Transcriptome Sequencing

If genome is said to be the static molecular part, then the transcriptome, consisting all of the mRNA, rRNA, tRNA and ncRNA etc., can be called as the dynamic part. Transcriptome sequencing or RNA-Seq is an important tool, that utilizes deep sequencing technologies and facilitates to understand the functional structure and large-scale expression profiles of the genes. It has the potential to enhance our understanding of the relationships between the genotypes and the phenotypes, in relation to varying biology and environment, which in turn would explain involvement of the genes, through their expression profiles, influencing a particular trait.

Fish-T1K (Transcriptomes of 1,000 fishes) project was launched in 2013, jointly by Beijing Institute of Genomics (BGI) and China National Genebank (CNGB) to generate large-scale transcriptome sequences for 1,000 diverse fish species, for evolution studies in fishes. Over 98,400 RNA-Seq reads data on fish species can be found in NCBI SRA database (https://www.ncbi.nlm.nih.gov/ sra/?term= RNA-Seq+AND+Fishes, accessed on August 22, 2022). It has resulted in greater understanding of biotic- (bacterial and fungal), abiotic- (hypoxia, ammonia, salinity, temperature etc.) stress tolerance mechanisms and understanding of biological processes, such as growth, reproduction, disease resistance etc. In India, the transcriptome sequencing works have been undertaken for identification of genes controlling important production traits like growth, disease resistance and reproduction; and marker discovery. The species include Indian major carps (*Labeo rohita* and *Catla catla*), hilsa shad (*Tenualosa ilisha*), magur (*Clarias magur*), Nile tilapia (*Oreochromis niloticus*), common carp (*Cyprinus carpio*), Indian white shrimp (*Fenneropenaeus indicus*), spotted snakehead (*Channa punctata*).

Molecular Markers Discovery

Rapidly advancing molecular and computational tools have led to generation of gigantic information and associated population level molecular markers. These provides indispensable insights onto the taxonomic position, phylogeographic positions, conservation management units, population profiles and demographic history of the species of concern. Studies have demonstrated the application of genomics led conservation studies (Garner *et al.*, 2016; Stockwell *et al.*, 2016). Mitochondrial markers and genomic (microsatellite) marker panels have been developed for several freshwater and marine fish species, useful in stock characterization across their natural range of distribution, which have applications in conservation as well as selective breeding programs. Large-scale Single nucleotide polymorphism (SNP) were recently identified in riverine populations of *L. rohita*, which have the potential to be valuable genomic resource.

Future Prospective and Action Points

Integrative multi-omics technologies need to be carried out for specialised, commercially and evolutionary important freshwater and brackish/marine species, for unique insights into the deeper fundamental biological understanding of their genomic architecture. These omics technologies may include genomics, transcriptomics, proteomics and metabolomics. This will facilitate effective genome mining for bioprospecting of novel genes and alleles from unexplored genetic diversity, for important production traits, stress (biotic and abiotic) tolerance and their biomarkers. The mechanism of osmoregulation in response to long term salinity challenge, the integrated analyses of metabolomics and transcriptomics has been successfully studied (Qin *et al*., 2022). These technologies also help in overcoming the diseases in aquaculture, by studying gene expression profiles in combination with immune-related biosynthetic pathways during host-pathogen interactions. Innovative multi-omics strategies can also be formulated to discover natural products, especially the marine metabolites and novel molecules with biological activity, which may have the potential for converting them into commercial products.

For application of Integrative multi-omics technologies, consortium mode research would prove to be the pre-eminent way to operate data intensive projects, where the pooling of expertise from different domains can provide paramount output for public goods.

Indian major carps (IMCs) are the backbone of Indian freshwater aquaculture and Ganga basin is the home of their origin. Extensive genomic resources of IMCs need to be generated for different populations to identify selection signatures, to understand genome diversity and variations for the genetic basis for domestication and adaptation to diverse environments. Availability of genomic resources would allow to identify the genomics regions/genes under selection and their link to important production traits. This would lead to the development of tools for genomic selection, to be utilized for future selective breeding programs for increased production.

Genome information forms the basic information for various genome editing technologies, which has potential to transform the aquaculture and trade. Most of the gene editing research is focussed on economic traits, like growth, disease resistance, sterility etc. It looks possible in future, to design a tailor-made fish through genome editing technologies, as per the needs of aquaculture trade or consumer preference, like skin colouration and pigmentation, nutritional profile, meat quality, texture etc.

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