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Application of omics technologies in aquaculture: Current advances and future perspectives

Deepika*, Bindu Sharma
Department of Zoology, Chaudhary Charan Singh University, Meerut, Uttar Pradesh, India
Corresponding Author: Deepika*
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Abstract
The modern aquaculture industry heavily relies on omics technologies. The development of omics technologies has made it possible to comprehend the fundamental processes of fish reproductive development and has paved the way for new advancements in the field of fisheries. New concepts for selective breeding, growth, adaptations, etc., for many fish species are being shaped by several genome-based studies. Epigenetics deals with the changes in gene expression for a variety of economically significant traits that are independent of DNA modifications. Proteomics helps in the analysis of fish protein profiles and their quality. Fisheries research is being conducted in new areas of omics, such as glycomics, the study of complex sugar compounds; lipidomics, the study of cell lipid profiles; and metabolomics, the study of intermediate metabolic products. Fish RNA sequencing or next-generation sequencing, or transcriptomics, can be used to find unknown genes and analyze their expression patterns. These tactics do more than just maximize aquaculture; they also strengthen conservation efforts and create resilient, sustainable futures for fish species around the world.

Keywords: Aquaculture, genomics, epigenomics, transcriptomics and metabolomics

Introduction

Aquaculture is a fast-growing field for food and livelihood. Suboptimal reproductive performance in fish is a major economic limitation of aquaculture by restricting the production of quality seed and limiting population growth (Honji *et al.*, 2025) [13]. Comprehensive evaluations of population dynamics, genetic composition, species identification and gene functional characterization are necessary for the sustainable growth of the sector. Accordingly, the application of genetics and biotechnology provides essential tools for advancing research and innovation (Tripathy *et al*., 2022) [33]. Analysis of stock, genetic composition, identification of unidentified species, functional aspects of genes, etc., are all necessary for the development of any industry that interacts with living things. Biotechnology and genetics are supporting this. In the early 2000s, researchers were able to examine the interactions between different molecular strata thanks to the development of mass spectrometry, next-generation sequencing and sophisticated data integration, which marked a paradigm change towards biology. Omics technologies are a collection of high-throughput methods intended to objectively examine the structure, function and interactions of biomolecules, such as genes, transcripts, proteins, lipids, and metabolites, inside biological systems (Horgan and Kenny, 2011) [15]. The primary omics fields in aquaculture systems are genomics, epigenomics, transcriptomics, proteomics, metabolomics and metagenomics (Fig.1)

"Multi-omics analysis" is a biological research approach that entails the simultaneous study of multiple types of molecular data from a biological sample. These kinds of data can be generated by genomic, transcriptomic, proteomic, metabolomic and other "omics" methods. Researchers can learn more about biological systems and the complex interactions between different substances and metabolic pathways by using multi-omics analysis. By combining a range of data types, multi-omics analysis helps create customized treatment tactics, identify new biomarkers and illuminate diseases that were previously unknown (Turanli *et al.*, 2018) [34]. Multi-omics analysis generates large and complex data sets that require the use of advanced computational and statistical methods. For instance, integrating metabolomics data can assist in finding metabolic pathways linked to particular diseases, while combining proteomics and genome data can help identify post-transcriptional modifications that affect protein function. (Ohashi *et al.*, 2015) [24].

A multi-omics approach, also known as poly-omics, pan-omics, trans-omics, integrative omics, vertical omics or systems omics, integrates two or more omics layers and provides a thorough framework for analyzing intricate biological processes in aquaculture organisms (Bashura *et al.*, 2021) [3]. Initiatives in precision medicine that employ multi-omics to determine genetic profiles unique to each patient have grown in popularity. These days, the incorporation of multi-omics data not only enhances our comprehension of biological systems but also expedites the diagnosis of diseases, the search for new drugs, and the creation of customized treatment regimens, confirming its status as a pillar of contemporary biomedical research. Advancements in high-throughput technologies and bioinformatics have led the field of multi-omics research to move from discrete single-omics investigations to a comprehensive, integrated approach. To understand the genetic foundations of diseases and the regulatory frameworks that accompany them, research has mostly focused on genomics and transcriptomics (Xu *et al.*, 2017) [37].

Multi-omics studies are becoming more and more important in fields pharmaceutical development and oncology research, etc. The integration of different omics data types is advancing both our understanding of complex biological systems and the creation of new insights into the underlying

molecular causes of disease (Bansal *et al.*, 2023) [2]. However, the integration and analysis of multi-omics data sets can be challenging and needs advanced computational resources, specialist knowledge from several domains and the development of new analytical methods. The development of new therapies and cures as well as our understanding of biological systems, could be completely transformed by the formidable technique of multi-omics analysis.

Despite the fact that the fundamental genetic information is recorded in genomic sequences, intricate regulatory interactions between genotype, expressed phenotype and environmental factors dictate performance and production characteristics. (Wang *et al.*, 2009; Hill and Kirkpatrick, 2010) [36, 13]. High-throughput datasets that shed light on specific molecular and cellular components are available across these disciplines (Mohanty *et al.*, 2019) [21] to better understand genetic diversity, structural organization and heredity. The entire DNA repertoire of an organism, tissue, or cell is examined via genomics (Mushtaq *et al*., 2025) [22]. Epigenomics studies how chemical and structural changes to DNA and RNA affect chromatin dynamics, gene regulation and epigenetic inheritance without changing the nucleotide sequence (Russell, 2010) [29]. In order to quantify gene activity, alternative splicing patterns and regulatory processes involving both coding and non-coding RNAs. The worldwide expression profile of RNA transcripts is the main focus of transcriptomics. In order to describe the structures, functions, post-translational modifications and molecular interactions of proteins, proteomics examines the entire proteome. Metabolomics shows cellular fluxes, metabolic regulation and biochemical pathways by analyzing the entire spectrum of metabolites (Davis, 2005) [6].

Genomics

The structure, function, evolution, mapping and editing of genomes are all considered in the biological area of genomics. An organism's whole DNA collection is called its "genome." The sequencing, assembly, and study of the entire genome's structure and function are all included in genomics. In order to sequence and comprehend genes, gene interactions, genetic elements and the structure and development of genomes, this subdiscipline of genetics combines classical and molecular biology. Genomic resources like whole-genome reference sequences, high-density SNP genotyping arrays and genotyping-by-sequencing are being used for several aquaculture species. When combined, these resources can be effective tools for a variety of studies and for identifying the genetic components that regulate complex features in the aquaculture industry. Fish genome analysis can be useful in several ways, from developing breeding plans to determining the causes of any species captive breeding failures and fish growth. DNA sequencing and genotyping are two of the key technologies in genomics. DNA sequencing identifies the nucleotide order of a DNA molecule. In contrast, genotyping includes identifying genetic differences, such as single nucleotide polymorphisms (SNPs), in a specific region of the genome (Devyatkin *et al*., 2024) [7].

Applications for genomic data include population genetics research, predicting treatment responses and identifying mutations that cause disease. For example, genomic data has been used to identify cancer cell mutations that drive tumor growth and to develop customized therapies that target these mutations (Ferguson *et al*., 2015) [9]. It has also been used to identify genetic differences associated with drug response, opening the door to individualized medical therapies that consider a patient's genetic profile. Genomics, a crucial multi-omics data type, offers a plethora of information about the genetic makeup of an organism and its possible effects on health and disease.

One of the primary problems is the enormous amount of genomics data; DNA sequencing can produce terabytes of data, which need specialized processing power and knowledge to manage and assess. (Schmidt *et al*., 2017 & Varsamis *et al*., 2023) [30, 35]. However, advances in data processing methods and sequencing technology have made genomics data more accessible and affordable in recent years. Genomics, a key multi-omics data type, provides important insights into an organism's genetic composition and potential impacts on health and illness. It can lead to important findings in several fields, including evolutionary biology, drug development and personalized medicine.

Proteomics

Proteomics is the study of every protein expressed by a cell, tissue, or organism that can provide insight into the functional and regulatory networks that govern cellular functions. Proteomics data can be generated using a variety of techniques like protein microarrays, mass spectrometry and high-throughput sequencing (Pelletier *et al*., 2020 & Ran *et al*., 2020) [25, 27]. One of the main applications of proteomics is the identification of biomarkers for disease prognosis and diagnosis. By examining the proteomes of patients with different conditions or illness stages, researchers can identify proteins that are mislocalized, post-translationally modified, or expressed differentially. These proteins can then be used as possible therapeutic targets or as markers for diagnosis or prognosis.

Proteomics data can be used to investigate protein–DNA interactions, protein–small molecule interactions, and protein–protein interactions. By mapping these connections, researchers can identify key regulatory networks and communication pathways that govern biological processes. For example, proteomics data can be used to identify the proteins that interact with a specific transcription factor (TF) and map its downstream targets. Proteomics has another important use in the field of structural biology, which aims to understand the three-dimensional structures of proteins and how they interact with other molecules. Proteomics data can be used to identify protein complexes and techniques like cryo-electron microscopy or X-ray crystallography can be used to study their structures (Schmidt *et al*., 2017) [32]. Structural biology has greatly benefited from neural networks, particularly in the area of protein folding. Their capacity to reliably anticipate protein structures and produce new ones creates new opportunities for medicine development, biotechnological application advancement and biological process knowledge. Like transcriptomics data, proteomics data requires complex data processing techniques and computational tools.

AI and machine learning techniques can be used to predict unknown protein functions and large-scale proteomics datasets can be examined for trends and correlations. Our understanding of how proteins work and are regulated depends on proteomics, a critical multi-omics data type (Liang *et al*., 2020) [18]. In the rapidly evolving field of

proteomics, several new emerging technologies and methods are transforming the research and analysis of proteins. For example, a new technique called single-cell proteomics allows researchers to look at the proteome of a single cell rather than a tissue or cell population. This could clarify cell-to-cell variance and make it easier to find new biomarkers or treatment targets. PTM research is another emerging area of proteomics (Hashiguchi *et al*., 2016) [12]. PTMs are chemical changes that occur after a protein is made and may have an effect on the stability, structure and functionality of the protein. Using proteomics methods like protein microarrays and mass spectrometry, PTMs can be identified, measured and their functional role in biological processes examined.

Metabolomics

Metabolites are intermediates and products of metabolism. To put it another way, it can be described as the methodical investigation of the distinct chemical signatures of particular biological functions. The whole collection of metabolites in a biological cell, tissue, organ or organism that are the byproducts of various cellular processes is referred to as the metabolome in metabolomics. Currently, aquaculture uses two popular metabolomic techniques: mass spectrometry (MS) and nuclear magnetic resonance (NMR). Fingerprinting is a metabolomics technique that builds a model based on all analytical variables derived from metabolite detection through high-throughput analysis of a large number of fish species. This method can be applied to in fish farming. Comparably, profiling is an additional method that is predicated on the identification of analytical variables produced by the biological system's nonselective analysis (Roques *et al*., 2020) [29]. For qualitative analysis of metabolic pathways caused by internal or external causes, metabolite identification is crucial.

Research on fish nutrition, health and welfare as well as how the environment affects fish has benefited from metabolomics in aquaculture. Environmental metabolomics examines how physical, chemical and biological stresses affect fish metabolism. Metabolic pathways are affected by internal or external factors; metabolite identification is crucial for qualitative analysis. The illness caused by pathogen infection in farmed fish is currently being investigated using metabolomics. Fish nutrition research is the most significant application of metabolomics in aquaculture systems. Sampling and analytical sample preparation, data capture, data processing, statistical analysis and biological interpretation are the fundamentals of the metabolomics workflow. The two primary tissues that are examined for metabolism and metabolic pathways are muscle and liver. Metabolomic techniques, many important biological and environmental biases to be taken into account, including season, tank influence, fish gender, sexual development, and ambient or water quality parameters. Metabolic pathway studies in aquaculture are investigated through plasma, serum, stomach contents, feces, mucus, skin, etc.

Transcriptomics

Transcriptomics is the study of the transcriptome, which deals with the total of an organism's RNA transcripts. The last ten years have seen a revolution in molecular biology techniques for aquaculture development due to the use of new next-generation sequencing technology to investigate the entire collection of transcripts of a particular organ or tissue. In order to compare various physiological or environmental variables, investigations using a control and a treated specimen in the same experiment have benefited from modern RNA-sequencing technologies using a transcriptomics method. In transcriptomics, Next-Generation Sequencing (NGS) tools like Illumina, Pyrosequencing, PacBio, etc. are used for library creation and sequencing following sample collection and RNA isolation. Trimmomatic software transforms the raw readings produced by NGS into high-quality reads. After that, Trinity software is used to prepare the high-quality reads for de novo pooled transcriptome assembly in a single file. SAM tools, BWA and the CD Hit test are used to predict and validate various gene segments, or Unigenes. Trans Decoder, BWA, and SAM tools employ these unigenes to predict Coding Sequences. The anticipated CDS is then used for three different kinds of analysis. First, BLASTX predicts the functions of various genes, or functional annotation. Next, Blast2GO classifies genes to their corresponding functional categories, or gene ontology. The expression of various genes from the samples is ascertained by quantifying CDS using DESeq for differential gene expression analysis. KEGG performs gene pathway analysis. Recently, the transcriptomics technique has been used to identify distinct genes and their expression for the development of aquaculture species.

Metagenomics

The study of genetic material obtained directly from environmental samples is known as metagenomics, a branch of genomics. Researchers use terms like environmental genomics, ecogenomics, and community genomics as synonyms for metagenomics. Captive stress conditions that result in a variety of diseases are the main issue facing the aquaculture sector. Similar to other vertebrates, fish have microbial communities in their guts that boost their general size, immunological response and eventually, defense against other infections.

Microbiomes are microbial populations that are beneficial to the environment, whereas gut microbiomes are not. Probiotics can help combat the rise in antimicrobial-resistant (AMR) bacteria that cause fish illnesses in recent years (Yukgehnaish *et al*., 2020) [40]. To employ them as probiotics for aquaculture, research based on gut microbiome metagenomics is crucial. Probiotics are far superior to conventional antibiotics in aquaculture because the latter eventually lead to the development of AMR bacteria. When it comes to the application of probiotics in aquaculture, there are numerous noteworthy accomplishments. *Oncorhynchus mykiss*, or rainbow trout, have been treated with *Aeromonas hydrophila* as a probiotic to prevent *Aeromonas salmonicida* infection (Irianto and Austin 2002) [16]. According to Granados-Amores *et al*., (2012) [10] is employed in *Crassostrea corteziensis* (Lions-pay scallop) to improve growth and sur*vivo*rship. Metagenomics can be used to identify helpful bacteria in soil and water in addition to researching the anti-pathogenic effects of various gut microbiota. This will aid in the monitoring of aquaculture water quality metrics in the future. Gathering samples from natural sources (soil, water, or fish stomach) is the initial step in the metagenomics analysis process, depending on the type of inquiry. It is necessary to collect DNA from these bacterial habitats

before building a metagenomic DNA library. The libraries are used to mine DNA sequences and clones. After that, these DNA sequences are separated into two categories: long inserts (Fosmids/Bacterial Artificial Chromosomes (BACs)/cosmids) and short inserts (plasmids). Short inserts are taken for sequence-based analysis, while extended inserts are analyzed functionally. Good clones and appropriate sequences are then extracted for special bacteriological or other biotechnological uses. Similar to this, environmental DNA (eDNA), which is derived from collected soil or water samples, is currently utilized for pond biomass calculations, fish species identification from natural sources and metagenomic analysis of biodiversity.

Neurogenomics

The study of an organism's genome in connection with its neurological system is known as neurogenomics. Functional genomics and neurobiology are combined in this field. In certain commercial and ornamental fish species, parental care is crucial for the survival of offspring, the continuation of the race and protecting offspring from predators, etc. Fish that exhibit parental care include tilapia, cichlids, African lungfish, darter fish, stickleback fish and fighter fish. In order to benefit from neurogenomics, it is crucial to investigate these parental concerns and the associated neurological behavior. Neurogenomics can be used to analyze associated life events, such as phases of territory building, pair bonding, dispersal, etc., and to research parental care at the molecular level (Bukhari *et al*., 2019) [5]. Measuring gene expression (RNA-Seq) in the male and female brains of fish allows for the analysis of neurogenomic dynamics. In addition to shedding light on the riddles surrounding mating, egg care, hatching and fry care, this will provide more understanding of the genes and their expression during parental care. RNA-Seq, RNA-Seq informatics, and the subsequent identification of several DEGs (Differentially Expressed Genes) comprise the neurogenomics methodology. Following the identification of distinct genes, functional analysis is carried out after Transcriptional Regulatory Network (TRN) analysis. Additionally, neurogenomics will aid in the research of neural behavior associated with reproduction, photoperiodism, brain hormone secretion, etc.

Pangenomics

Another new area of genomics that examines the pan-genome is called pangenomics. A species full gene set across all strains is called its pan-genome. Disease outbreaks are a significant issue in the aquaculture sector, particularly in prawn or shrimp farming. Determining each strain and the bacterium's virulence is essential to fighting it. Pangenomics enables detection of the core genome, which contains genes shared by all strains in the clade, as well as genes that are important contributors to strain-specific virulence. The predicted genes can be annotated against the NCBI non-redundant database, Gene Ontology (GO) and Swiss-Prot databases using DIAMOND software. The genome sequences of the causative bacteria and virus can be obtained through RNA-Seq or from previously submitted sequences in the National Center for Biotechnology Information (NCBI) database (Buchfink *et al*., 2014; Nourdin-Galindo *et al*., 2017) [4, 23]. KEGG database is used to retrieve the metabolic pathways. Gene sequences and an out-group are then used for phylogenetic and phylogenomic analyses. The NCBI BLASTp algorithm is used to evaluate the core and pan genomes and identify virulence factors in the pan genome (Altschul *et al*., 1990) [1] and the Virulence Factor Database are utilized. The 5S, 23S and 16S rRNA gene sequences of every strain are then predicted using RNAmmer software (Lagesen *et al*., 2007) [17] for genomic comparisons across the various strains and genogroups using NCBI BLASTn (Altschul *et al*., 1990) [1].

Epigenomics

The full collection of epigenetic modifications on a cell's genetic material, or "epigenome," is the subject of epigenomics. The study of heritable variations in gene expression that are unrelated to variations in DNA sequence is known as epigenetics. The study of fish epigenetic mechanisms is still in its early stages. This can show how aquaculture animals respond to their environment in terms of phenotypic plasticity, or the ability of a single genotype to display a range of phenotypes under different environmental conditions. Additionally, aquaculture species have high variety, high fecundity, amazing flexibility and substantial economic advantages, presenting good study prospects in the field of fisheries epigenomics for the upcoming blue revolution. The addition of a methyl group (CH3) to position 5 of a cytosine's pyrimidine ring (5mC) is known as DNA methylation, and it is the most extensively researched method in aquaculture epigenomics. In eukaryotic cells, these 5mC primarily occur on the transcription start site of a gene or a cytosine-phosphate-guanine (CpG) island, which modifies the expression of a gene. Additionally, by altering the chromatin organization of nearby genes, the DNA methylation process can control their transcriptional activity. An additional source of heritable variation apart from genetic diversity is provided by these epigenetic mechanisms, which can differ between fish species and be preserved at the individual level and eventually passed on to later generations. (Metzger and Schulte 2016) [20]. Single-base-pair resolution, intermediate resolution, and low-resolution assessment of global DNA methylation are the three methods used to study epigenomics using DNA methylation.

One of the most quantitative techniques for figuring out whole-genome DNA methylation levels at low resolution rates is reverse-phase high-performance liquid chromatography (RP-HPLC). DNA is first broken down into single nucleotides using this technique. Because cytosines and methylated cytosines have distinct molecular masses, HPLC or liquid chromatography combined with tandem mass spectrometry (LC–MS/MS) can efficiently quantify them. Low resolution measurement of DNA methylation can also be aided by ELISA-based techniques. Purified genomic DNA is first hybridized to test wells using ELISA-based techniques. An antibody specific to methylated cytosines is then used to identify methylated DNA. A secondary enzyme-linked antibody is then used for colorimetric measurement. Several manufacturers are selling commercial kits for these methods. These methods have a low-resolution rate and only detect very big deviations, which are their two main shortcomings.

Another technique for evaluating DNA methylation patterns at intermediate resolution is the methylation-sensitive amplified polymorphism analysis (Reyna-López *et al*., 1997) [28]. Genomic DNA is first broken down by methylation-sensitive and non-methylation-sensitive

isoschizomeric restriction enzymes, Hpa II and MspI, respectively. Fluorescent-tagged primers are used to amplify the DNA fragments once they have been ligated to adapters. The PCR data are then assessed using gel electrophoresis or capillary electrophoresis. The methylation status of a certain locus is determined by the band pattern of digested DNA using the restriction enzymes Msp I and Hpa II. Differentially methylated genes can then be identified by isolating and sequencing these bands that are visible on gel electrophoresis or capillary electrophoresis. Once more, this method's drawbacks include poor reproducibility, anonymous locus screening and low-resolution rates.

The bisulfite conversion process can be used to methylate DNA with single-base-pair resolution. This approach involves first treating the DNA with either metabisulfite or sodium bisulfite. The unmethylated cytosine bases (C) are transformed into uracil (U) as a consequence of this bisulfite treatment. However, methylated cytosines (5mC) do not create uracil. PCR amplification changes the original sequence from a C to a T in unmethylated places, while methylated positions remain Cs. This helps to estimate DNA methylation accurately. Methylated DNA immunoprecipitation and sequencing (MeDIPseq) and methyl CpG binding domain immunoprecipitation and sequencing (MDBseq) are two new techniques to lower the cost of whole-genome bisulfite sequencing (WGBS). These days, several restriction-enzyme-based techniques for DNA methylation are used, such as EPIRAD Seq and reduced representation bisulfite sequencing (RRBS). The RRBS approach precisely targets CpG patterns by digesting the genomic DNA with a methylation-insensitive restriction enzyme, such as MspI. Following bisulfite treatment, these fragments are sequenced. As an alternative to the RRBS method, EpiRADseq enables sequencing efforts to be focused mainly on areas of the genome that are likely to be methylated (Gu *et al*., 2010) [11]. Two restriction enzymes—methylation-insensitive PstI and methylation-sensitive HpaII—are utilized in EpiRADseq to doubly digest the genomic DNA.

Since the methylation-sensitive restriction enzyme can only cut unmethylated DNA, the methylation can be ascertained by comparing the frequencies at which loci are tested. Therefore, this method solely yields data regarding the methylation status at the enzyme cut-sites. Fish muscle quality development, selective breeding, color, location-based commercially significant phenotypic alterations and other aspects of aquaculture are already being addressed by epigenomics.

Lipidomics

The vast field of study known as "lipidomics" is concerned with the networks and pathways of cellular lipids in biological systems. The entire lipid profile found in a cell, tissue, organism, or ecosystem is referred to as the "lipidome." Currently, research efforts are mostly focused on improving the quality of fish muscles. For this reason, it is crucial to first research the lipid profile of muscle and the various environmental factors that impact muscle quality. Fish muscle is first sampled and stored in vials filled with liquid nitrogen. The muscle samples are taken for the extraction of lipids after being homogenized and freeze-dried. Ultrahigh-performance liquid chromatography (UHPLC) is then used to inject these lipid extracts. Mass spectrometry (MS) is then applied to the separated samples. One analytical method for ionizing samples and determining their mass-to-charge ratio (m/z) is mass spectrometry. After that, the MS raw data are displayed for additional statistical analysis and interpretation. Fatty Acids, Fatty Acid Derivatives, Fatty Acids Metabolism, Glycerolipids, Glycerophospholipids, Sphingolipids, Isoprenoids, Sterols, Lipids CLASS, Phospholipids, Wax Esters, Olive Oil Phenols, etc. may all be analyzed using lipidomics in aquaculture.

Glycomics

The study of an organism's whole collection of free or more complicated sugar molecules is known as glycomics. Glycans are chain-like structures made of single sugar molecules (monosaccharides) that are linked to proteins and lipids in living things, while glycomes are the total amount of carbohydrates in a cell. Human central nervous system development, cartilage formation, muscle dystrophies, skeletal disorders, neuromuscular transmission abnormalities, neurocutaneous illnesses and inflammatory bowel disease are among the several glycan-based diseases. In the near future, these can be treated and researched using the zebrafish model of glycomics. The synthesis and processing of glycans, which are essential for numerous biological processes, are thought to account for 1% to 2% of the vertebrate genome (Yamakawa *et al*., 2018) [39]. Tissue samples are first dissected, cleaned, homogenized using a mechanical disperser and then freeze-dried for fish glycomics. The tissues are then removed to purify glycans, specifically N-linked glycans (NGs), O-linked glycans (OGs), and glycosphingolipids (GSLs). After being purified, the glycans are extracted in chloroform, repeatedly cleaned with water, permethylated using NaOH/dimethyl sulfoxide and then taken for MS analysis. For additional analysis, monosaccharide analysis, lipid derivatizations, IHC, WB and qPCR are performed. Glycomics can help detect bacterial and viral illnesses because glycoproteins and glycolipids are the cell surface detectors for these infections. Studying cellular signaling pathways, innate immunity, cancer development, protein stability and folding, the pathway and destiny of glycoproteins, etc. can all benefit from it. Glycomics can be used to develop several new medications and glycoconjugate vaccines in the near future.

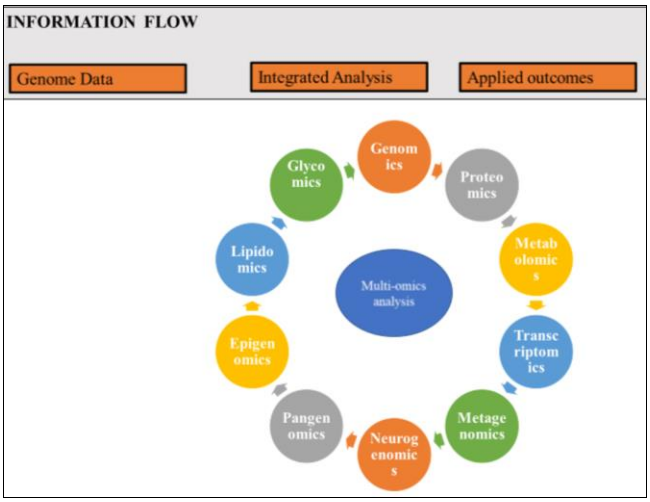

Fig 1: Diagrammatic representation of Omics technologies in aquaculture

Conclusion

Numerous novel approaches for unique gene identification, marker-assisted selection, selective breeding, reproductive biotechnology, disease detection, and nutrition have been influenced by omics in aquaculture with the development of RNA-Seq and NGS. The development of aquaculture, which will lead to the blue revolution, will benefit from these new studies. Numerous new omics research studies conducted on mammals, such as foodomics, pharmacogenomics, toxicogenomics, psychogenomics, connectomics, tomomics, cellomics, etc., may soon be used in the biotechnology field of fisheries and aquaculture.

Future perspectives

In order to understand the complex molecular and physiological processes driving reproductive development, gametogenesis, and spawning, future studies on fish reproduction should prioritize the integration of multi-omics techniques, such as transcriptomics, proteomics, metabolomics, and phenomics. The use of metabolite profiling and advanced molecular diagnostics can provide early insights into reproductive health, enabling accurate broodstock monitoring and prompt identification of reproductive problems. While phenomics techniques help clarify the intricate connections between genotype, phenotype, and reproductive features like fecundity and hormone regulation, nutritional omics will be essential in creating species-specific diets that maximize reproductive success and offspring quality. Furthermore, the long-term preservation of genetic diversity in endangered or commercially valuable species will be aided by the incorporation of omics into cryopreservation and germplasm conservation. Combining these strategies could enhance precision aquaculture, boost reproductive efficiency, ensure genetic sustainability, and support effective fish population management and conservation.

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