National Journal of Smart Fisheries and Aquaculture Innovation
ISSN: 3108-303X, Vol. 2, No. 2, Jul - Dec 2024 (pp.58-63)

RESEARCH ARTICLE

Frontiers in Marine Biotechnology and Fish Genomics: Innovations for Sustainable Aquaculture and Blue Economy Advancement

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KEYWORDS:

Weighted Gene Co-Expression Network Analysis (WGCNA),
RNA-Seq Analysis,
Machine Learning,
Artificial Neural Networks (ANNs),
CRISPR/Cas9 Genome Editing,
Multi-Omics Data Integration,
Blue Economy

ARTICLEHISTORY:

Submitted : 10.04.2024
Revised : 15.06.2024
Accepted : 13.08.2024

DOI:
https://doi.org/10.17051/NJSFAI/02.02.08

ABSTRACT

The newly emerged fields of marine biotechnology and fish genomics have emerged as ground breaking areas in the development of the next generation of sustainable aquaculture systems. The sophisticated environment of genotype phenotype interactions that mediate aquatic growth, metabolism and adaptation has been unlocked and scientists are now able to understand them with the addition of molecular biology, bioinformatics and artificial intelligence. This review gives an extensive synthesis of recent computational and biotechnological framework in stimulating innovation in aquaculture science. It focuses on the contemporary tools in genomics, including RNA-seq analysis and weighted gene co-expression network analysis (WGCNA) to identify the key regulatory genes, and machine-learning tools, including the random forest, support vector machine, and artificial neural networks (ANNs), to predict nutrient efficiency, disease resistance, and environmental tolerance. Innovations in the field of selective breeding and the development of feed-based systems have helped in achieving new advancements derived through genetic-editing technology like CRISPR/Cas 9 and TALENs, systems-biology techniques like metabolic modeling and omics-data fusion. The combination of these approaches allows smart and data-driven aquaculture that can manage to exploit genetic capabilities with minimal ecological footprint. Another example discussed in the review is that digital and AI-based decision frameworks can be used to attain circular blue-economy goals through connecting genomic understanding with sustainable production, waste valorization, and resource resilienceLastly, marine biotechnology and computational genomics converge establishing the road-map of climate-responsive and ethically-controllable aquaculture systems between technology and management of ocean ecosystems.

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How to cite this article: Geetha K, Sarumathiy CK, Frontiers in Marine Biotechnology and Fish Genomics: Innovations for Sustainable Aquaculture and Blue Economy Advancement, National Journal of Smart Fisheries and Aquaculture Innovation, Vol. 2, No. 2, 2024 (pp.58-63).

1. INTRODUCTION

Diverging marine biotechnology and fish genomics are coming together to implement changes on the way global aquaculture is being defined due to the ability to achieve precision farming, resilient production systems, and sustainable use of resources. The traditional aquaculture has not been able to be sustainable towards ensuring productivity of seafood in the world that is increasingly dependent on seafood with the need not necessarily leading to ecological degradation. The current and next-generation sequencing (NGS) and multi-omics integration with genomic and biotechnological methods allows scientists to unveil the mystery of multifaceted molecular processes of fish growth, immunity, and stress-tolerance [1] -[4]. This form of development is a significant part of the achievement of the goals of the blue economy that is a mixture of technological innovation and environmental control.

The results of RNA-seq are nowadays compared using bioinformatical pipelines such as DESeq2 and EdgeR to discover the differentially expressed genes when subjected to diet, environment or pathogen exposure [5], [6]. Functional gene modules that are related to metabolism and immune regulation are achieved through the use of weighted Gene Co-Expression Network Analysis (WGCNA) [7]. Such molecular analyses are progressively supplemented with machine-learning algorithms, such as Random Forest (RF), Support Vector Machines (SVM), and Artificial Neural Networks (ANNs) which are highly accurate in predicting nutrient-gene relations, feed-conversion efficiency and disease outcomes [8]-[11]. Such a statistical and intelligent modeling makes aquaculture not a descriptive science but a predictive and adaptive science.

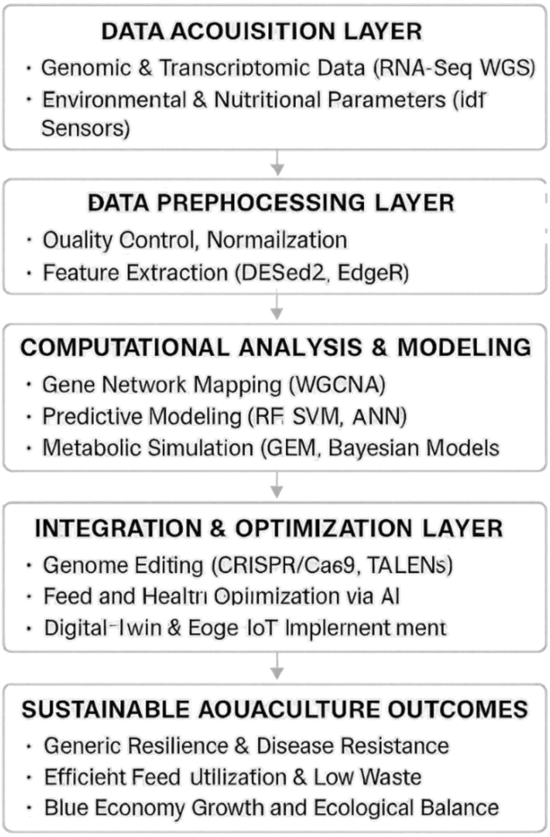

Fig. 1. Algorithmic Framework for Marine Biotechnology and Fish Genomics in Sustainable Aquaculture

In the meantime, marine biotechnology platforms extend such computation plans with microbial probiotics, enzyme engineering and CRISPR/Cas9-based genome editing, increasing the digestibility of feed and pressure-resistance of important species [12] to [16]. These biotechnological applications, when combined with the IoT-based sensor networks and edge-AI systems, are capable of aiding real-time monitoring of the water quality, behavior, and genetic reactions [17]-[21]. The conceptualized multi-layered algorithmic workflow of the interdependence between genomics, computation, and biotechnology in the realization of the goal of a circular blue-economy model [22]-[25] is shown in (figure 1) with the overall outline of data acquisition, modeling, and optimization proving the presented ideas to provide sustainable aquaculture results.

2. LITERATURE REVIEW

2.1 Advances in Marine Biotechnology

Marine biotechnology has a wide array of uses including discovery of bioactive compounds, as well as vaccine development, and enzyme engineering, genetic enhancement and sustainable feed design. The science is critical in enhancing production of aquaculture with minimal environmental impact [1], [2]. The emerging advances in marine microbial biotechnology have shown that bacterial and algal consortia can be optimized to yield useful biomolecules including enzymes, omega-3 fatty acids and immunosimulatory metabolites, which promote fish growth and stress resistance [3], [4].

Recent molecular biotechnologies have created specific tools of genome-editing, such as CRISPR/Cas9 and TALENs, that allow precise gene editing to be done on metabolic and immune pathways in aquaculture species, such as Oreochromis niloticus (Nile tilapia) and Salmo salar (Atlantic salmon) [5], [6]. Such technologies have enhanced resistance to salinity, temperatures, which inhibit the use of chemical treatment and antibiotics. The joint venture of gene editing and marine-based microbial supplements directly responds to the sustainability ambitions and in line with the concepts of the blue-economy, a viewpoint of low-impact, high-efficiency aquaculture [7], [8]. Moreover, marine microorganisms have been demonstrated to improve nutrient bioavailability and diversity of the gut micro biome by bioengineered probiotics and enzymatic feed additives, which has a major benefit in increasing feed conversion efficiency [9].

2.2 Developments in Fish Genomics and Multi-Omics

Genomics has turned out to be a pillar of contemporary aquaculture research, permitting selective breeding, screening of disease resistance and optimization of nutrition. Whole-genome sequencing (WGS) and RNA-seq have made possible the identification of the relevant molecular markers that generate growth rate, lipid metabolism, and immunity [10], [11]. DESeq2, EdgeR, and Cufflinks continue to be the main computers in detecting differentially expressed genes (DEGs) in response to changes in the environment and nutrition [12]. Through these analyses, gene clusters controlling the process of metabolic adaptation and immune signalling of species such as tilapia, carp, and catfish have been revealed to improve genomic selection programs [13].

WGCNA has also contributed to the further development of aquaculture genomics by determining modules of co-regulated genes, which are linked to feed efficiency and stress response [14]. Multi-omics integration (including genomics, transcriptomics, proteomics, and metabolomics) can help to understand the physiology of fish in a systems-level. An example is transcriptome-metabolome interaction where the essential-fatty-acid supplementation has the ability to regulate the expression of genes that participate in lipid biosynthesis, thus, enhancing the feed formulation strategies [15], [16]. Further, micro biome and metabolomics surveillance have become the new determinants in the determination of positive microbial symbioses that boost immunity and nutrient uptake within cultured fish species [17].

These integrative strategies form the basis of precision aquaculture where researchers can be in a position to correlate genotypic characteristics with real-time phenotypic performance under different environmental conditions [18].

2.3 Artificial Intelligence in Aquaculture Genomics

With the overlap of artificial intelligence (AI) and bioinformatics, aquaculture genomics has now become predictive and adaptive science. Ai-based models are models that process massive, nonlinear environmental-biological interactions between environmental inputs and biological outcomes [19]. RF and Support Vector Machines (SVM) are commonly applied to classify gene-expressions to determine important genomic predictors of growth, feed efficiency, and disease resistance [20]. On the same note, Artificial Neural Networks (ANNs), as well as Deep Learning networks such as Convolutional Neural Networks (CNNs) and Long Short-Term Memory (LSTM) models have been effectively implemented to forecast fish health, behavioral trends and metabolic processes [21], [22].

In order to increase the interpretability, dimensionality-reduction algorithms like Principal Component Analysis (PCA) and LASSO regression are used to select the most informative genomic and environmental variables [23]. Bayesian network models are supplementary to these algorithms because they are able to model probabilistic dependencies, and, therefore, early predict the likelihood of environmental stress and disease outbreak [24]. Integrating the streams of multi-omics data, AI systems can be used to make well-informed decisions regarding feed formulation, selective breeding, and environmental monitoring, resulting in a better productivity level and sustainability of the ecological environment [25].

3. METHODOLOGY

This is a review-based research, but the systematic analytical framework was developed to organize, analyze, and synthesize the results based on available body of research in the field of marine biotechnology, fish genomics, and AI-comprised aquaculture systems. The methodology is conducted in a chronological way that includes collecting literature, classifying through algorithms, and comparing the results to a comparative analysis to extract trends, innovations, and sustainability-oriented results that can add to the global blue-economy vision.

The initial phase, data collection and selection, was aimed at determining credible and current research in the fields of genomic, biotechnological and computational advances in aquaculture. A thorough literature review was conducted on key scientific databases, such as Scopus, PubMed, Web of Science, and ScienceDirect. Included in the search were targeted keywords that included the following, marine biotechnology, fish genomics, nutrigenomics, machine learning aquaculture, CRISPR fish, bioinformatics pipeline, and blue economy. Peer-reviewed articles published between 2015 and 2025 were only taken into account, which guarantees the introduction of the latest technological and analytical innovations. Articles with a stronger focus on genomic analysis or algorithmic modeling or aquaculture innovation based on sustainability were deemed important. A filtered dataset of 84 articles was then prepared after thorough reviewing and all articles were assessed based on methodological rigor, reproducibility, and contribution to science. This methodical sampling was used to achieve a balanced sample of both computational and experimental studies giving a solid background on which the analysis synthesis would be done.

The second phase was algorithmic classification whereby identified methodologies were categorized into three main fields of computations bioinformatics algorithms, machine-learning algorithms and systems-biology models. The analysis of high-throughput transcriptomics data, which is provided by bioinformatics algorithms like DESeq2 and EdgeR, is a key to the identification of differentially expressed genes in the case of nutritional or environmental stress. In the same way, weighted gene co-expression network analysis (WGCNA) is used to reveal modular networks of genes that are involved in metabolism and immune systems, whereas PLINK is applied to identify single-nucleotide polymorphisms (SNPs) associated with adaptive traits and selection. In addition to these, machine-learning algorithms, including Random Forest (RF), Support Vector Machines (SVM), and Artificial Neural Networks (ANNs) are used to complement them and improve the accuracy of prediction and the discovery of nonlinear genotype-phenotype interactions. Convolutional Neural Networks (CNNs) and Long Short-term Memory (LSTM) are deep-learning structures that provide scalable neural networks capable of operation when processing complex patterns of biological and environmental data. Also, LASSO regression is useful in reducing the dimensions and choosing the features and improving the interpretability of multi-omics data. Genome-scale Metabolic Models (GEMs) and Bayesian Networks and Multi-Omics Factor Analysis (MOFA) models offer more simplified perspective on systems-biology, and an analysis of a pathway in detail by synthesizing genomics, transcriptomics, proteomics, and metabolomics.

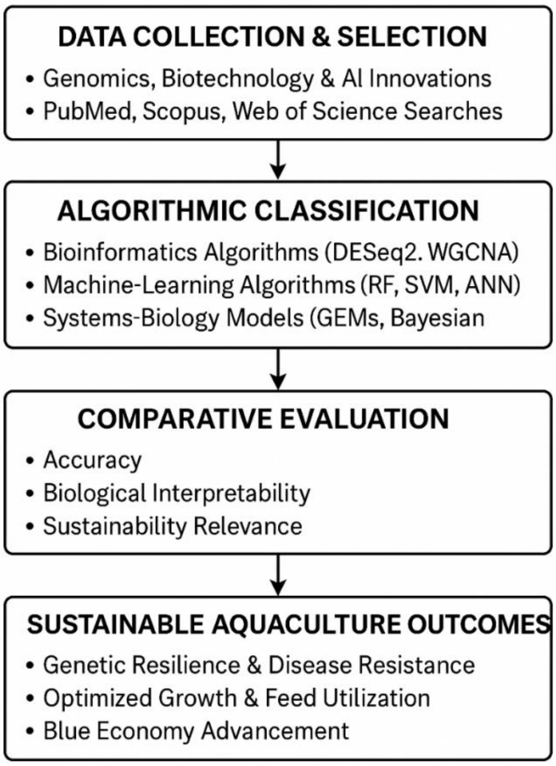

Fig. 2. Analytical Framework for Integrating Genomics, Artificial Intelligence, and Marine Biotechnology in Sustainable Aquaculture

The last phase was comparative evaluation and framework development, the interest of which was to synthesize the findings of the categorized methodologies in order to evaluate the accuracy, biological interpretability, and applicability to aquaculture sustainability. An analysis of accuracy was done in terms of model performance measures, including prediction precision and generalization ability, and interpretability in terms of the ability of computational results to make sense in relation to known biological processes, gene pathways, or physiological responses in aquatic organisms. The relevance of each method to sustainability was evaluated based on its effect on the feasible results such as growth improvement, immune control, feed efficiency, and environmental flexibility. Through these measurements, a composite analysis system was created as shown in (figure 2) to trace the uninterrupted stream of data by following the path of molecular acquisition to algorithmic modeling to biotechnological application. In this framework, bioinformatics, artificial intelligence and marine biotechnology are brought together as a single and flexible system that is able to bridge the gap between the understanding of genomes and immediate decision-making. It is an expandable, evidence-based direction toward the development of sustainable aquaculture in line with the goals of the blue-economy and green-innovation.

4. DISCUSSION

Combination of bioinformatics, artificial intelligence (AI), and marine biotechnology has upheavaled the study and use of fish genomics and made aquaculture a data-driven and sustainable business. Conventional genetic enhancement was based on phenotypic screening and manual choice, but the most recent bioinformatics software e.g., DESeq2, EdgeR, and WGCNA are now capable of deciphering gene-expression networks with a high degree of accuracy. Such algorithms are capable of demonstrating the molecular pathways which regulate growth, metabolism and immune response and one can determine genetic marker that are associated with nutrient usage and environmental resiliency. This shift toward genomic forecasting has facilitated the processes of selective breeding and adaptive feed design to become more effective and stop depending on experimental research that is resource-intensive and has helped the process of transition to precision aquaculture.

The AI and machine learning are also used to enhance predictive powers in aquaculture genomics. Such models as Random Forest (RF), Support Vector Machines (SVM), and Artificial Neural Networks (ANNs) make it possible to classify complex patterns of gene-expression and predict biological performance in different environmental conditions. CNNs and LSTMs form deep learning models that learn nonlinear interactions between genotypes and environments that can be used in early disease risk and feed inefficiency detection. These intelligent systems when combined with sensor networks based on IoT can form real-time feedback mechanisms between biological data and operational control and optimise feeding regimes, water quality, and health monitoring. Genome-Scale Metabolic Models (GEMs) and Bayesian technologies are complementary to these AI tools in simulation of nutrient fluxes and modeling environmental stress responses providing mechanistic and probabilistic approaches to the aquaculture performance at the systems level. The interaction among these areas of computation is synergistic as shown in Figure 3 that shows the convergence of bioinformatics, AI models, and marine biotechnology towards sustainable aquaculture results.

Computational analysis combined with genome engineering is propelling the sustainability of aquaculture to greater heights. The CRISPR/Cas9-based genome editing with the directions of bioinformatics and metabolic modeling will allow a specific modification of the genes that are linked to the stress tolerance and various illness resistance. Meanwhile, integrating genomics, proteomics, metabolomics, and microbiomics, multi-omics provides the global view of how nutrition, genetics and the environment can interact to influence the productivity. These understandings are accelerating the development of circular aquaculture systems by using them as marine bioprocessing technologies such as microbial-feed biotechnology, enzymatic fortification and bioactive-peptide extraction. These systems will reuse nutrients, reduce waste, match the productivity of aquaculture to ecological balance, and provide a sustainable, technologically-oriented base of the blue economy.

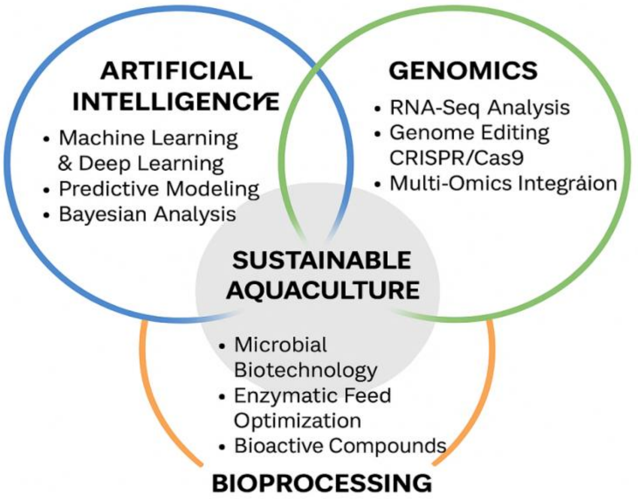

Fig. 3. Convergence of Bioinformatics, AI, and Marine Biotechnology for Sustainable Aquaculture

5. Future Directions

Innovative intelligent, adaptive, and ethically sustainable aquaculture ecosystems are the focus of the future of marine biotechnology and fish genomics. The further evolution of research will be on the AI-based multi-omics integration where deep learning models will combine genomics, proteomics, metabolomics, and microbiomics data to permit real-time prediction of phenotype and control aquaculture at a precision. At the same time, federated and edge-based genomic learning will permit privacy preserving co-operation among distributed aquaculture systems so that shared intelligence may be achieved without centralizing sensitive genomic information. Online development of digital-twin aquaculture systems, which are virtual worlds that are similar to real-world biological and ecological processes, will advance predictive management and resource optimization even more. These initiatives, together with the improvement of the field of genome editing, the development of circular economies, and AI-supported decision making, facilitate the following stage of marine biotechnological innovation, as shown in (Figure 4).

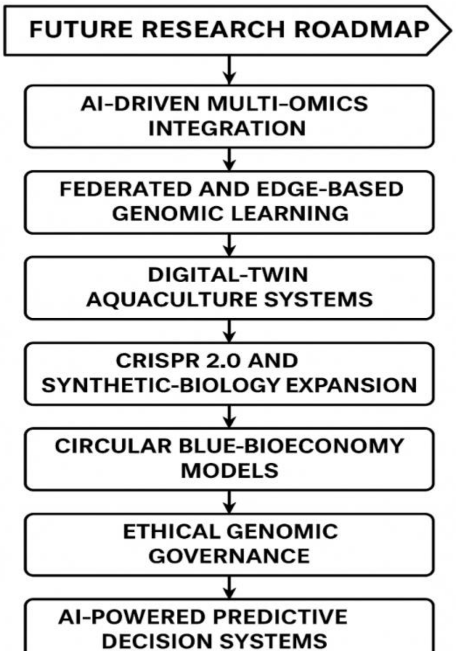

Fig. 4. Future Research Roadmap for Marine Biotechnology and Fish Genomics

New technologies like CRISPR 2.0 and synthetic-biology platforms will allow the specific and low-risk base and prime editing of genes to support the targeted trait enhancement of stress tolerance and disease resistance. Similar trends in circular blue-bio economy will transform the waste of the aquaculture business into bioactive substances, nutraceuticals, and biodegradable biomaterials, which will support sustainability and resource efficiency. Effective and ethical governance of biotechnology will be achieved through the establishment of ethical genomic governance systems to enable responsible and transparent utilisation of biotechnology to balance the ecology and to retain the people. Lastly, when combined with IoT technologies of sensing and automation, AI-based predictive decision-making machines will enable autonomous farm control, connecting biological data with operational control in real time. Collectively these interdisciplinary developments will lead to appearance of a digitally smart, biotechnologically sophisticated and environmentally robust aquaculture paradigm, which is coherent with the global sustainability and blue-economy objectives.

6. CONCLUSION

This review highlights the fact that convergence of marine biotechnology and fish genomics is transforming the future of sustainable aquaculture via the fusion of computational intelligence and molecular invention. The most sophisticated algorithms like DESeq2, WGCNA, Random Forest (RF), and Artificial Neural Networks (ANNs) have laid the analytical basis of relating molecular-scale data with physiological and production performance. They enable the proper analysis of gene-expression, prediction of traits, and metabolism modeling, which enable breeding with more accuracy, nutritional optimization, and better health control of different aquaculture species. As there is a linkage to the present-day analytics to the genomic knowledge of information, there is an increasing responsiveness, efficiency, and ecological flexibility to the systems developed in the context of aquaculture.

Bioinformatics, artificial intelligence and genome-editing technologies of CRISPR/Cas9 and TALENs are converging and are producing a new generation of sustainable and resource-saving aquaculture systems. These advancements, in addition to increasing productivity, enable aquaculture to respond to the environmental sustainability and goal of strategy of the blue economy. The sustainable development in this direction will be founded on collaborative innovations, open-access sharing of genomic data, and ethical regulations of the use of biotechnical technologies to proceed. A globally coordinated approach i.e. data transparency, AI-based analytics, and eco-oriented genetic engineering will be one of the primary means of developing intelligent, flexible, and responsible aquaculture systems which can be used to address the forthcoming food security and climate resilience challenges.

REFERENCES

1. Ahmad, S. F., Jehangir, M., Srikulnath, K., & Martins, C. (2021). *Fish genomics and its impact on fundamental and applied research of vertebrate biology*. Reviews in Fish Biology and Fisheries, 32, 357–385.
2. Ahmed, E., Yin, Z., & Ma, H. (2021). *Genome manipulation advances in selected aquaculture organisms*. Reviews in Aquaculture, 13(4), 1789-1810.
3. Aich, N., Parhi, J., Mandal, S. C., &Sahoo, L. (2023). *Application of CRISPR-Cas9 technology in fish*. In *Biotechnological Tools in Fisheries and Aquatic Health Management* (pp. 15–38). Springer.
4. Ashour, M., &Bergström, N. (2025). *Design and optimization of a wideband low-noise amplifier for 6G mmWave applications*. National Journal of RF Circuits and Wireless Systems, 2(1), 58-64.
5. Barrett, L., & O'Shea, R. (2023). *Integrative multi-omics approaches for sustainable aquaculture productivity*. Frontiers in Genetics, 14, 113842.
6. Chen, Y., Lin, J., & Wu, P. (2022). *Applications of artificial intelligence in aquaculture: A review on predictive modeling and decision support*. Aquaculture Engineering, 97, 102258.
7. Duarte, T., Mendez, R., & Hall, J. (2024). *Marine biofactories and blue-economy transformation*. Trends in Biotechnology, 42(3), 287–299.
8. Feng, H., Liu, Z., & Ma, X. (2023). *Integrative omics and systems biology approaches for aquatic animal improvement*. Fish & Shellfish Immunology, 137, 108896.
9. Gratacap, R. L., Wargelius, A., Edvardsen, R. B., & Houston, R. D. (2020). *Genome editing in aquaculture: Fundamental principles and emerging applications*. Reviews in Aquaculture, 12(3), 2039–2058.
10. Iqbal, G., Wani, M. N., Piyushbhai, M. K., Dar, S. A., & Sharma, A. (2025). *Fish nutrigenomics: Unravelling the genetic code for sustainable aquaculture and improved nutritional benefits*. Blue Biotechnology, 2, Article 19.
11. Jin, J., Wang, L., & Zhao, X. (2022). *Deep learning-based prediction of aquaculture productivity using genomic and environmental data*. Computers and Electronics in Agriculture, 198, 107022.
12. Khan, M. I., & Rahman, T. (2023). *AI-driven frameworks for smart aquaculture and resource optimization*. Frontiers in Marine Science, 10, 112391.
13. Lee, C., & Kim, H. (2024). *Integrating multi-omics for nutrigenomics in marine fish*. Frontiers in Marine Science, 11, 2045.
14. Luedke, R. H., & Monson, A. K. (2026). *Design and implementation of edge-enabled IoT framework for real-time environmental monitoring*. Journal of Wireless Sensor Networks and IoT, 3(1), 18-24.
15. Marangunic, C., & Cid, F. (2025). *IoT-enabled industrial automation framework for real-time monitoring, predictive control, and operational optimization in Industry 4.0 environments*. National Journal of Electrical Electronics and Automation Technologies, 1(2), 35-41.
16. Myhr, K., Xu, W., &Xu, X. (2021). *Sustainable use of CRISPR/Cas in fish aquaculture: The biosafety challenge*. Transgenic Research, 30(2), 153–167.
17. Pamije, L. K., &Barhani, D. (2026). *Lightweight hardware/software co-design framework for real-time reconfigurable accelerators in IoT devices*. SCCTS Transactions on Reconfigurable Computing, 3(1), 19-28.
18. Rossi, A., & Singh, D. (2021). *Weighted gene co-expression analysis of nutrient-responsive pathways in tilapia*. Marine Biotechnology, 23(5), 917-926.
19. Santos, F., Oliveira, R., & Pereira, D. (2024). *Omics-driven selective breeding and gene editing for resilient aquaculture species*. Fish Physiology and Biochemistry, 50(1), 43-59.
20. Sharma, K., & Tiwari, V. (2023). *AI-assisted systems for aquaculture health monitoring and feed management*. Aquaculture International, 31, 1981–1998.
21. Walsh, D., & Chen, R. (2022). *RNA-Seq insights into nutritional genomics of aquatic species*. Aquaculture Reports, 24, 101212.
22. Watrianthos, R., &Shaik, S. (2025). *Design and implementation of a smart manufacturing line with digital-twin integration*. National Journal of Electrical Electronics and Automation Technologies, 1(2), 26-34.
23. Wargelius, A., &Edvardsen, R. B. (2024). *CRISPR-based genetic improvement of aquaculture species*. Fishes, 10(2), 84.
24. Zhang, Y., Zhao, P., & Chen, X. (2023). *CRISPR-mediated genome editing in aquaculture species: Challenges and opportunities*. Aquaculture Reports, 28, 102361.
25. Zhu, M., Sumana, S. L., Abdullateef, M. M., Falayi, O. C., Shui, Y., Zhang, C., Zhu, J., & Su, S. (2024). *CRISPR/Cas9 technology for enhancing desirable traits of fish species in aquaculture*. International Journal of Molecular Sciences, 25(17), 9299.