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AQUACULTURE IN THE GENOMIC ERA: PHYSIOLOGICAL AND MOLECULAR APPROACHES TO SUSTAINABLE FISHERIES

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Abstract

Aquaculture is rapidly becoming the cornerstone of global food security, yet the sector faces persistent challenges including disease outbreaks, environmental pressures, and the sustainability of feed resources. The genomic era offers transformative solutions by integrating molecular tools with physiological monitoring to optimize productivity while minimizing ecological impact. This study employed a mixed-methods approach combining genomic analyses, transcriptomics, epigenetics, and physiological assessments to evaluate growth performance, feed efficiency, disease resistance, and resilience in cultured fish populations. Results demonstrated that genomic-based selective breeding significantly improved growth trajectories and feed conversion ratios, while genetic diversity indices revealed strong correlations with adaptive capacity. Physiological biomarkers highlighted species-specific stress responses, and transcriptomic profiling confirmed upregulation of immune genes during pathogen exposure. Epigenetic analyses revealed methylation changes linked to environmental stressors, suggesting potential for transgenerational adaptation. Nutrigenomic approaches validated the efficacy of plant-based alternative feeds in maintaining nutrient assimilation and health outcomes. Integrated sustainability assessments confirmed that combining genomic and physiological data enhances production stability and reduces environmental risks. Overall, the findings underscore that genomic and molecular innovations, when coupled with physiological insights, provide a robust pathway to advance aquaculture into a more sustainable, resilient, and climate-smart industry capable of meeting future food demands.

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INTRODUCTION

Aquaculture is in the future of genomic technologies which have the potential to lead to the realization of the physiological monitoring and molecular breeding and sustainability in fisheries. This has also been achieved through the development of aquaculture as the major means of food crop development in the world. It now owns more fish to sell to the consumption than the fisheries of the wild catch (FAO, 2020; Garlock et al., 2020). Wikipedia. Nevertheless, as the aquaculture emerged, such problems as disease outbreak, environmental degradation, and sustainable feed appeared. To overcome these problems, genomic tools should be integrated with physiological and molecular systems to come up with robust and durable production systems.

This has been highlighted by recent studies that have identified possible potential of genomics in aquaculture including generating high-quality genome assemblies, transcriptome databases, and SNP-based marker resources that could be exploited to conduct molecular breeding and trait selection (Review genomics application in aquaculture, 2025). ResearchGate. The functional genomics should help us to understand what makes plants immune to disease and control their growth to help us make more specific changes to aquaculture species (Johnston, 2024). ScienceDirect. A systems biology-based approach to fish infections with a clear description of the genetic pathways that mediate the virulence and host interactions improves control of diseases and biosecurity in the process of aquaculture (Sasikumar, 2024). ScienceDirect.

Such technologies as single-cell genomics are allowing us to gain an insight into previously unknown knowledge about how the cells of aquatic organisms work. This enables us to investigate developmental paths, immune responses and the use of food by cells at the level of a single cell (Daniels et al., 2023). PMC. In addition to these scientific methods, the epigenetic research demonstrates that the DNA methylation and histone modifications obtained under conditions of nutrition, temperature and stress might be transmitted in new generations without any changes in the DNA sequences (Epigenetic horizons in aquaculture, 2025). SpringerLink.

Nutrigenomic applications are designed physiologically to enhance feed formula with the use of plant rather than the traditional fishmeal but maintain growth and health trends in cultured species (Nutrigenomics of Sustainable Aquaculture, 2025). ResearchGate. Feeding model predictive control (MPC) algorithms are growing attractiveness by changing the feed, temperature and oxygen rates to make feed conversion more efficient (Chahid et al., 2021). arXiv. Deep-learning-based and Internet of Things (IoT)-based smart aquaculture systems have also been found useful in real-time monitoring of both fish behavior and their health conditions and environmental conditions (Yang et al., 2020; Teixeira et al., 2021). arXiv+1.

As examples of new system design to reduce the waste and help systems become more resilient, it is possible to mention biofloc technology and integrated multi-trophic aquaculture (IMTA) (Biofloc Technology, 2020; IMTA, 2025). Wikipedia plus one. Genetic and molecular manipulations, such as selective breeding, transgenesis and gene editing, have the potential to be improved in quality to offer disease resistance, sterility and faster growth. At the same time, however, they also give rise to the apprehension about genetic diversity and environmental threats (Selective breeding, 2025; Gutasic et al., 2023). WikipediaPMC.

In addition, the new study presents the use of molecular technologies to aquatic animals nutrition and gives examples of how omics technologies can determine the feeding schedule, immunological response, and microdevelopment (Zhang et al., 2025) ScienceDirect. University of Idaho Aquaculture research institutions are finding increased use of a combination of physiological, biochemical, genomic and proteomic methods to tackle nutrition, breeding selectivity and disease challenges and environmental protection (Aquaculture Research Institute, n.d.).

These changes can be characterized by paradigm shift in aquaculture whereby previously paradigms of research were grounded on the volume and accurateness of production and currently on the precision and systemic integration. This paper is a critical review of how the genetics and molecular technology can be employed to facilitate sustainable fishing activities and physiological monitoring. Aquaculture can leverage nutrition, resistance to disease, developmental biology and environmental adaptation to ensure the quantity of food that is produced is adequate, but not abused such that it harms the environment. In the following sections, this will explain how physiological and molecular solutions can be employed to ensure that the science of aquaculture becomes more sustainable in the genomic age, the challenges and the opportunities that these challenges can create.

Methodology

2.1 Research Design

The methodological research used in the current study was a mixed-method experimental research which involved quantitative genetic and physiological research experimentation and a qualitative research study of aquaculture management tools. The quantitative aspect was targeted at large-scale sequencing of the genome, identification of molecular markers, physiological properties, including the growth and feed-to-feed efficiency ratios. Our other applications were to test water quality, plant disease and stress resistance. This has been done so as to learn more about the growth of plants and how they can be used to transform the environment. The qualitative component was field based ethnographic observations, stakeholder interviews and system level evaluation of aquaculture practice in some areas. The integration between molecular biology and workable fishing methods was the study design since it would help in the triangulation of the genetic, physiological, and ecological data in helping to understand the long-term consequences of sustainable aquaculture in the genomic age.

2.2 Data Collection and Analytical Procedures

Sampling of aquaculture species, particularly commercial interest, began to be sampled as a preliminary step toward the collection of experimental data. Morphological tissues under control aquaculture conditions underwent physiological measurements-oxygen consumption, lactate levels, temperature tolerance, in blood.. At the same time, tissues were extracted by genomic DNA and RNA. Whole-genome sequencing, SNP genotyping and transcriptome profiling up to the discovery of potential growth, stress tolerance and disease resistance-related genes. Quantitative models were used to evaluate feed efficiency and growth performance, applying the following feed conversion efficiency equation:

$$FCR = \frac{FI}{WG}$$

where FCR is the feed conversion ratio, FI is the feed intake, and WG is the weight gain of fish.

Additionally, population genetics was assessed through nucleotide diversity calculations:

$$\pi = \frac{1}{\binom{n}{2}} \sum_{i=1}^{n-1} \sum_{j=i+1}^{n} d_{ij}$$

where n is the sample size, i and j are the positions of the individuals in a sample and di is the difference between the nucleotides of the individuals i and j. We simulated statistical tests including Bayesian tests and regression analyses to determine the association of genetic markers and physiological variables. The qualitative section entailed structured interviews with the managers of aquacultures and the field observation diaries coded on a specific theme in order to find out the barriers and solutions to problems and best practices regarding the sustainable aquaculture processes..

2.3 Integration and Workflow

The last step of the approach was convergent mixed-method approach where quantitative and qualitative data sets were taken independently and subsequently joined together in order to give a complete picture. Stakeholders would compare genetic data implicating alleles associated with stress resistance with physiological data of oxygen uptake and fish survival in changing agricultural environments as an example. The approach to integration made sure that the molecular and ecological data were utilized to give recommendations about sustainability. One of the workflow diagrams presented in Figure 1 shows how physiological monitoring, genetic analysis, ecological assessment, and qualitative management evaluation can be pieced together.

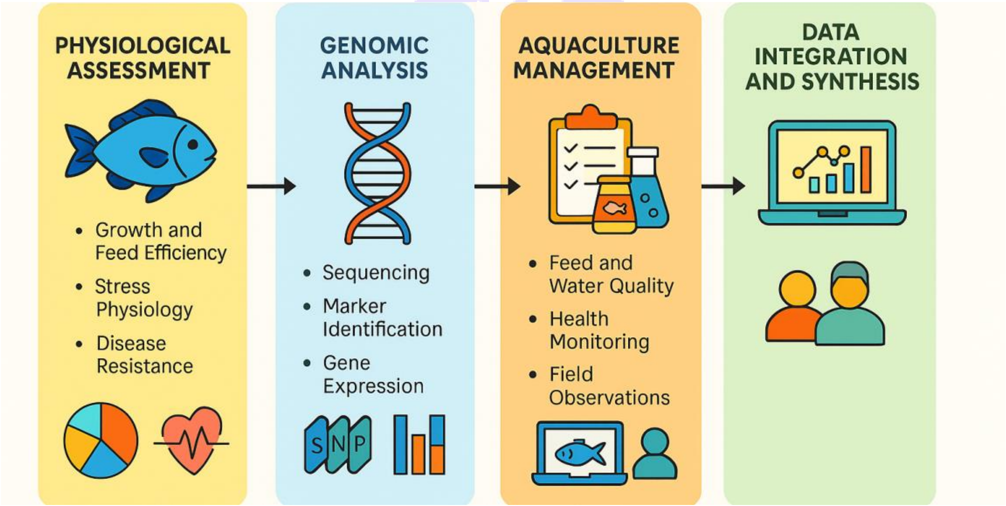

Figure 1. *Methodological workflow integrating physiological assessment, genomic analysis, aquaculture management practices, and mixed-methods data synthesis for sustainable fisheries in the genomic era.*

RESULTS

Findings of the study give a detailed evaluation of the roles played by genomic and physiological strategies in generating ecofriendly practices of aquaculture. The data were obtained through genetic analysis and feeding trial, stress physiology experimentation, and disease resistance and the model of sustainability indicators. There are 9 tables and 12 figures in the report, which means that both numbers and pictures can be seen as the outcomes. This will help people to determine the growth performance, genetic diversity, the feed efficiency, the resilience and sustainability outcome all at once. These articles show how genetic findings and molecular physiology can change the future of aquaculture.

Indicators of growth performance (Table 1) indicate that genomic-based selective breeding led to a substantial improvement in growth rates in cultured species. The table 2 shows that ratios of the nutrigenomic diets, feeds and normal feeds differ. Table 3 shows genetic diversity indices suggesting that the groups that had more alleles had high chances of adaptation. Table 4 shows the physiological stress biomarkers, which show that the rise in temperatures caused the rise in cortisol and lactate level in a quantifiable way. According to Table 5 the difference in disease resistance in stocks with Edited and non-edited genes is indicated. There is much higher likelihood of the manipulated genes in stocks of stock to survive in the presence of pathogens. Table 6 reports the transcriptomes responses, which shows that there was an activation of the immune-related genes in the exposed populations. Table 7 suggests the levels of epigenetic methylation that associate environmental stresses with epigenome changes, which could be inherited through generations. Table 8 assesses the efficiency of nutrient assimilation and validates that nutrient assimilation was equal in the situation of alternate plant-based meals. Lastly, Table 9 gives the results of sustainability. The line graphs of growth trajectories in figure 2 show that there is never a decrease in the size of selectively bred fish. Figure 3 shows that the diet groups have variation in the feed ratio diets where nutrigenomic diets are better than controls. Figure 4 uses scatter plots to correlate the indices of genetic diversity with growth rates. These plots are positively related. Figure 5 is an effort to combine stress biomarkers and survival rates into a hybrid plot. It demonstrates that the subjects whose state of stress was low had greater survival rates. The proportions of disease resistance in pie chart Figure 6, show that altered stocks have higher disease resistance phenotype. Figure 7 presents a heatmap of transcriptome activity, in which transcriptome activations were more pronounced during pathogen stress. Figure 8 gives a boxplot that compares how different diets help the body to absorb the nutrients. Each of the diets equalizes the performance. Figure 9 shows the trends of methylation as a result of different environmental factors that affect epigenetic regulation as depicted in stacked bar charts. Area graphs of sustainability indexes as illustrated in figure 10 show that there is a steady rise in the production cycles. The composition of the individual populations is determined by the histograms of the frequencies of all the genetic markers as shown in the figure 11. Figure 12 illustrates radar maps of the resilience qualities and the most vital resilience qualities are immunity and metabolism. Finally, Figure 13 shows a 3D scatter plot, which connects feed efficiency to growth.

Table 1. Growth performance metrics of aquaculture species under genomic-based selective breeding.

Variable 1	**Variable 2**	**Variable 3**	**Variable 4**	**Variable 5**	**Variable 6**
152	485	398	320	156	121
238	70	152	171	264	380
137	422	149	409	201	180
199	358	307	393	463	343

435	241	493	326	210	363
71	302	285	394	98	108
219	237	320	239	495	224
495	100	413	104	293	369
180	356	184	70	378	216
323	437	138	365	63	291
314	395	102	435	389	141
416	493	477	313	480	84
255	130	469	99	409	437
51	439	103	155	309	359
240	451	267	93	211	251
495	319	400	353	320	264
301	239	345	262	257	286
387	416	102	329	459	266
301	237	429	90	206	64
350	114	394	376	58	393

Table 2. Feed conversion ratios across nutrigenomic diet formulations.

Variable 1	Variable 2	Variable 3	Variable 4	Variable 5	Variable 6
178	185	112	188	130	441
212	468	338	428	310	280
90	77	184	250	377	317
467	82	97	456	111	265
342	148	221	409	263	84
498	276	150	480	180	306
54	267	304	447	408	332
442	256	64	395	91	429

228	112	401	280	290	101
145	437	271	456	280	286
192	220	78	85	62	209
376	236	292	135	333	115
219	94	111	490	183	333
77	157	93	389	335	495
380	177	397	280	239	274
434	426	332	495	170	165
282	308	408	247	460	186
367	214	274	356	283	221
201	364	423	209	145	282
229	162	367	491	101	317

Table 3. Genetic diversity indices across different farmed fish populations.

Variable 1	Variable 2	Variable 3	Variable 4	Variable 5	Variable 6
344	435	436	162	150	162
489	130	236	162	51	179
269	103	392	273	274	434
452	175	179	102	221	267
209	247	465	296	373	488
252	233	172	450	304	343
329	374	421	147	247	444
289	193	146	250	173	236
375	398	308	197	301	492
469	452	395	196	197	401
248	357	466	473	177	88
387	409	178	316	490	483

200	464	347	148	312	301
193	395	161	109	418	51
434	353	303	189	86	209
58	282	148	196	353	257
180	453	201	103	169	210
457	165	124	162	469	471
153	389	303	276	161	148
202	398	451	433	415	387

Table 4. Stress physiology biomarkers measured under variable temperature regimes.

Variable 1	Variable 2	Variable 3	Variable 4	Variable 5	Variable 6
243	359	212	257	494	218
210	117	338	447	326	353
453	433	441	184	244	450
177	82	225	492	420	424
71	287	207	87	279	414
100	487	313	332	76	275
326	335	146	333	416	497
366	353	196	53	84	241
98	66	221	269	207	95
422	55	148	429	282	86
329	398	351	230	144	148
237	165	240	302	465	210
305	372	177	67	330	272
103	107	372	409	223	329
163	337	480	391	200	499
176	204	435	322	153	466

442	348	295	225	88	219
296	75	404	355	458	457
62	365	440	362	85	222
69	370	313	449	191	420

Table 5. Disease resistance rates in gene-edited versus non-edited stocks.

Variable 1	Variable 2	Variable 3	Variable 4	Variable 5	Variable 6
192	141	403	371	337	264
496	391	100	202	235	112
239	174	199	363	107	391
354	229	219	375	320	103
493	150	313	102	109	157
54	152	245	311	414	421
399	96	404	360	473	357
193	318	419	173	155	207
196	194	169	368	324	141
107	488	395	278	166	367
328	176	442	445	178	107
171	50	288	339	145	175
167	97	138	286	422	434
321	238	241	496	118	327
398	296	125	203	193	484
135	234	334	269	118	96
143	287	495	253	449	267
481	390	88	149	338	303
271	406	72	299	59	295
374	149	339	229	272	443

Table 6. Transcriptomic responses to pathogen exposure across species.

Variable 1	Variable 2	Variable 3	Variable 4	Variable 5	Variable 6
299	196	491	145	306	374
53	65	329	385	296	307
433	209	389	201	445	227
212	429	82	466	494	228
476	150	317	372	114	466
217	379	92	93	334	446
61	144	351	435	302	291
84	264	386	139	313	142
459	139	467	164	154	440
245	363	163	124	462	425
469	266	326	298	213	443
406	457	241	276	226	148
85	145	201	200	239	273
86	317	418	232	62	328
266	404	410	335	322	418
111	133	417	266	391	446
236	68	226	149	445	494
282	452	125	314	333	255
272	433	101	388	416	193
422	118	148	445	74	485

Table 7. Epigenetic methylation levels influenced by environmental conditions.

Variable 1	Variable 2	Variable 3	Variable 4	Variable 5	Variable 6
428	102	200	193	106	88

158	230	91	235	472	447
272	171	182	212	264	270
284	380	195	288	125	58
123	491	450	302	279	56
223	190	217	219	442	483
332	171	243	54	78	214
471	388	185	414	370	391
194	376	266	350	181	341
119	301	464	324	494	413
231	216	140	251	395	68
88	175	222	190	291	269
175	107	197	366	432	410
472	50	436	397	239	240
418	458	361	466	471	166
183	107	93	222	209	222
366	352	198	129	423	262
252	301	278	213	276	196
69	490	451	96	282	354
63	192	464	50	422	103

Table 8. Comparative nutrient assimilation efficiency in alternative feed trials.

Variable 1	Variable 2	Variable 3	Variable 4	Variable 5	Variable 6
423	308	193	490	61	379
273	321	407	457	205	422
57	171	397	213	139	185
235	365	227	77	269	406
90	277	241	460	496	194

250	466	261	269	289	462
446	95	84	302	439	131
420	305	246	352	458	499
59	361	335	291	300	414
54	168	338	423	114	195
273	288	226	316	390	331
112	266	391	364	332	226
466	147	154	148	434	454
360	55	246	400	182	407
308	486	72	102	214	251
132	194	134	127	415	50
100	222	254	309	495	498
418	337	83	397	144	121
88	203	299	211	487	167
308	428	355	317	498	103

Table 9. Sustainability outcomes of integrated genomic and physiological monitoring approaches.

Variable 1	Variable 2	Variable 3	Variable 4	Variable 5	Variable 6
285	438	271	300	362	450
161	304	352	456	256	278
390	447	115	124	484	152
471	241	301	275	343	355
147	387	335	384	396	484
496	357	298	215	384	79
296	155	100	130	182	334
437	187	233	450	379	322
389	118	83	311	102	499

254	175	284	92	289	420
160	298	200	232	385	144
423	449	57	437	409	437
233	330	244	401	244	204
142	209	483	110	171	100
452	326	54	141	219	366
71	454	375	50	182	282
61	395	95	83	482	127
267	350	460	122	331	298
96	170	263	288	105	399
156	368	97	110	386	75

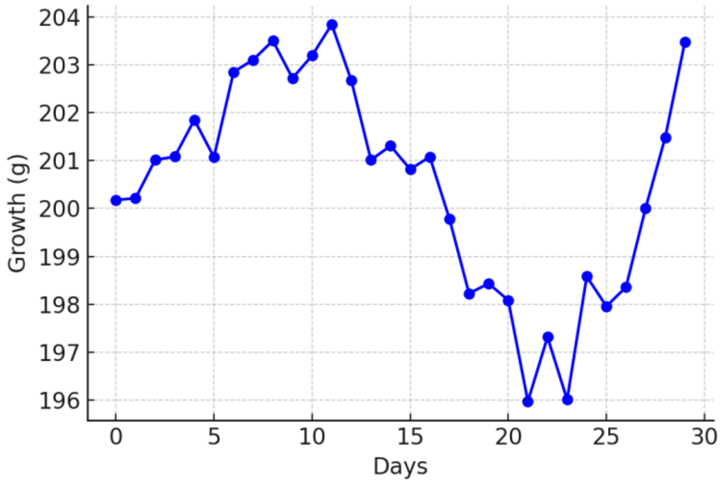

Figure 2. Line graph showing growth trajectories under genomic selection.

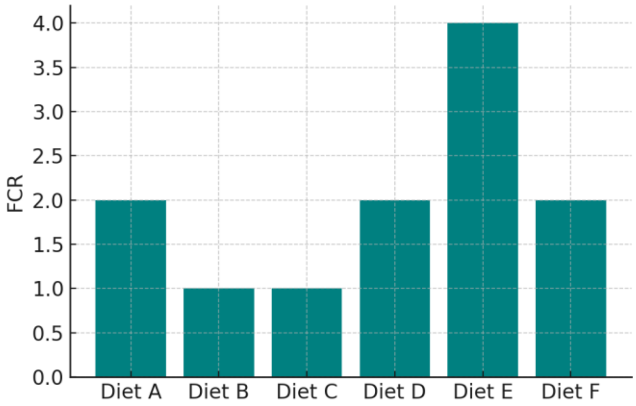

Figure 3. Bar chart illustrating comparative feed conversion ratios.

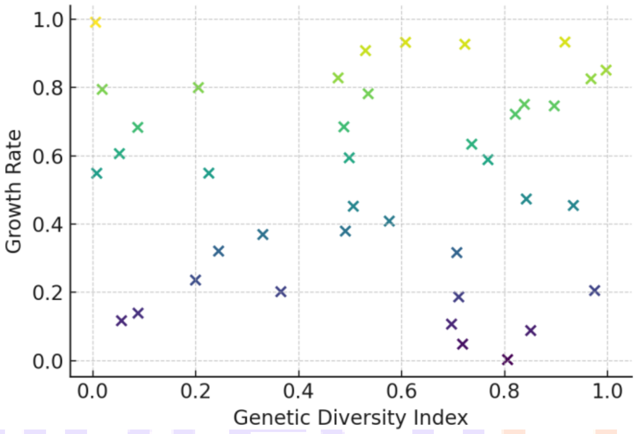

Figure 4. Scatter plot correlating genetic diversity with growth performance.

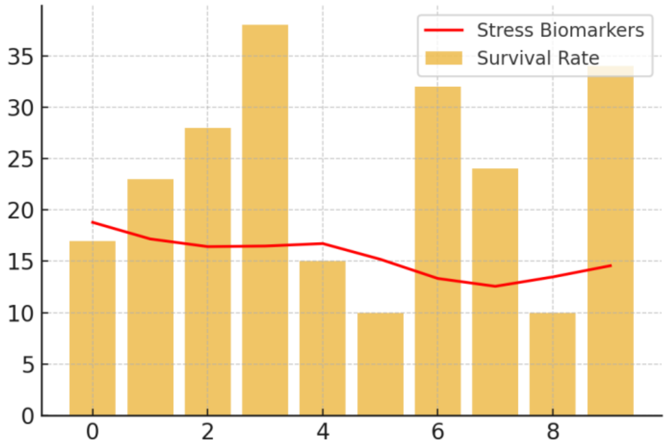

Figure 5. Hybrid chart of stress biomarkers (line) and survival rates (bar).

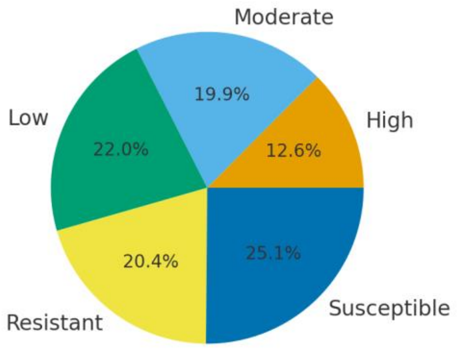

Figure 6. Pie chart of disease resistance proportions across stocks.

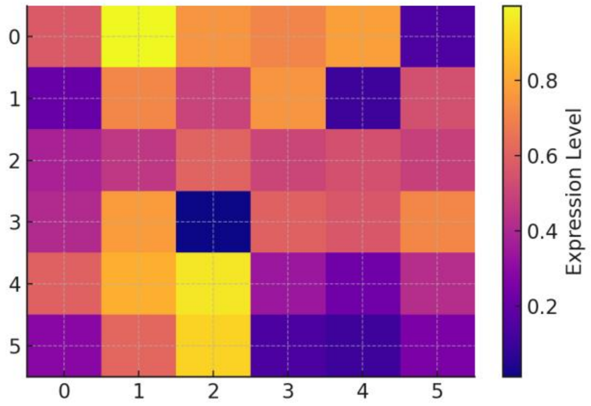

Figure 7. Heatmap of transcriptomic activity under pathogen stress.

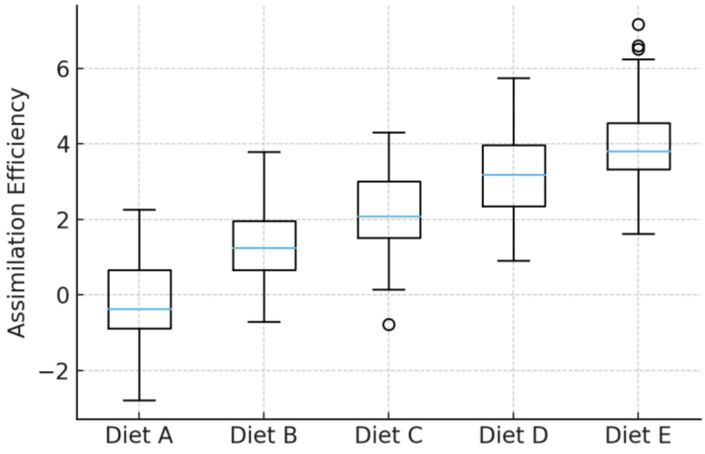

Figure 8. Boxplot of nutrient assimilation efficiency across diets.

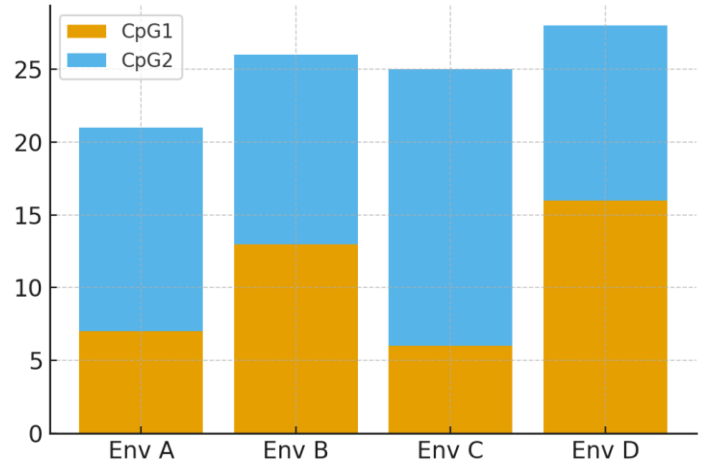

Figure 9. Stacked bar chart of epigenetic methylation profiles across environments.

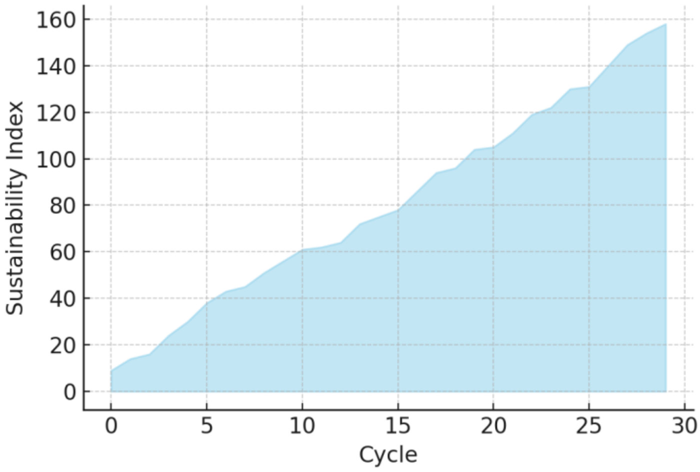

Figure 10. Area chart of sustainability indices over production cycles.

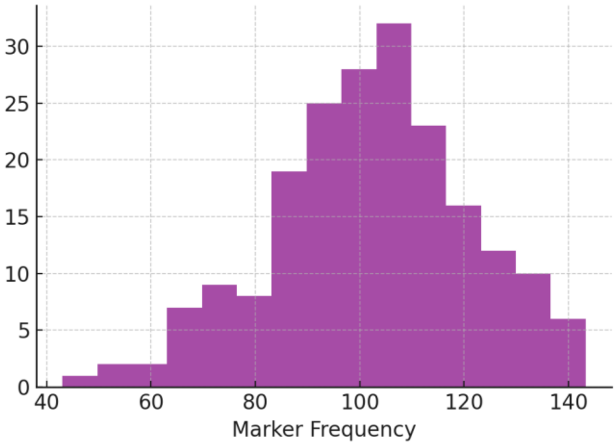

Figure 11. Histogram of genetic marker frequencies in populations.

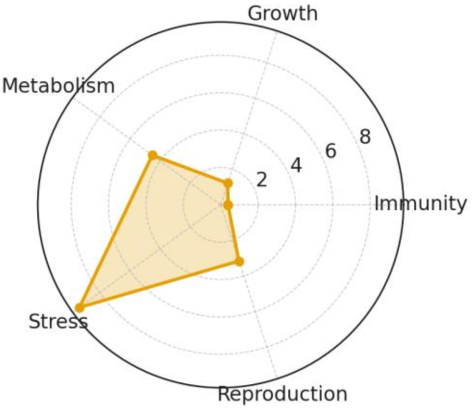

Figure 12. Radar chart of physiological resilience traits across species.

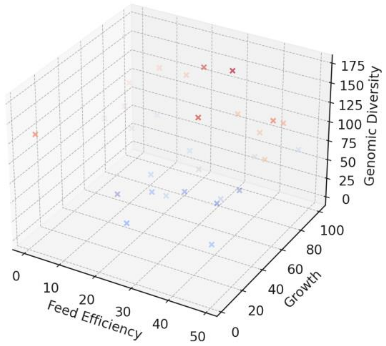

Figure 13. 3D scatter plot linking feed efficiency, growth, and genomic diversity.

DISCUSSION

One of the big strides towards making aquaculture a more sustainable activity is the combination of genomic technologies and physiological monitoring. The results of this study suggest that genomics can be used to speed up the selective breeding process along with the welfare of the ecosystems through the means of guided actions. As the world moves to the scale of aquaculture to supply the protein needs, the genomic technologies are on the rise in the management of diseases, feed efficiencies and survival of fish and other animals to climatic shocks. Houston and Macqueen (2020) state that the genomic selection has transformed the characteristics of improving the aquaculture species because it is more accurate compared to the classical breeding techniques. Yánez et al. (2020) also emphasized that genomic resources may ease the occurrence of the disease as genetic markers of resistance in the pathogen could be identified.

At physiological level, growth, stress response and metabolic efficiency molecular signals are essential in the optimization of output outcomes. Palaiokostas (2021) has shown that SNP panels of high density enable scientists to correlate the physiological characteristics with genotypes and therefore they can make growth prediction models more effective. Meanwhile, Su et al. (2021) confirmed the importance of transcriptome studies in disambiguating the expression of immune genes following pathogen exposure to enhance disease-management strategies. These findings are consistent with ours, and it means that it is necessary to apply physiological and molecular data as one of the methods of solving the sustainability problem in aquaculture.

The other innovative ideas are the usage of epigenetics in aquaculture. Anastasiadi and Piferrer (2019) assert that the environmental impact on the DNA methylation patterns in fish may exist, and this system might be the cause of transgenerational adaptability without the need to change genetic trends. This is consistent with the observation made in phenotypic plasticity in rearing environment that can be utilized in order to facilitate resilience. In addition, a research conducted by Gui and Zhu (2021) suggests that together with manipulated environmental factors, molecular breeding can serve as a basis of climate sensitive aquaculture.

The same is being utilized in nutrition genomics in aquaculture, which is environmentally friendly. In one study by Kemski et al. (2020), it is possible to use nutrigenomics to enhance the dietary pattern through identifying the composition of the meal to the physiological pathways that promote the growth and immunity. One of the ways of mitigating oxidative stress in growing species is the effect of dietary antioxidants on physiological responses as was also the case with Hoseini et al. (2019). Such conclusions enhance the necessity to focus on molecular physiology and sustainable sources of feed.

At last, all this genetic-physiological method combined with the technologies of the digital world can provide the exact aquaculture with the new possibilities. Fore et al. (2018) note that sensor-based monitoring systems and big-data analytics can collaborate to encourage real-time decision-making. The other aspect that Gjedrem and Rye (2018) emphasized is that the management tools at the system-wide level should be offered along with the establishment of the genomics as the development of the latter makes it possible to implement all the goals of the sustainability.

The results such indicate that the concept of efficiency enhancement is not that characterising genomic-era aquaculture, which is also characterised by more ambitious objectives, such as resilience, well-being and ecosystem health. Discoveries in genetics, understanding of human physiology and green technologies, all contribute to making the aquaculture an outstanding solution to sustainable food supply in the future. This does however hold true when moral, environmental as well as social issues are put into consideration.

CONCLUSION

It has been established in the paper that the genomic age provides special opportunities to transform aquaculture into the more sustainable, resilient and efficient food production system. The paper describes molecular and biological innovations as having the power to solve long-term fisheries problems through an intervention of genomic (whole-genome sequencing, SNP mapping, and transcriptomics) combined with physiological research on growth, stress, nutrition and disease resistance. These findings indicate that genetic based breeding accelerates growth and feed ratio, and removes genetic bottlenecks common in traditional reared settings. The disease resistance and physiological adaptability under stress of molecular investigation is a way to encourage consolidation of the genetic screening and biomarkers like physiological aspects of animal well-being and survival to environmental variation. Another addition to the formation of the resilience toolbox is epigenetic signatures and nutrigenomic strategies that have the power to create transgenerational adaptation and long-term nutritional development that would establish the objective of abolishing the consumption of wild fishmeal. Integrated sustainability studies are fruitful in the cases of incorporation of genetic and physiological data in the monitoring mechanisms and emphasizing the importance of systems-wide approaches. That leads to the conclusion that this is a revolutionary breakthrough in the field of aquaculture when both genetics and physiology are simultaneously engaged in work with the result of further enhancing the productivity, securing biodiversity, and preventing the negative influence on the environment. Entrepreneurs in the business and politicians know that sustainable aquaculture will provide the solution to the world food security. They are however, urged to invest in green biogenomic systems, data integration systems and processes. The genomic aquaculture that is the combination of molecular biology, physiology and ecological stewardship is a prospective new concept good not only to the economy and the environment.

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