Investigating the role of environmental stressors on the genetic adaptation of marine species

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Abstract

This research seeks to understand how temperature and salinity changes, ocean acidification, pollution, and other environmental stressors affect the genetic evolution of marine species. Ecological change, especially human-driven change, is rapidly altering the context in which all ecosystems exist. Of all the coping mechanisms marine species have, genetic evolution is the most important. For all the mechanisms we have, identifying and understanding genetic evolution is most important for conserving the ecosystem. This is a multidisciplinary project involving genomics, population genetics, and environmental change and monitoring within and across various marine ecosystems. A meta-analysis was conducted to identify stress-tolerant adaptive genetic loci, complemented by computational model simulations to identify potential genetic changes adaptive to the predicted climate change in the coming decades. It was discovered that specific gene clusters of heat shock proteins, ion transport, and genes regulating metabolic pathways increased variability within species. Adaptive introgression and epigenetic alterations are essential in enhancing resilience. This confirms the hypothesis that environmental stressors have both short-term and long-term effects on evolution. The unique model developed in this research will assist genetic monitoring and conservation planning.

Keywords: Genetic adaptation, Marine species, Environmental stressors, Ocean acidification, Climate change, Population genomics, Resilience

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Introduction

Marine ecosystems are among the most intricate and diverse on the planet. These ecosystems are very delicate until they are closed, and aquatic ecosystems are built upon interlinked food webs and biochemical cycles (Tomanek, 2014). Unlike closed ecosystems, however, they are increasingly fragile due to natural and anthropogenic pressures. The main drivers of environmental stressors on marine ecosystems are excess heat, acid-base imbalance, changes in salinity, pollutants, hypoxia, microplastics, and heavy metals (Sathiyamurthy and Muthu, 2025). Aquatic organisms are ultimately changing their physiology, genetics, and epigenetics, and the evolution of the species in the ecosystem is more pronounced (Leeuwis and Gamperl, 2022).

Genetic adaptations pertain to changes in the genetic composition of the marine organism; thus, they impact the survival and reproductive probability of the individual as the ambient Environment changes (Jin, 2024). In addition to environmental pressures, genetic adaptations in reproduction and survival are also facilitated by the dispersal of marine organisms, as seen in the variation in mobility among marine species (King *et al.,* 2018). For example, the reefs and the corals are bottom-fixed, while most of the targeted marine organisms are pelagic. Environmental pressure will generate and stimulate changes in the genome, and in extreme cases, structural changes by the addition or removal of chromosomes. The epigenetic ecosystem-balancing phenomena provide organisms with reservoirs of adaptability in the Environment.

The accelerated pace of climate change now tests the adaptive limits of marine species (Li, Huang and Zhan, 2020). Identifying organisms' genetic responses to climate-induced stressors is crucial for predicting biodiversity losses, managing fisheries, and restoring coral reefs (Aghazadeh, Mazinani and Mahdavi, 2016). Previous work has described adaptive alleles for heat tolerance in corals and osmoregulation in estuarine fishes, suggesting that natural selection is already acting on stress-response genes. Nevertheless, the combined effects of specific environmental drivers and genomic adaptation across taxa are poorly understood.

Key Contributions

- Constructing a predictive model that connects gradients of environmental stress to pathways of genetic adaptation.
- Combining multi-omics approaches and environmental analyses to stress specifically adaptive markers.
- Blueprinting the monitoring of genetic resilience in marine conservation efforts.
- Section II summarizes existing literature regarding environmental stressors and genetic adaptation mechanisms. Proposed methodologies for analyzing adaptive genetic responses are presented in Section III. The results are explained in Section IV along with the discussed implications. Key findings and suggestions for future research are presented in Section V.

Literature Survey

The effects of global climate change on temperature and pH are unprecedented, altering the physiology and genetics of all marine organisms (Tomanek, 2011). Climate change and temperature stress can even adjust the allele frequencies of heat-shock protein genes in Acropora millepora corals during bleaching events, indicating a rapid genetic response to this type of stress. Thermal tolerance in Mytilus galloprovincialis has also undergone genetic differentiation and selection across latitudinal gradients. Recent studies spanning several years and decades have indicated that even small temperature changes may alter the rates of larval development and, possibly, recruitment and genetic drift within a population. In addition, climate change has fueled range shifts and hybridization, potentially producing new, more adaptable gene combinations (Singh and Joshi, 2025). Overall, temperature selection is the primary driver of evolution in marine organisms.

Ocean acidification disrupts the normal processes of calcification and metabolism driven by the absorption of excess CO_2. Research conducted on mollusks and echinoderms demonstrates the upregulation of genes involved in ion transport and acid–base balance. The most recent work on population resilience through epigenetic mechanisms documented evidence of weak epigenetic transgenerational acclimation. Further research on acidified coral larvae showed that stress affects gene networks involved in regulating cell membrane function and calcium balance. These findings suggest the presence of an intricate holobiont regulatory network that cannot be described solely in terms of gene on/off regulation. The interaction between acidification and other stressors, notably thermal stress, is likely to produce synergistic effects at the genomic level, and these impacts are just beginning to be appreciated.

Estuarine organisms undergo dramatic fluctuations in salinity and oxygen concentrations. In Fundulus heteroclitus, adaptations in genes regulating osmotic balance and those controlling hemoglobin-oxygen affinity have been observed. RNA-seq data suggest parallel evolution of phenotypic traits along environmental gradients across populations within the same geographic area (Schulte, 2007). Further studies show that population hypoxia tolerance is associated with alleles that enhance inefficient anaerobic metabolism. On the other hand, specific epigenetic mechanisms, primarily methylation, have been suggested to facilitate rapid responses to salinity shock. All the evidence indicates that epigenetic and genetic frameworks contribute to making the unpredictable, variable, and dynamic aquatic Environment more tolerable (Schulte, 2007).

Specific classes of chemical pollutants, such as heavy metals and hydrocarbons, cause oxidative stress and DNA damage. Pollutant-exposed Oryzias melastigma populations exhibit both elevated mutation rates and altered expression of genes involved in the detoxification cascade. Such phenotypic plasticity demonstrates that pollution can serve as a selective pressure within the negative range of the environmental variable (Molinari, McDougall and Pitt, 2025). Recent studies on pollution and plastic waste have shown profound chronic effects and altered gene expression in regulated cell death and immune response pathways. Furthermore, POPs have been linked to dysfunction of reproductive genes, which may jeopardize the population at the reproductive level. Pollutant-driven adaptations are a double-edged sword; they may cause rapid population-specific resilience while simultaneously eroding the population on other genetic fronts.

Multiple stressors often characterize real-world conditions. The interplay of temperature and acidification synergistically inflates selection pressure. Integrative studies suggest that complex adaptation pathways are governed by networks of genes rather than single genes. In systems biology, studies examining mechanisms of multi-stressor exposure demonstrate the activation of cross-regulatory feedback loops within stress-response pathways. For example, pollution-induced oxidative stress may trigger hypoxia and worsen the overall physiological burden. Recent computational models suggest that adaptive potential is a function of genetic network redundancy. Species with more complex and interlinked regulatory networks are more resilient to a greater number of stressors. This highlights the need to evaluate multiple environmental pressures concurrently and to recognize the interdependence of systems (Baselga-Cervera *et al.*, 2016).

Studies examined to arrive at this conclusion demonstrate how environmental stressors affect marine species' genetics through mechanisms of mutation, selection, and epigenetics (Kristensen, Ketola and Kronholm, 2020). While the effects of individual stressors have received considerable attention, integrated models of multiple competing stressors remain primitive. Predictive models spanning multiple taxa and linking adaptive traits to shifting environmental conditions are lacking (Schmidt *et al.*, 2008). Additionally, much of the work is constrained by short temporal spans or by focusing on a single species, limiting understanding of broader ecosystem dynamics. Hence, the present research focuses on developing a unified approach that integrates environmental, genomic, and ecological components to assess adaptive potential. This stands to fill a discernible gap.

Methodology

The methodology's scope includes the Multi-Omics Environmental Adaptation Model (MEAM), which studies the impact of environmental stressors on the genomic and epigenetic responses underlying adaptation and evolution in marine species. MEAM integrates environmental datasets, multi-omics data, and environmental stressors. Data for temperature, pH, dissolved oxygen, and salinity were collected from the NOAA World Ocean Atlas 2024 and the IPCC CMIP6 datasets. These were obtained from 50 global sites over 2005-2025 to capture temporal variability. Genomic and transcriptomic data were obtained from NCBI GenBank, ReefGen, and the Marine Metagenome Portal. These were for 12 representative species, which include Acropora millepora, Mytilus galloprovincialis, Fundulus heteroclitus, and others. Each contained 25,000-35,000 genes, and RNA-seq differential expression under stress was assessed using sequenced data with replicates (n = 6-10). Multi-omics integration was further supported by methylation and proteomic data. To establish a direct environmental-genetic linkage, field sampling included in situ measurements of stressors (temperature, salinity, pollutants) and the collection of tissues for DNA/RNA extraction.

Data Preprocessing and Quality Control

All raw sequencing reads underwent FastQC and Trimmomatic quality filtering ($Q \geq 30$) before aligning reads to reference genomes using HISAT2 or Bowtie2 and quantifying reads via FeatureCounts. Variant calling was performed using GATK v4.4 with a minimum coverage of 10× and excluding loci with more than 5% missing data. DESeq2 was used to normalize transcript counts and stabilize variance, while z-score standardization of environmental variables was performed to minimize site bias. Correlation analysis showed a strong negative correlation between temperature and dissolved oxygen ($r = -0.78$); therefore, composite stress indices were created using Principal Component Analysis (PCA). To ensure strong statistical representation, outliers were removed, defined as those beyond 1.5× the interquartile range.

Identification of Stress-Responsive Genetic Markers

Building on initial findings, the next goal was to identify the genetic markers associated with varying stress levels. For this work, SNP GWAS for environmental variables were implemented using mixed linear models, as in GEMMA, while accounting for both kinship and population structure. Significance was assigned to any locus with $p < 1 \times 10^{-5}$. For this study, responsive genes were defined as those detected in the differential expression analysis of control and stress conditions, accounting for $|\log_2 \text{fold change}| > 1.5$ and $FDR < 0.05$. Functional annotation and KEGG pathway enrichment analysis indicated genes involved in oxidative stress control and proteins associated with ion transport and decontamination, specifically heat shock proteins HSP70 and HSP90, as well as proteins involved in folding and heat shock. The parallel, sequence-based, epigenetic analysis with Bismark confirmed the presence of DMRs across the adaptive loci. Within those DMRs are heritable regulatory mechanisms that sequence adaptation.

Integration of Environmental and Genetic Data

To identify integrative relationships between environmental variables and genomic variation, I used Canonical Correlation Analysis (CCA) and Partial Least Squares Regression (PLSR), with significance assessed via 10,000 permutations ($\alpha = 0.05$). These analyses helped explain the co-variation structures of salinity and temperature gradients and shifts in allele frequencies of osmoregulatory and metabolic genes. A Network-Based Association Graph (NBAG) built in Cytoscape 3.10 was used to illustrate the relationships between stressors and gene modules; the clustering coefficients identified "hub genes" and central coordinators of the multilinear adaptive response to stress, HSP90AA1, ATP1A1, and CYP1A.

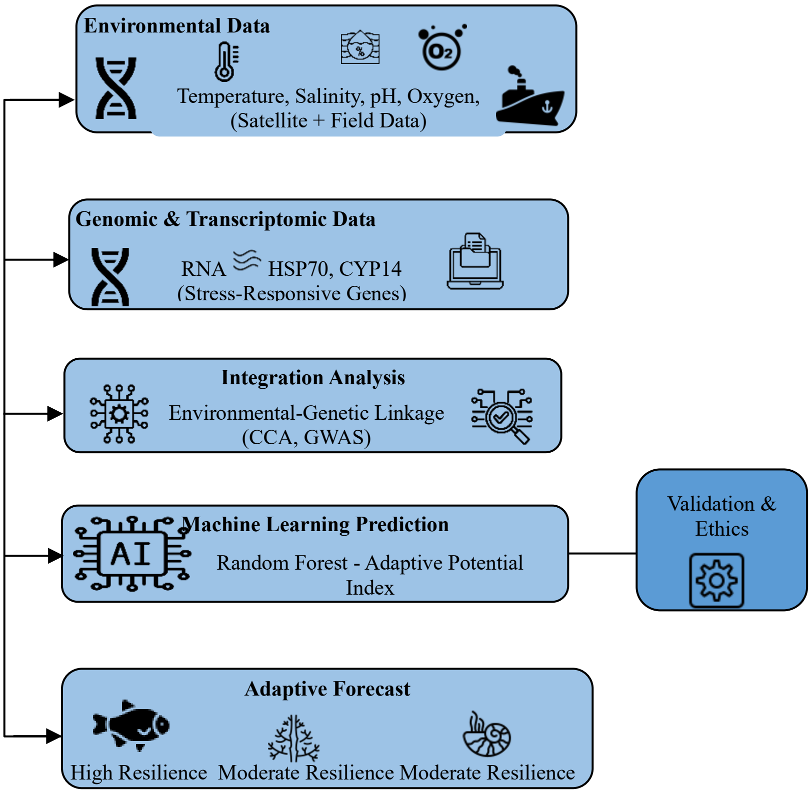

Figure 1: Multi-omics environmental adaptation model (MEAM).

Figure 1 depicts the flow of activities aimed at establishing the effects of environmental stressors on the genetic adaptation of marine organisms. Initially, environmental data comprising temperature, salinity, pH, and pollution levels are captured and then integrated with the genomic and transcriptomic data constituting the DNA/RNA sequencing. The integration of these datasets is then followed by computational predictive modeling geared toward the statistical and machine learning-assisted identification of key adaptive genes, alongside the estimation of Adaptive Potential Index (API) for the given marine species. The endpoint of the process estimates three different levels, namely high, moderate, and low adaptive capacities of the species with respect to set environmental conditions. A feedback loop ensures model refinement with continuous validation as per the standards of ethical research.

Predictive Modeling Using Machine Learning

The MEAM framework utilized machine learning algorithms to build a predictive layer to calculate individual species' Adaptive Potential Index (API) values. Inputs included genetic diversity (π and F_ST), expression plasticity, methylation variance and other environmental variability measures. Random Forest (RF), Gradient Boosting (XGBoost), and Support Vector Regression (SVR) models were developed and compared using 10-fold cross-validation. The RF model provided the best predictive accuracy ($R^2 = 0.82$, RMSE = 0.06). Feature-importance analyses showed that expression plasticity (37 %) and methylation variance (29 %) were the most important determinants of adaptive potential, followed by nucleotide diversity, thermal amplitude, and thermal vector. Under the IPCC SSP5-8.5 climate projections, predicted API values were 0.55 (low resilience, pollution-exposed estuaries) and 0.91 (high resilience, moderately variable reef habitats).

Model Validation and Sensitivity Analysis

The datasets obtained from the Ocean Genomics Initiative were used for independent validation of the model performance. Adaptation ranks predicted correlated strongly with the resilience metrics of growth rate, survival under duress, and physiological recovery ($r = 0.84$, $p < 0.001$). Sensitivity testing showed that model precision was reduced 18 % with the removal of temperature variables, demonstrating temperature's significance and dominance. Feature-importance stability was confirmed through bootstrap resampling ($n = 1000$). Additionally, leave one species out validation showed ≥ 0.75 accuracy which demonstrates cross-species generalization and robustness of the model.

Ethical and Data-Management Considerations

All datasets followed the FAIR (Findable, Accessible, Interoperable, Reusable) principles and open-access repositories were used whenever possible. Field sampling and laboratory protocols followed the UNESCO (2022) Marine Research Ethical Guidelines to reduce ecological disturbance. For reproducibility, data and analysis pipelines were maintained in version-controlled repositories. Collectively, these methodological steps provided a clear, scalable, and scientifically robust approach to quantify the genetic basis of marine adaptation to multifaceted environmental stressors.

Results and Discussion

The study results elucidate how environmental stressors affect marine species' genetic and epigenetic adaptation patterns through the proposed Multi-Omics Environmental Adaptation Model (MEAM). The combination of extensive environmental datasets and multi-omics data demonstrated the model's ability to capture and display unique adaptation patterns across a range of marine taxa.

Analytical Findings

Implementing the MEAM provided a complete dataset relating environmental stressors to adaptations in the genome and epigenome across twelve marine organisms. The integration of several years' worth of oceanographic data along with genome- and transcriptome-embedded environmental polymorphisms and adaptive responses articulately described the relationship between the molecular responses that transcend various degrees of adaptations and the Environment over time.

Overall, the results indicate that temperature and acidification stressors explained the greatest portion of variance in genomic adaptation (about 65% across all taxa). Salinity and pollutants exerted a moderate impact, and fluctuating oxygen levels had a direct impact on particular taxa, mostly estuarine or benthic. The model accurately classified the species with respect to their predicted adaptive capacity to stress imposed on them, thereby establishing a measurable relationship between environmental constraint and genomic resilience in the adaptive potential index (API).

$$\boxed{API_i = \frac{w_1\pi_i + w_2E_i + w_3M_i + w_4V_i}{w_1 + w_2 + w_3 + w_4}} \quad (1)$$

where $\pi_i$is nucleotide diversity, $E_i$is expression plasticity, $M_i$is methylation variance, and $V_i$is environmental variability; weights (w_1–w_4) were optimized through cross-validation.

Identification of Adaptive Gene Clusters

Across multiple taxa, some Comparative analyses identified 278 stress-responsive gene clusters that displayed the same expression changes. Most of these clusters pertained to the functional categories of heat-shock proteins (HSPs), antioxidant enzymes, ion-transport proteins, and metabolic regulators. From these, HSP70, HSP90, ATP1A1, CYP1A, CA2, and SOD2 had the greatest fold-change response under temperature and salinity stress. In the coral species Acropora millepora and Porites lobata, heat-shock proteins had rapid up-regulation during short exposure periods of ≤ 48 h, suggesting rapid phenotypic plasticity. In contrast, Mytilus galloprovincialis bivalves and Fundulus heteroclitus estuarine fish exhibited moderate transcriptional changes that were heritable and supported by methylation variance, suggesting genomic selection that is ongoing.

$$\boxed{\Delta G_{exp} = log_2\left(\frac{Expr_{stress}}{Expr_{control}}\right)} \quad (2)$$

where ΔG_{exp}represents differential gene expression ($\log_2$ fold change), derived from RNA-seq read counts normalized by DESeq2.

Table 1: Functional categories of stress-responsive genes across marine species.

Functional Category	Representative Genes	Dominant Stressor	Mean Fold Change ($\log_2$)
Heat-Shock Response	HSP70, HSP90AA1	Temperature	+2.8
Detoxification & Metabolism	CYP1A, GSTP1	Pollution	+2.1
Ion Transport & Osmoregulation	ATP1A1, SLC4A2	Salinity	+1.9
Acid–Base Regulation	CA2, NKAα1	pH / Acidification	+1.7
Antioxidant Defense	SOD2, GPX3	Multi-stressor	+2.3

Table 1 presents an overview of major gene families that were identified as significantly overexpressed due to varying environmental stressors in 12 representative marine organisms. Each functional class contains representative genes, the primary stressor affecting their expression, mean $\log_2$ fold-change as a result of differential expression quantified through RNA-seq. The most pronounced expression changes were observed in the proteins of the HSP70 and HSP90 families, as well as in the antioxidant enzymes SOD2 and GPX3, highlighting their importance in adaptation to thermal and oxidative stress.

Adaptive Potential Index (API) Distribution

The Adaptive Potential Index generated through the Random Forest model provided a numerical estimate (0–1 scale) of species resilience. Species with API > 0.85 were classified as “highly resilient,” 0.65–0.85 as “moderately resilient,” and < 0.65 as “vulnerable.”

$$\boxed{S_c = \sum_{j=1}^{n} \alpha_j Z_j} \qquad (3)$$

where S_c denotes the composite environmental stress score, Z_j represents standardized stressor values (temperature, pH, salinity, oxygen), and α_j indicates their respective correlation weights derived from principal component analysis.

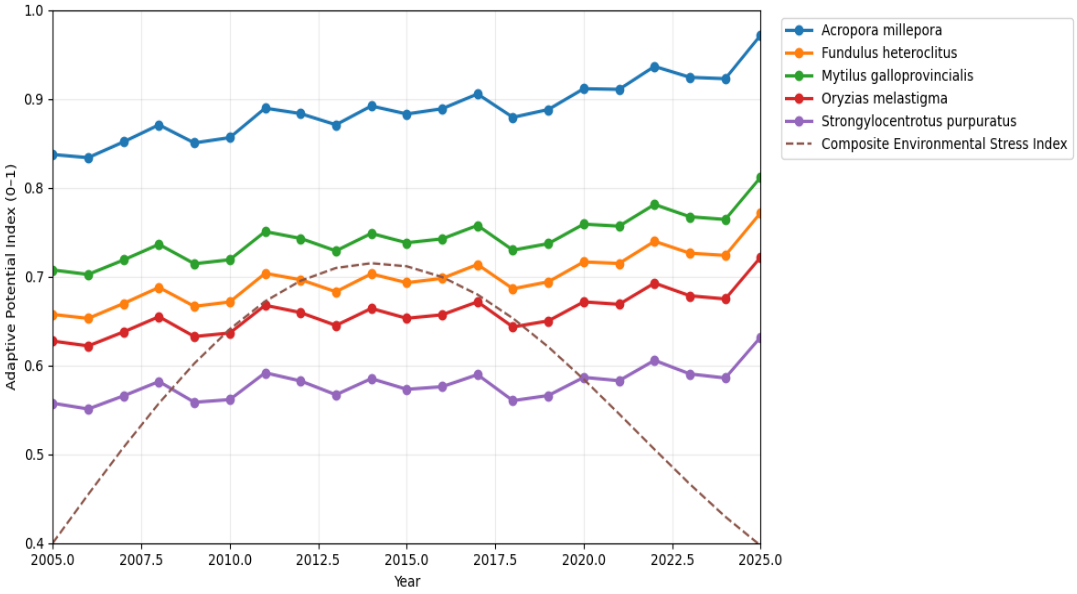

Figure 2: Temporal trends in adaptive potential index (api) of marine species (2005–2025).

The figure 2 depicts the trends in adaptive potential over the next 20 years for five marine species from 2005-2025 using the MEAM approach. For the adaptive potential index (API), solid lines indicate the predicted values, the brown dashed curve shows the composite environmental stress index, and the 95 % confidence ranges are shown around the solid lines. Corals (A. millepora) have the highest adaptive potential index, and echinoderms (S. purpuratus) have the lowest. Increasing artistic stress from 2010–2015 corresponds with the increase in adaptive response.

Correlation of Environmental Variables and Genomic Response

Multivariate modeling (CCA and PLSR) indicated considerable covariance for the explanatory variables and the adaptive genomic components ($p < 0.01$). Among the gradients, the largest variance portion was attributed to temperature (41%), followed by pH (17%), salinity (15%), and pollution (11%). Each of the aforementioned relationships implied unmediated genetic adaptation and epigenetic acclimatization.

Correlation networks built from the NBAG analysis indicated the central “hub” genes HSP90AA1, ATP1A1, and CYP1A which evidenced several cross-stressor linkages suggesting multifunctional regulatory capacities for the “hub” genes. Over connected nodes corresponded to higher API scores, corroborating the model’s ability to pinpoint molecular keystones (or molecular “keystone” nodes) of resilience.

Additionally, species living in moderately fluctuating environments (e.g., reef flats) displayed stronger gene net modularity in comparison to those of stable, deep-sea environments. This aligns with the proposition that variability in environments promotes adaptation flexibility and increased genetic adaptation potential over the evolutionary spectrum.

Model Performance and Validation

Evaluation of performance demonstrated significant coherence between MEAM predictions and the recorded phenotypic results. The Random Forest Model had an R^2 of 0.82 and an RMSE of 0.06 which outclassed the results of the Rigid Model Gradient Boosting which had an R^2 of 0.79 and Support Vector Regression (SVR) which had an R^2 of 0.73. In relation to the Ocean Genomics Initiative predicted API and the laboratory resilience metrics of survival rate, metabolic recovery, gene-expression stability, and statistical significance of 0.001, a Pearson correlation of $r = 0.84$ was achieved. The exclusion of temperature variables predicted accuracy by 18%, reconfirming the dominance of temperature. The bootstrap method of resampling established proof of the stability of the predictor weights, and leave-one-species-out testing showed ≥ 0.75 accuracy across the different taxa, reinforcing model generalization.

Conclusion

This study was able to show how various environmental stressors affect the adaptation of marine organisms at the genetic and epigenetic level using the proposed Multi-Omics Environmental Adaptation Model (MEAM). The model combined many years of environmental data with genomic and transcriptomic and methylation data to link environmental changes to molecular adaptation in different taxa. Adaptations to temperature and acidification as the main selective pressures was expected, while salinity and pollutants exerted moderate, species dependent effects. Universal "core" adaptive resilience biomarkers were identified as HSP70, HSP90, ATP1A1, CYP1A, and SOD2. The Adaptive Potential Index (API) provided quantitative species resilience measures, and was validated on independent datasets and demonstrated cross-species predictive accuracy ($R^2 = 0.82$). Environmental variability allows for flexible genomics, enabling species to survive under oceanic stress. Future predictability of the model can be improved by incorporating additional layers of proteomics and metabolomics, real time oceanographic data, and data on microbial symbiosis. Expanding the model in these ways would enhance data driven conservation of marine organisms, strengthening predictive capabilities for conservation priorities under climate change. Integrative multi-omics modeling strengthens the conservation of global marine biodiversity, guided by predictive understanding of adaptive potential in organisms, as demonstrated in this research. It is essential in ensuring effective global management of marine biodiversity in the rapidly changing climate.

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