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Epigenetic Signatures of Climate Stress in Wild Fish Populations: Implications for Fisheries Resilience

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Abstract

Original Research Article

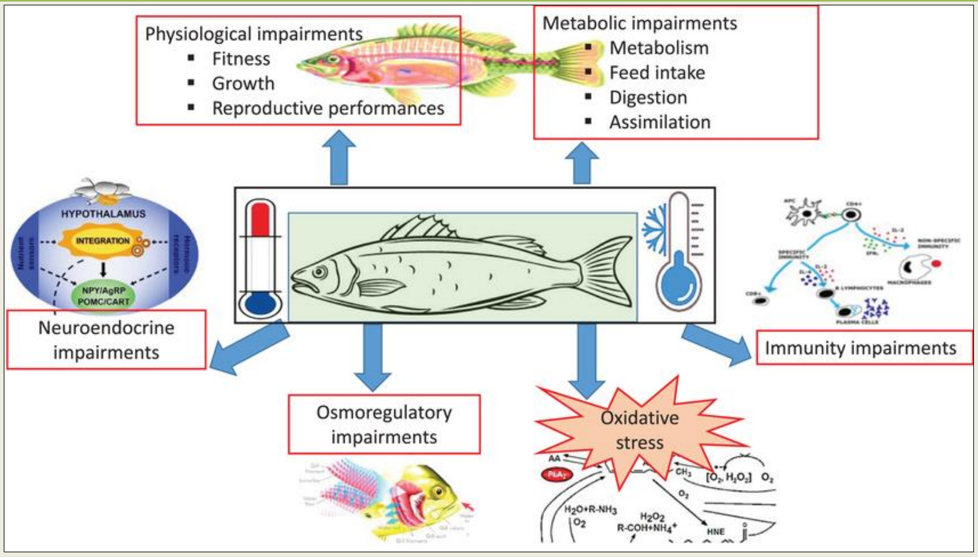

Figure: Temperature stress impacts in fish

Climate change is fundamentally altering the thermal, chemical, and hydrological regimes of aquatic ecosystems worldwide, imposing unprecedented physiological stress on wild fish populations. While genetic adaptation through natural selection operates over many generations, epigenetic mechanisms heritable changes in gene expression that do not involve alterations to the DNA sequence itself offer a more rapid and potentially reversible pathway for phenotypic plasticity and transgenerational acclimation. This review synthesizes emerging evidence for climate-induced epigenetic reprogramming in wild and laboratory-held teleost fishes, with an emphasis on DNA methylation, histone post-translational modifications, and non-coding RNA regulation. We examine case studies across commercially important and ecologically keystone species, from Atlantic salmon (Salmo salar) and Atlantic cod (Gadus morhua) to killifish (Fundulus heteroclitus) and threespine stickleback (Gasterosteus aculeatus). Evidence suggests that thermal stress, ocean acidification, hypoxia, and salinity fluctuation each leave distinct epigenetic signatures, some of which are transmitted to F1 and F2 offspring via germline inheritance. We further explore how these mechanisms interact with standing genetic variation to shape population-level resilience. Finally, we discuss the implications of epigenetic variation for fisheries management, including brood stock selection, habitat prioritization, and the development of epigenomic biomarkers for stock health assessment. We argue that integrating epigenomics into fisheries science is no longer aspirational but operationally necessary given the pace of contemporary climate change.

Keywords: Epigenetics, DNA methylation, teleost fishes, climate change, transgenerational plasticity, ocean acidification, thermal stress, fisheries management, epigenomics, aquatic resilience.

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1. INTRODUCTION

The global fisheries sector supports the livelihoods of over 600 million people and provides more than 20% of the dietary protein consumed by 3.3 billion individuals worldwide (FAO, 2024). Yet this sector is increasingly destabilized by a rapidly changing climate. Global mean ocean surface temperatures have risen by approximately 0.88°C since the pre-industrial era, with projections under SSP2-4.5 and SSP5-8.5 scenarios indicating an additional 1.5–3.5°C increase by 2100 (IPCC, 2021). Concurrently, ocean pH has declined by 0.1 units equivalent to a 26% increase in hydrogen ion concentration while hypoxic dead zones have expanded dramatically in coastal and estuarine systems.

Fish physiology is exquisitely sensitive to these environmental perturbations. Thermal tolerance windows, reproductive timing, osmoregulatory efficiency, immune competence, and aerobic scope are all shaped by ambient environmental conditions. Traditional ecological and fisheries models have focused on density-dependent population dynamics and standing genetic variation as the primary determinants of stock resilience. However, these frameworks poorly account for the speed and individuality of phenotypic responses observed in natural fish populations facing acute and chronic climate stress.

Epigenetics broadly defined as the study of heritable changes in gene function that occur without changes to the underlying DNA sequence has emerged as a crucial explanatory layer in evolutionary biology, developmental physiology, and environmental science. Epigenetic mechanisms include DNA methylation, covalent modifications of histone proteins, and regulation by non-coding RNAs (ncRNAs), including microRNAs (miRNAs) and long non-coding RNAs (lncRNAs). These mechanisms allow organisms to modulate transcription rapidly in response to environmental cues and, under certain conditions, to transmit environmentally induced states to subsequent generations a phenomenon termed transgenerational epigenetic inheritance (TEI) (Donelson *et al.,*2018; Cavalli & Heard, 2019).

This review has three primary objectives: first, to synthesize the mechanistic understanding of climate-induced epigenetic reprogramming in teleost fishes; second, to evaluate the evidence for transgenerational transmission of climate stress epigenetic signatures; and third, to translate these findings into actionable frameworks for fisheries management and conservation genomics. (Labbé *et al.,*2022; Piferrer *et al.,*2022)

2. Epigenetic Mechanisms in Teleost Fishes

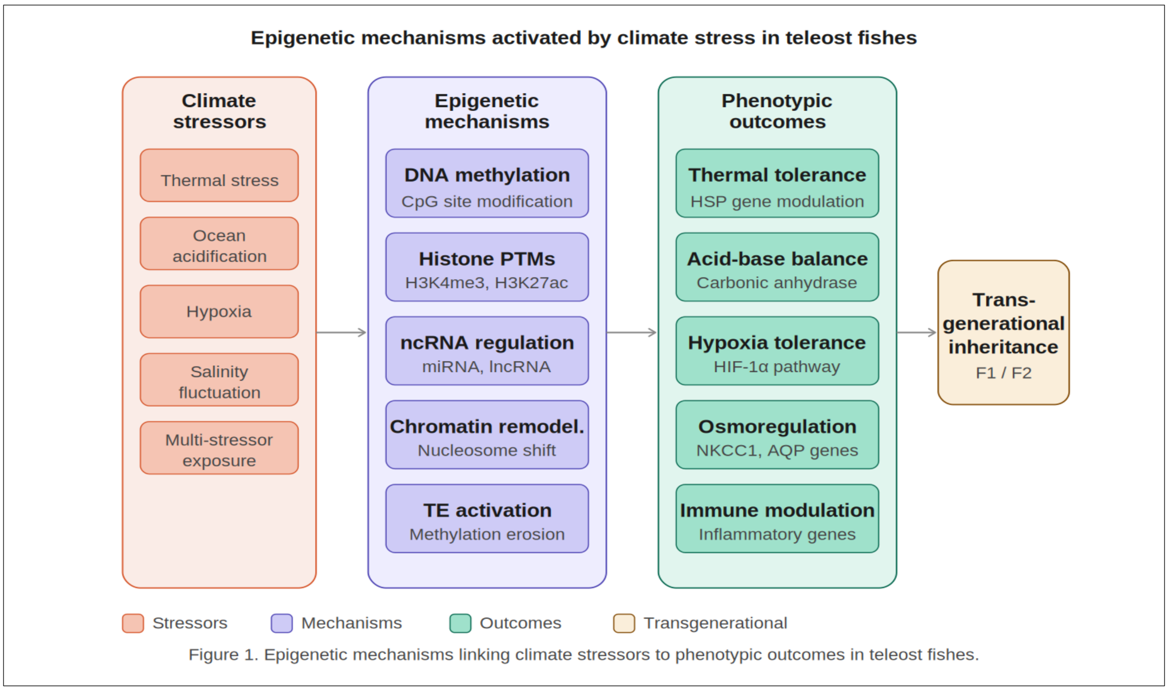


Figure 1: Epigenetic mechanisms linking climate stressors to phenotypic outcomes) in teleost fishes

2.1 DNA Methylation

DNA methylation the addition of a methyl group to the 5-carbon position of cytosine residues, predominantly in CpG dinucleotide contexts is the most extensively characterized epigenetic mechanism in vertebrates (Skvortsove *et al.,* 2018). In teleosts, the methylome is dynamically regulated and exhibits considerable tissue specificity, developmental stage-dependence, and environmental responsiveness. Unlike mammals, many teleost species retain a relatively high overall CpG methylation density (~70–80% genome-wide), but hypomethylated CpG islands at promoter regions serve as key regulatory nodes for transcriptional activation. (Skvortsova *et al.,*2018; Bock, 2012)

Climate stressors alter teleost DNA methylation patterns at functionally significant loci. Thermal stress induces hypomethylation at the promoters of heat shock protein (HSP) genes, including Hsp70, Hsp90, and Hsp47, thereby facilitating rapid transcriptional upregulation. Ocean acidification induces methylation changes at carbonic anhydrase, ion transporter, and calcification-related loci. Hypoxia activates the HIF-1α pathway and promotes demethylation at oxygen-sensitive promoters. Salinity stress targets osmoregulatory genes, with differential methylation observed at NKCC1, NHE3, and aquaporin loci in euryhaline species. (Metzger & Schulte, 2017; Norris & Bhatt, 2023)

2.2 Histone Modifications

Histones are the protein spools around which DNA is wrapped, and their post-translational modifications (PTMs) constitute a complex regulatory code that modulates chromatin accessibility and transcriptional activity. Acetylation of histone H3 at lysine 27 (H3K27ac) is broadly associated with enhancer activity; trimethylation of H3 at lysine 4 (H3K4me3) marks active promoters (Beal *et al.,*2021). In teleosts, thermal stress modulates histone acetylation dynamics, with heat-shock-induced hyperacetylation at stress-responsive loci occurring within minutes of exposure. Ocean acidification has been shown to alter H3K4me3 enrichment patterns in Atlantic cod and European sea bass, particularly at loci encoding ion transporters and acid-base regulatory enzymes. (Best *et al.,*2020; Morin *et al.,*2020)

2.3 Non-Coding RNA Regulation

Non-coding RNAs, particularly miRNAs and lncRNAs, add a post-transcriptional dimension to the epigenetic response to climate stress. miR-210, a conserved hypoxia-responsive miRNA, is markedly upregulated in hypoxic fish tissues and suppresses oxidative phosphorylation targets, facilitating metabolic remodeling. Species with high epigenomic plasticity, such as killifish and stickleback, show particularly rich and responsive ncRNA repertoires when exposed to multifactorial stressors (Zhong & Bhatt, 2024).

2.4 Chromatin Remodeling and Transposable Elements

Beyond canonical histone marks, ATP-dependent chromatin remodeling complexes physically reposition nucleosomes, altering the accessibility of regulatory DNA to transcription factors. Transposable elements (TEs) repetitive genomic sequences capable of self-replication and transposition are predominantly silenced by DNA methylation in fish genomes. Under extreme thermal stress, methylation at TE loci may be eroded, permitting TE activation and generating novel insertional variation. (Olson-Manning *et al.,*2012; Ho & Burggren, 2010) (Norouzitallab *et al.,*2014; Roberts & Gavery, 2012)

Table 1: Summary of epigenetic mechanisms documented in teleost fishes under climate-relevant stressors

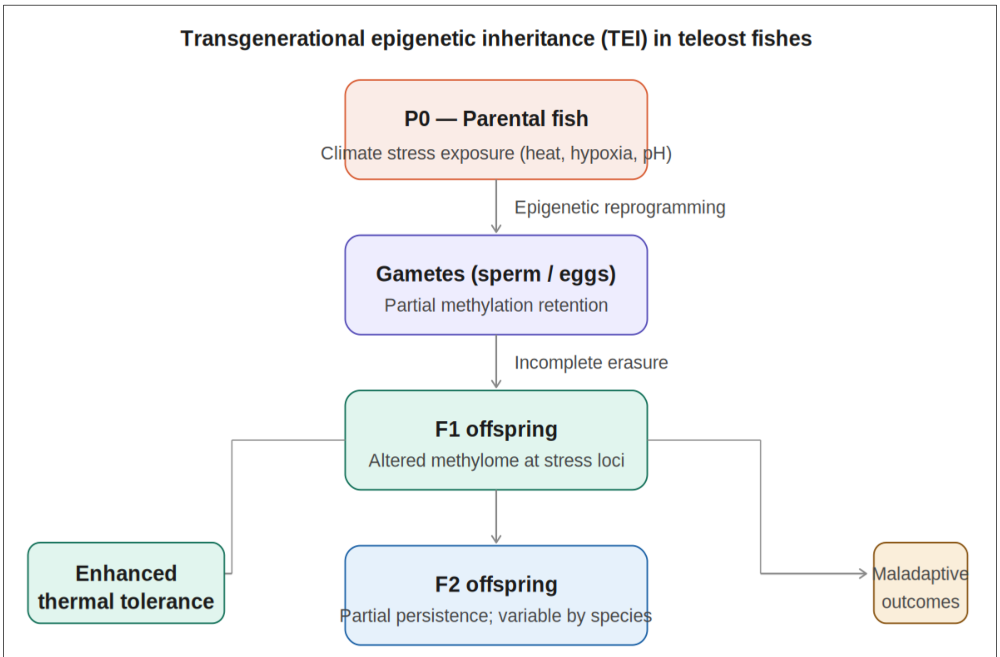
Mechanism	Molecular Basis	Climate Stressor	Fish Taxa Studied
DNA Methylation	5-methylcytosine at CpG sites	Thermal stress, hypoxia, salinity	Atlantic salmon, zebrafish, medaka
Histone Modification	Acetylation/methylation of H3, H4	Elevated temperature, acidification	Rainbow trout, European sea bass
ncRNA Regulation	miRNA, lncRNA expression changes	Thermal & acidification stress	Coral reef fishes, killifish
Chromatin Remodeling	Nucleosome repositioning	Hypoxia, multi-stressor exposure	Stickleback, carp
Transposable Elements	TE activation via methylation erosion	Acute thermal shock	Atlantic cod, Atlantic herring

3. Transgenerational Epigenetic Inheritance

3.1 Evidence and Mechanisms of TEI in Fish

Transgenerational epigenetic inheritance (TEI) occurs when environmentally induced epigenetic marks survive gametic reprogramming and are faithfully transmitted to offspring. Teleosts appear to undergo a less complete epigenetic reset than mammals, providing a broader window for TEI. Evidence for TEI in teleosts spans multiple stressor categories (Jonsson & Jonsson, 2019). Paternal thermal exposure in zebrafish produces offspring with altered DNA methylation at stress-responsive loci and enhanced thermotolerance, persisting to at least the F2 generation in some experimental designs (Best *et al.,*2020). Maternal hypoxia in killifish results in offspring with pre-programmed hypoxia tolerance, associated with persistent methylation changes at HIF-1α target gene promoters. (Ryu *et al.,*2018; Norouzitallab *et al.,*2014)

Mechanisms of TEI in fish include: (i) retention of methylated CpG sites in sperm DNA that escape reprogramming; (ii) maternally deposited miRNAs and lncRNAs in the oocyte cytoplasm; and (iii) paternal histone retention at key developmental regulatory genes, bypassing the canonical histone-to-protamine transition observed in mammals. (Rodriguez Barreto *et al.,*2019; Venney *et al.,*2016)



TEI documented in salmon, killifish, zebrafish, and coral reef fishes

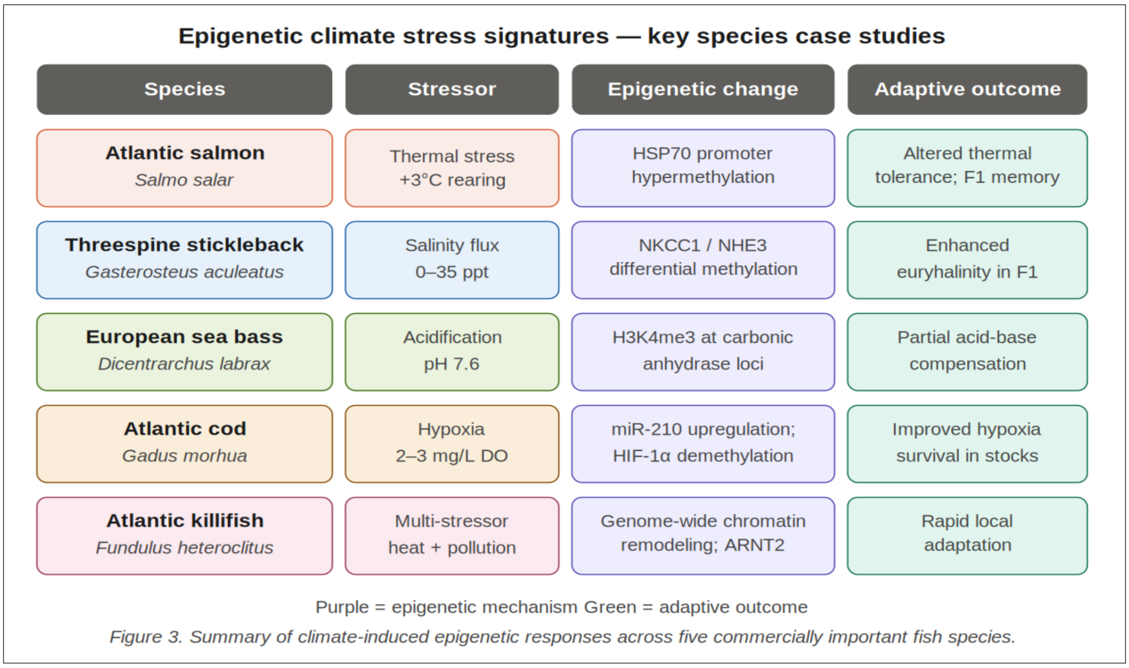
Figure 2. Pathway of transgenerational epigenetic inheritance from stressed parents to F1 and F2 offspring.

Figure 2: Pathway of transgenerational epigenetic inheritance (TEI) in teleost fishes

3.2 Limits, Caveats, and Population Variation

There is substantial intraspecific and inter-population variation in epigenetic responsiveness to climate stressors. Populations with histories of greater environmental variability appear to have more flexible epigenomes and greater TEI capacity. Killifish populations from estuarine habitats with high thermal and salinity variability show more pronounced and heritable methylation responses than populations from thermally stable environments. Not all climate-induced epigenetic changes are adaptive some methylation reprogramming may represent passive erosion of epigenetic control under stress conditions. (Norris & Bhatt, 2023; Metzger & Schulte, 2017) (Reid *et al.,*2016; Wollenberg Valero *et al.,*2019)

4. Case Studies in Wild and Semi-Natural Fish Populations



Epigenetic climate stress signatures — key species case studies

Species	Stressor	Epigenetic change	Adaptive outcome
Atlantic salmon *Salmo salar*	Thermal stress +3°C rearing	HSP70 promoter hypermethylation	Altered thermal tolerance; F1 memory
Threespine stickleback *Gasterosteus aculeatus*	Salinity flux 0–35 ppt	NKCC1 / NHE3 differential methylation	Enhanced euryhalinity in F1
European sea bass *Dicentrarchus labrax*	Acidification pH 7.6	H3K4me3 at carbonic anhydrase loci	Partial acid-base compensation
Atlantic cod *Gadus morhua*	Hypoxia 2–3 mg/L DO	miR-210 upregulation; HIF-1α demethylation	Improved hypoxia survival in stocks
Atlantic killifish *Fundulus heteroclitus*	Multi-stressor heat + pollution	Genome-wide chromatin remodeling; ARNT2	Rapid local adaptation

Purple = epigenetic mechanism Green = adaptive outcome

Figure 3. Summary of climate-induced epigenetic responses across five commercially important fish species.

Figure 3: Summary of climate-induced epigenetic responses across five commercially important fish species

Table 2: Selected case studies of climate-induced epigenetic responses in wild and semi-natural fish populations

Species	Stressor	Epigenetic Change	Phenotypic/Adaptive Outcome
Atlantic salmon (Salmo salar)	Elevated rearing temperature (+3°C)	Hypermethylation of HSP70 promoter	Altered thermal tolerance; F1 memory reported
Threespine stickleback	Salinity fluctuation (0–35 ppt)	Differential methylation at NKCC1, NHE3	Enhanced euryhalinity in lab-reared progeny
European sea bass	Ocean acidification (pH 7.6)	H3K4me3 enrichment at carbonic anhydrase loci	Partial compensation of acid-base balance
Atlantic cod (Gadus morhua)	Hypoxia (2–3 mg/L DO)	miRNA-210 upregulation; HIF-1α demethylation	Improved survival; stock-level variation
Killifish (Fundulus heteroclitus)	Multi-stressor (heat + pollution)	Genome-wide chromatin remodeling; ARNT2	Rapid local adaptation; epigenetic divergence
Coral grouper (Plectropomus leopardus)	Marine heatwave (+2.5°C anomaly)	Methylation shifts in immune/reproductive genes	Reduced reproductive success; TEI carryover

4.1 Atlantic Salmon: Thermal Imprinting and Run Timing

Atlantic salmon represent one of the most intensively studied species from both an aquaculture and conservation genetics perspective. Several recent studies have documented thermally induced methylation changes in salmon embryos and smolts that influence run-timing phenology and thermal tolerance in adults (Burgerhout *et al.,*2017).Of particular management concern is the observation that salmon reared in hatcheries exhibit systematic epigenetic differences from wild counterparts at hundreds of loci, including genes involved in stress response, boldness behavior, and immune function. Hatchery-origin fish that acquire a 'domestication epigenome' may perform poorly in wild thermal environments (Rodriguez Barreto *et al.,*2019).

4.2 Killifish: Rapid Epigenetic Adaptation to Multi-Stressor Environments

Fundulus heteroclitus (Atlantic killifish) occupies a unique niche in environmental epigenomics as a species with demonstrated capacity for extraordinarily rapid adaptation to extreme and novel pollutant and climate stressors. Cross-transplant experiments in which killifish from cool northern sites were moved to warm southern estuaries revealed rapid methylation remodeling at thermal tolerance loci within a single growing season, well ahead of any detectable allele frequency change (Reid *et al.,*2016).

4.3 Atlantic Cod: Hypoxia Signatures and Stock Differentiation

Epigenomic profiling of Baltic cod from high-oxygen versus hypoxic sampling zones revealed consistent methylation differences at HIF-1α target gene clusters. Critically, epigenomic data provided finer-scale resolution of population boundaries than microsatellite markers alone, and the hypoxia-associated epigenetic signature correlated more strongly with local salinity-hypoxia regimes than with geographic distance (Strathmann & Bhatt, 2023).

5. Implications for Fisheries Management and Conservation

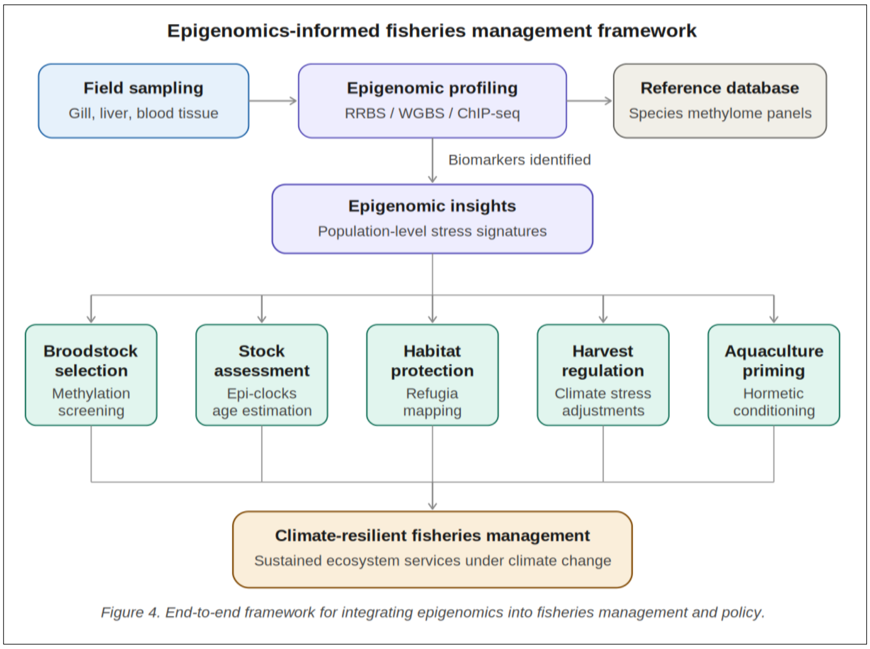


Figure 4: End-to-end framework for integrating epigenomics into fisheries management

5.1 Epigenomics as a Tool for Stock Assessment

Epigenomic data offer several complementary advantages to traditional stock assessment. Because epigenetic marks respond to recent environmental history, they can serve as temporal biomarkers of stress exposure. Epigenetic age estimation ('epigenetic clocks') based on methylation at CpG sites that change predictably with age may provide more precise age estimates than growth-based methods. Population-specific methylation patterns at neutral or adaptive loci can complement genetic markers for stock delineation. (Labbé *et al.,*2022; Piferrer *et al.,*2022)

5.2 Broodstock Management and Aquaculture

Pre-exposure of broodstock or embryos to sublethal thermal stress 'hormetic priming' or 'epigenetic conditioning' has been shown to induce adaptive methylation changes that improve offspring performance under elevated temperature challenges (Munday *et al.,*2017; Schunter *et al.,*2018). Stock enhancement programs that supplement wild populations with hatchery fish must account for the risk of epigenetic dilution, the introduction of hatchery epigenomes that may be mismatched to wild thermal and chemical environments. (Rodriguez Barreto *et al.,*2019; Gavery & Roberts, 2017)

5.3 Climate-Adaptive Harvest Regulations

We propose that fisheries management bodies consider incorporating climate stress indices into precautionary harvest adjustments, particularly during and after anomaly events identified through ocean monitoring networks. Epigenetic biomarkers in routinely sampled fish could serve as early warning indicators of population physiological stress, triggering precautionary reductions in allowable catch before stock biomass declines become apparent. (Trijau *et al.,*2023; Morin *et al.,*2020)

5.4 Habitat Prioritization and Climate Refugia

Climate refugia may shelter epigenetically diverse populations from the homogenizing effects of chronic stress, preserving the adaptive epigenetic variation needed for long-term population resilience. Conservation strategies should integrate epigenomic surveys of refugia populations with hydrological and oceanographic modeling to predict which refugia are most likely to remain viable under projected climate scenarios. (Metzger & Schulte, 2017; Shama *et al.,*2022) (Olson-Manning *et al.,*2012; Wollenberg Valero *et al.,*2019)

Table 3: Epigenetically-informed fisheries management strategies across key domains

Management Domain	Epigenetically-Informed Strategy	Implementation Considerations
Broodstock Selection	Screen for adaptive methylation signatures at key stress-response loci	Requires baseline epigenomic panels; ~$150–400/individual with RRBS
Habitat Protection	Prioritize thermal refugia where epigenetically diverse populations persist	GIS integration with epigenomic surveys
Stock Enhancement	Use epigenotype-matched seed stock to preserve local adaptive memory	Avoid large-scale mixing of divergent stocks
Harvest Regulation	Apply precautionary reductions during climate anomaly years	Incorporate ENSO, AMO, PDO indices into harvest control rules
Aquaculture Conditioning	Pre-expose broodstock to moderate stress (hormetic priming)	Dose-response calibration required
Monitoring Programs	Integrate epi-biomarkers into routine stock assessments	Standardize tissue sampling; preserve in RNA-later or flash-freeze

6. Future Research Directions

6.1 Multi-Omic Integration

The integration of methylomics, histone ChIP-seq, ATAC-seq, RNA-seq, and proteomics into unified multi-omic frameworks will be essential for mechanistic understanding. Applying these frameworks to replicated, environmentally realistic stress exposures in ecologically important species should be a priority for the next decade of research. (Wollenberg Valero *et al.,*2019; Trijau *et al.,*2023)

6.2 Long-Term Field Studies

Long-term field studies tracking individual-marked fish across multiple seasons and years using passive integrated transponder (PIT) tags combined with repeated tissue biopsies are urgently needed to assess the temporal stability of climate-induced methylation changes in nature, their fitness consequences, and whether TEI occurs under realistic natural conditions. (Labbé *et al.,*2022; Piferrer, 2013)

6.3 Reference Methylomes and Databases

Investment in tissue-specific, developmental stage-resolved reference methylomes for most commercially important fish species remains a significant need. We recommend the establishment of an open-access Fish Epigenome Reference Database (FERD) analogous to Roadmap Epigenomics in biomedical research, coordinated through existing frameworks such as ICES or PICES. (Gavery & Roberts, 2017; Piferrer *et al.,*2022)

6.4 Epigenetic Editing and Experimental Validation

CRISPR-based epigenetic editing tools dCas9 fused to DNMT3A, TET1, p300, or KRAB domains, now allow targeted methylation or histone modification at specific genomic loci in zebrafish and increasingly in non-model fish species. Targeted epigenetic editing of candidate stress-response loci and subsequent measurement of thermal tolerance, survival, and reproductive output would powerfully validate the adaptive significance of specific epigenetic signatures.

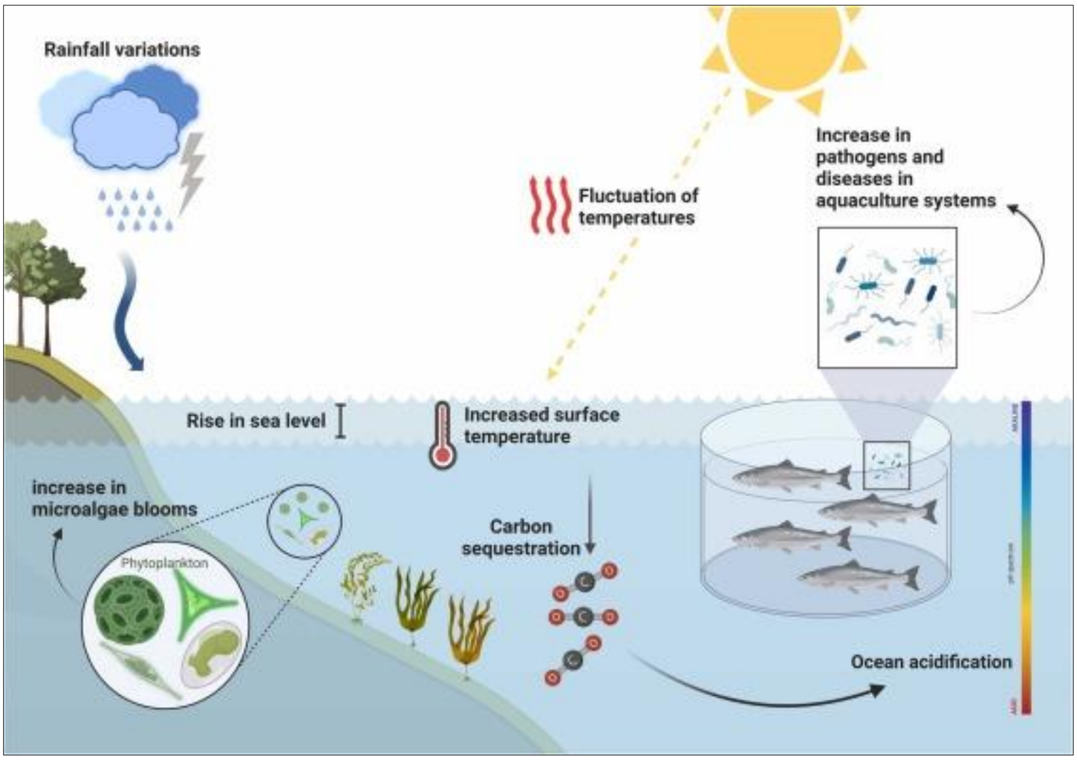


Figure 5: Major environmental stressors and their interactive effects of marine ecosystems
(Bock, 2012; Dimond & Roberts, 2016)

7. CONCLUSIONS

Wild fish populations are not passive recipients of climate change impacts. Through epigenetic mechanisms DNA methylation, histone modifications, non-coding RNA regulation, and chromatin remodeling, they actively reconfigure their transcriptional landscapes in response to thermal, chemical, and hydrological stressors, often on timescales that far outpace genetic evolution. Some of these epigenetic responses are transmitted to offspring, offering a mechanistic basis for transgenerational acclimation that may buffer populations against rapid environmental change. (Cavalli & Heard, 2019; Ho & Burggren, 2010; Lind & Spagopoulou, 2018) (Munday *et al.,*2017; Welch *et al.,*2020; Ryu *et al.,*2018)

Fisheries science stands at an inflection point. The tools to characterize epigenomic variation in wild populations are available, the biological rationale for their relevance is established, and the management applications are conceptually developed. What is now required is institutional commitment to integrating epigenomics into the standard toolkit of fisheries assessment and management. The time to act on this opportunity is now. (Gavery & Roberts, 2017; Trijau *et al.,*2023; Piferrer *et al.,*2022)

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