

Feature Review

Open Access

Effects of Salinity Variation on Growth and Health of Yellowfin Seabream (*Acanthopagrus latus*)

Ming Li, Congbiao You ✉

Hainan Tropical Agricultural Resources Research Institute, Tropical Microbial Resources Research Center, Sanya, 572025, Hainan, China

✉ Corresponding author: congbiao.you@hitar.org

International Journal of Marine Science, 2026, Vol.16, No.2 doi: [10.5376/ijms.2026.16.0009](https://doi.org/10.5376/ijms.2026.16.0009)

Received: 19 Feb., 2026

Accepted: 28 Mar., 2026

Published: 11 Apr., 2026

Copyright © 2026 Li and You, This is an open access article published under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Preferred citation for this article:

Li M., and You C.B., 2026, Effects of salinity variation on growth and health of yellowfin seabream (*Acanthopagrus latus*), International Journal of Marine Science, 16(2): 111-126 (doi: [10.5376/ijms.2026.16.0009](https://doi.org/10.5376/ijms.2026.16.0009))

Abstract Salinity is one of the most important environmental factors affecting the growth, physiological regulation, and health status of marine fish. Yellowfin seabream (*Acanthopagrus latus*) is an economically valuable aquaculture species with strong environmental adaptability; however, fluctuations in seawater salinity caused by climate change and intensive aquaculture practices may negatively affect its production performance. This review summarizes the effects of salinity variation on the growth performance, physiological responses, immune function, and molecular regulatory mechanisms of yellowfin seabream. Changes in salinity influence feeding activity, nutrient utilization, energy allocation, osmotic regulation, antioxidant capacity, and disease resistance through complex physiological and biochemical pathways. Salinity stress can induce oxidative damage, alter hematological parameters, and regulate the expression of osmoregulatory and stress-related genes, including ion transporters and antioxidant-related factors. Case studies under different salinity conditions further demonstrate the importance of maintaining suitable salinity ranges for improving growth efficiency and aquaculture sustainability. Future research integrating multi-omics approaches, environmental monitoring technologies, and selective breeding strategies will provide new insights into salinity adaptation mechanisms and promote climate-resilient aquaculture of yellowfin seabream.

Keywords Yellowfin seabream; Salinity variation; Growth performance; Osmoregulation; Aquaculture health management

1 Introduction

Yellowfin seabream (*Acanthopagrus latus*) is a euryhaline sparid widely distributed in the Indo-West Pacific and is recognized as an economically important coastal fish in several Asian production regions. In the northern South China Sea, it has been described as the most economically important sparid species, highlighting its commercial relevance to regional fisheries and aquaculture. The species is also important in the Pearl River Estuary and adjacent traditional fishing grounds, where its value is tied to both capture fisheries and habitat-linked population dynamics (Tang et al., 2023). Its culture potential is strengthened by strong environmental plasticity, because *A. latus* tolerates broad changes in salinity and temperature and can be reared in ponds or cages (Zhao et al., 2025). This euryhalinity is not only commercially useful but biologically distinctive, since the species naturally occupies coastal environments with large and frequent salinity fluctuations and therefore serves as a suitable model for studying teleost osmoregulation. Field evidence further shows that *A. latus* uses habitats spanning low- to moderate-salinity estuarine waters and more marine environments across its life cycle, with repeated migration between these habitats common in many individuals. This ecological pattern helps explain why salinity is a central variable in yellowfin seabream production: hatchery, nursery, pond, and cage systems often expose fish to abrupt or seasonal changes caused by rainfall, freshwater inflow, evaporation, and estuarine mixing. For aquaculture, salinity is therefore not simply a background water-quality parameter; it is a production factor that shapes growth rate, feed use, survival, physiological stability, and ultimately economic return (Seale et al., 2024).

Salinity variation affects fish physiological ecology because osmotic imbalance alters ion and water homeostasis and forces reallocation of energy toward osmoregulation and stress defense (Mkulo et al., 2025). In teleosts, this regulation depends mainly on coordinated responses of the gill, intestine, kidney, and associated epithelial transport systems, which sense environmental change and switch between salt uptake and salt secretion strategies. Across

fishes, growth often improves at intermediate salinities because osmotic costs can be reduced under near-isosmotic conditions, whereas unfavorable salinity increases metabolic demand and suppresses performance. In juvenile yellowfin seabream specifically, a 56-day trial showed that increasing salinity from 6 to 12‰ improved growth, but salinity above 24‰ suppressed growth, indicating that tolerance does not imply equal performance across all salinity levels. Other studies on *A. latus* show that acute salinity challenge causes rapid but partly reversible endocrine and metabolic disturbance: glucose and lactate rise shortly after transfer, cortisol responds at both low and high salinity, and juveniles can acclimate to 5-35 ppt within 48 h under experimental conditions. Gill tissue appears especially important in this adjustment, being highly sensitive under hypoosmotic stress and increasing Na^+/K^+ -ATPase activity to limit ion loss, while the liver shows pronounced oxidative stress responses (Lin et al., 2020). Intestinal responses are also substantial: hypoosmotic exposure reshapes microbial composition, suppresses intestinal Na^+/K^+ -ATPase activity in freshwater, challenges antioxidant defense, and shifts the balance from probiotic taxa in brackish water toward potentially pathogenic bacteria under stronger dilution stress. Salinity-driven microbiota remodeling is not unique to this species, as comparable work in yellow drum found that high salinity altered intestinal microbiota and increased potentially harmful *Vibrio*, reinforcing the idea that fish health under salinity stress includes microbial as well as host physiological dimensions. More recent work in juvenile yellowfin seabream likewise indicates that 10 ppt and 30 ppt conditions produce contrasting gut microbial and transcriptomic states, with brackish water enriching *Cetobacterium* and seawater enriching *Vibrio* alongside different metabolic and immune gene-expression profiles.

Against this background, research on salinity adaptation in yellowfin seabream is significant for both mechanism and application. From a mechanistic perspective, the species is an excellent model because its genome and comparative genomics resources now provide direct entry points into the molecular basis of euryhalinity, including expansion of osmoregulation-related gene families such as *ARRDC3* and *GSTA* and chromosomal resources for studying adaptation across Sparidae. More broadly, omics studies in teleosts show that salinity acclimation involves interacting ion-transport, stress-response, metabolic, and microbiome pathways rather than a single osmoregulatory axis. This systems view is consistent with emerging evidence in *A. latus*: saline-alkaline exposure alters gill histology, increases malondialdehyde, and co-enriches immune- and energy-metabolism pathways even when growth is not significantly changed, suggesting that performance alone can miss substantial sublethal stress. It is also consistent with population-level evidence that salinity-associated SNPs in wild yellowfin seabream are enriched in pathways linked to cellular process, metabolism, immune response, and environmental information processing, implying that adaptation operates through integrated regulatory networks shaped by local environments. For production, this line of research supports species- and stage-specific salinity management rather than assuming that a euryhaline fish performs equally well across its tolerance range. It also supports using salinity as a deliberate management variable to optimize growth, robustness, and disease resistance, while accounting for rate of transfer, developmental stage, and interacting factors such as temperature. Therefore, studying the effects of salinity variation on growth and health of yellowfin seabream is important not only for defining optimal culture conditions, but also for clarifying how physiological regulation, immunity, oxidative balance, and host-microbiota interactions together determine resilience in a fluctuating aquaculture environment.

2 Ecological Characteristics and Salinity Adaptation Basis of Yellowfin Seabream

2.1 Life history characteristics and environmental requirements of yellowfin seabream

Yellowfin seabream (*Acanthopagrus latus*) is a euryhaline sparid widely distributed in the Indo-West Pacific and is an economically important coastal fish in Asian waters (Lu et al., 2022). Its ecological value is closely tied to its broad habitat use, because this species occupies environments where salinity fluctuates frequently and strongly over time. In the Pearl River Estuary, otolith evidence indicates that early life stages are associated with low- to medium-salinity habitats such as mangrove and oyster-farm waters, which likely function as spawning or nursery grounds. Many individuals later move repeatedly between estuarine and marine environments, showing marked habitat plasticity across ontogeny (Tang et al., 2023). This repeated use of habitats with contrasting salinity regimes helps explain why yellowfin seabream is considered a suitable model for studying environmental adaptation in coastal teleosts.

The environmental requirements of yellowfin seabream are shaped not only by its broad tolerance range but also by life stage and the rate of environmental change. In fish generally, the ability to cope with salinity depends on developmental stage, and salinity tolerance often increases markedly from larval to juvenile phases as gill, kidney, and intestinal osmoregulatory functions mature. For yellowfin seabream specifically, experimental evidence shows that juveniles can tolerate wide salinity exposure, but tolerance is strongly modified by temperature and transfer regime. Fish held at 33‰ tolerated salinity as high as 66‰-67‰ when salinity increased gradually, whereas tolerance was lower under more abrupt challenge conditions. These patterns indicate that habitat suitability for this species depends on the interaction of salinity level, temperature, developmental stage, and the speed of salinity fluctuation rather than on a single fixed optimum.

2.2 Physiological regulation mechanisms of salinity adaptation in fish

Salinity adaptation in fish depends on the maintenance of internal osmotic and ionic homeostasis through coordinated regulation of the gill, kidney, intestine, and other epithelial surfaces. Euryhaline fishes are distinguished by their ability to shift dynamically between salt absorption and salt secretion strategies as external salinity changes. This adjustment begins with osmosensing and signal transduction, which detect the direction and magnitude of osmotic disturbance and activate transport and permeability effectors in osmoregulatory tissues. Because these processes consume energy and alter cellular conditions, salinity stress often affects much more than ion balance alone, extending into metabolism, tissue structure, and whole-animal performance. Salinity therefore acts as both an ecological factor and a physiological stressor in cultured fish.

The physiological response to salinity challenge is also mediated by endocrine, cellular-stress, and immune pathways. Hormones such as cortisol, prolactin, growth hormone, and thyroid hormones are central regulators of osmotic acclimation in teleosts, linking ion regulation with metabolism and growth (AlKatrani, 2022). At the cellular level, salinity stress can trigger conserved stress responses involving macromolecular protection, energy reallocation, and in severe cases apoptosis, showing that tolerance depends on the capacity to stabilize cells as well as fluids (Evans and Kültz, 2020). Recent omics-based work further shows that salinity adaptation includes regulation of ion transport genes, stress-response pathways, and microbiota-associated functions, indicating that osmoregulation should now be understood as a multi-system response rather than a single-organ process. This broader framework is especially relevant for euryhaline aquaculture species exposed to repeated environmental fluctuation (Figure 1).

2.3 Research progress on salinity tolerance of yellowfin seabream

Research on yellowfin seabream has moved from basic tolerance description to integrated evaluation of growth, endocrine regulation, tissue response, and molecular adaptation. A 56-day culture study showed that increasing salinity from 6‰ to 12‰ improved growth in juveniles, whereas salinity above 24‰ suppressed growth, indicating that broad tolerance does not mean equal performance across the full salinity range (Mozanzadeh et al., 2021). Short-term challenge experiments further found that juveniles acclimated to 20 ppt could adjust to 5-35 ppt within 48 h, with transient increases in cortisol, glucose, and lactate early after transfer followed by recovery toward basal levels. Together, these studies suggest that yellowfin seabream is physiologically resilient, but its optimal production salinity is narrower than its absolute survival range.

More recent studies have clarified that salinity tolerance in yellowfin seabream is tissue-specific and involves immune, oxidative, and microbial regulation. Under hypoosmotic stress, the gill showed the strongest osmoregulatory sensitivity through increased Na^+/K^+ -ATPase activity, whereas the liver exhibited the most severe oxidative stress response, demonstrating that different organs bear different parts of the acclimation cost. In the intestine, hypoosmotic exposure reshaped microbial composition and suppressed Na^+/K^+ -ATPase activity in freshwater, while potentially pathogenic genera such as *Vibrio* and *Aeromonas* became more abundant under lower salinity conditions (Lin et al., 2020). At the genomic level, chromosome-scale assemblies and population SNP analyses have also identified osmoregulation-related gene family expansion and salinity-associated adaptive loci, supporting a shift in the field toward multi-omics dissection of salinity adaptation mechanisms in this species.

Overall, current research shows that yellowfin seabream salinity tolerance is best understood as an integrated phenotype linking ecology, growth, endocrine response, immunity, and host-microbiota interactions.

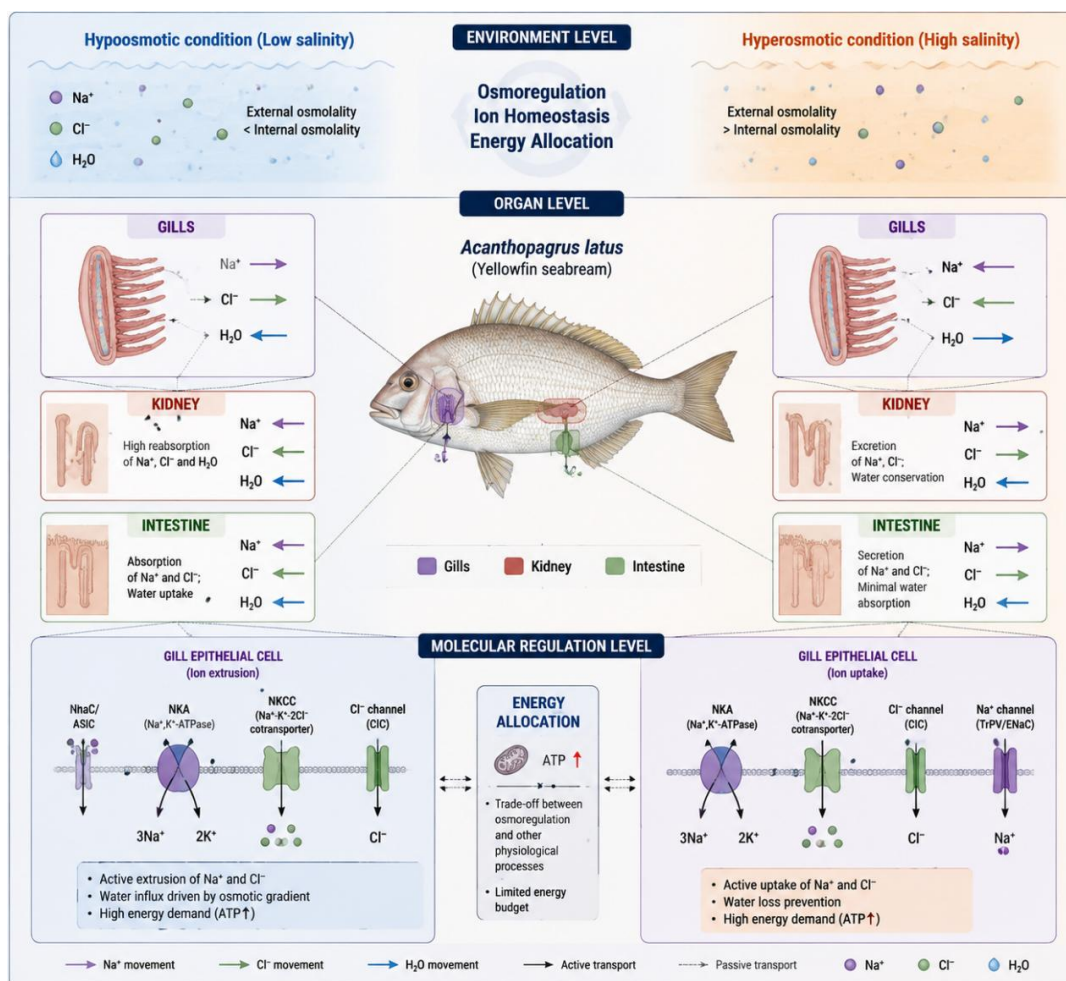


Figure 1 Multi-organ osmoregulatory mechanisms involved in salinity adaptation of euryhaline fish

3 Effects of Seawater Salinity Variation on Growth Performance of Yellowfin Seabream

3.1 Effects of salinity on growth rate and weight gain performance

Salinity variation directly affects growth rate and weight gain in yellowfin seabream, but the response is clearly nonlinear rather than monotonic. In a 56-day trial on juvenile *Acanthopagrus latus*, growth improved when salinity increased from 6‰ to 12‰, whereas further elevation beyond 24‰ suppressed growth, indicating that moderate brackish conditions support better performance than either lower or higher salinity extremes (Mozanzadeh et al., 2021). An earlier acclimation study reached a similar conclusion, showing that juveniles achieved their highest growth at 7 and 15 g/L, while fish transferred to 23 and 30 g/L exhibited poorer performance and even negative growth during the early stage after transfer. These results show that yellowfin seabream can tolerate broad salinity ranges, but its best growth occurs within a narrower intermediate window.

This pattern is consistent with evidence from other euryhaline fishes, where the best growth commonly appears near species-specific isosmotic or low-cost osmoregulatory conditions. In juvenile black sea bream, a closely related sparid, 15 psu was identified as the most favorable salinity for economic culture, with improved feed conversion and low oxidative burden compared with full-strength seawater. Comparable work in Asian seabass also found that intermediate salinity produced the highest weight gain and specific growth rate, whereas both hypo-saline and hyper-saline conditions reduced growth performance (Hassan et al., 2022). Mechanistically, these trends support the view that when salinity departs too far from the physiological optimum, more energy is diverted toward osmoregulation and less remains available for somatic growth.

3.2 Effects of salinity on feeding behavior and feed utilization efficiency

Salinity affects yellowfin seabream growth partly through changes in feeding behavior and feed utilization efficiency. In the same 56-day experiment, salinity above 24‰ not only reduced growth but also impaired feed utilization, showing that performance loss at elevated salinity reflects lower efficiency of converting feed into biomass rather than body weight change alone (Mozanzadeh et al., 2021). Supporting evidence from the 2014 acclimation study showed that the best feed conversion ratio occurred at 7 and 15 g/L, while higher salinity weakened conversion efficiency and coincided with transient weight loss after transfer. This suggests that the feeding response of yellowfin seabream is sensitive to both absolute salinity and acclimation stress.

Evidence from other cultured fishes indicates that salinity can modify feed intake itself as well as post-ingestive efficiency. In Asian seabass, intermediate salinity yielded the lowest feed conversion ratio, while discussion of the same experiment noted that increasing salinity can suppress appetite and thereby contribute to poorer growth. Similar declines in feed intake and protein utilization with rising salinity were reported in common carp and grass carp, where higher salinity increased feed conversion ratio and reduced protein intake, consistent with a shift of dietary energy toward maintenance and ionic regulation rather than tissue deposition. For yellowfin seabream aquaculture, this means that salinity management should be considered part of feeding strategy, because unsuitable salinity can reduce both appetite and feed-use efficiency even when fish remain alive.

3.3 Effects of salinity on body composition and nutrient metabolism

Salinity variation also changes body composition and nutrient allocation in yellowfin seabream. Juvenile *A. latus* reared at 23 and 30 g/L showed reduced proportions of protein, fat, and moisture together with increased ash content relative to lower-salinity groups, indicating that high salinity can alter both tissue deposition and carcass quality. More recent evidence in juvenile yellowfin seabream shows that salinity does not act only at the level of proximate composition, but also reshapes metabolic regulation: fish cultured at 10 ppt upregulated gut-associated metabolic, biosynthetic, and ion-transport genes, whereas fish at 30 ppt showed a stronger immune and redox-oriented transcriptomic profile (Peng et al., 2025). This implies that moderate salinity favors anabolic and nutrient-processing functions, while higher salinity shifts physiological investment toward stress adaptation.

Results from other euryhaline aquaculture species reinforce this interpretation. In GIFT tilapia, increasing salinity decreased whole-body lipid content but increased protein content, demonstrating that salinity can reorganize nutrient partitioning rather than simply depress overall growth. In blue tilapia, brackish-water culture improved growth and was associated with higher amino acid and fatty acid content together with activation of pathways related to unsaturated fatty acid biosynthesis and anabolic metabolism (Zhou et al., 2024). Taken together, these studies suggest that in yellowfin seabream, salinity-mediated differences in growth performance are closely linked to changes in nutrient metabolism, tissue composition, and the balance between anabolic processes and stress-related energy expenditure.

Salinity variation therefore affects yellowfin seabream growth performance through three coupled pathways: direct effects on growth rate and weight gain, indirect effects through feeding and feed conversion, and compositional effects through nutrient metabolism and tissue deposition. For *A. latus*, the evidence consistently indicates that moderate brackish salinity is more favorable than salinity extremes for efficient growth and better physiological allocation.

4 Effects of Seawater Salinity Variation on Physiological Health of Yellowfin Seabream

4.1 Changes in hematological physiological parameters under salinity stress

Salinity stress changes hematological and blood biochemical indices in yellowfin seabream mainly by disturbing osmotic balance and activating a short-term stress response. In juvenile *A. latus*, acute transfer from 20 ppt to 34, 12, or 5 ppt caused significant increases in blood glucose and lactate after 2 h, but both variables returned toward basal levels within 24-48 h, indicating that metabolic disturbance was rapid and largely reversible during acclimation. In the same study, blood electrolytes did not change significantly across salinity treatments, suggesting that juveniles were able to maintain ionic homeostasis even while stress-related metabolites fluctuated. Cortisol and

ALP also rose transiently after transfer and recovered within 24 h, which supports the view that endocrine and biochemical responses are driven more by the timing of challenge than by sustained blood failure.

Although detailed hematology in yellowfin seabream remains limited, studies in related and comparative fishes show a consistent pattern of salinity-induced changes in circulating cells, proteins, and ions. In black sea bream, serum ion concentration and osmotic pressure were actively adjusted within 6-12 h under acute low salinity, showing that blood homeostasis is maintained through rapid regulation rather than passively preserved. In common carp exposed to hypersalinity, total protein, albumin, and globulins decreased while blood glucose, cortisol, and sodium increased, indicating combined osmotic, metabolic, and endocrine strain (Ahmed et al., 2023). A freshwater catfish model showed an even clearer hematological cost, with higher white blood cells but lower red blood cells, hemoglobin, and packed cell volume under salinity exposure, which implies that blood indices are sensitive markers of osmotic challenge severity (Okomoda et al., 2024).

4.2 Effects of salinity variation on antioxidant systems and immune function

Salinity variation strongly affects antioxidant defenses and immune function in yellowfin seabream, but the response depends on tissue and salinity level. Under hypoosmotic stress, the liver showed the most severe oxidative disturbance in *A. latus*, as reflected by fluctuations in SOD and CAT activities together with changes in MDA content. Intestinal physiology was also clearly affected: freshwater exposure significantly inhibited Na^+/K^+ -ATPase activity and challenged the antioxidant defense system, indicating that reduced salinity can impair both ion regulation and redox stability in the gut. At the transcriptional level, hypoosmotic stress altered intestinal expression of genes linked to pathogen recognition, antimicrobial activity, pro-inflammatory cytokines, apoptosis, and antioxidant defense, showing that oxidative and immune responses are tightly coupled in this species.

The immune consequences of salinity stress extend beyond enzyme activity to broader host-microbe and tissue-level regulation. In yellowfin seabream intestine, brackish conditions favored *Lactobacillus* and *Pseudomonas*, whereas freshwater increased potentially pathogenic *Vibrio* and *Aeromonas*, suggesting that low salinity can shift the microbiota toward a less favorable immune context. A newer study likewise found that 30 ppt water enriched *Vibrio* and activated immune and redox-homeostasis genes, while 10 ppt favored *Cetobacterium* and metabolism-related genes, indicating that different salinity regimes bias the fish toward either defense-oriented or metabolic states (Peng et al., 2025). Evidence from black seabream supports the same time-dependent pattern: acute low salinity increased reactive oxygen species, MDA, and total antioxidant capacity early in exposure, then declined as adaptation progressed, showing that oxidative stress is often strongest in the initial adjustment phase (Figure 2).

4.3 Effects of salinity variation on tissue structure and cellular functions

Salinity variation affects tissue structure and cellular function in yellowfin seabream most clearly in organs directly involved in osmoregulation. In *A. latus*, the gill was the most sensitive tissue under hypoosmotic stress and responded by increasing Na^+/K^+ -ATPase activity to reduce Na^+ and K^+ loss, indicating that branchial ion transport is a primary compensatory mechanism. The intestine also showed functional disruption under freshwater exposure, with depressed Na^+/K^+ -ATPase activity and coordinated shifts in microbes, gene expression, and physiological traits, which indicates that salinity stress modifies epithelial function at both cellular and community levels. These findings fit the general teleost model in which gill, intestine, kidney, and other epithelia dynamically switch between salt absorption and salt secretion strategies as salinity changes.

Comparative structural studies show that salinity stress can progress from functional adjustment to overt tissue remodeling when exposure is stronger or more prolonged. In black sea bream, low salinity reduced the number and volume of gill chloride-secreting cells and was accompanied by more developed glomeruli and wider renal tubules, consistent with reduced salt secretion and enhanced ion reabsorption. Across fishes more broadly, salinity challenge can induce gill and liver damage, alter proteins involved in ion transport, metabolism, immunity, and apoptosis, and make gill and intestine the earliest and most responsive organs to structural stress (Su et al., 2025). Acute and chronic salinity experiments in other species similarly show dose- and time-dependent lamellar fusion, intestinal mucosal change, renal stress, and hepatocellular swelling, reinforcing that cellular adaptation has clear structural limits when

salinity moves beyond the optimal acclimation range. Overall, seawater salinity variation affects the physiological health of yellowfin seabream through rapid blood stress responses, tissue-specific oxidative and immune regulation, and remodeling of gill and intestinal function. In yellowfin seabream, physiological resilience is evident, but health costs rise when salinity departs too far from the acclimation range or changes too abruptly.

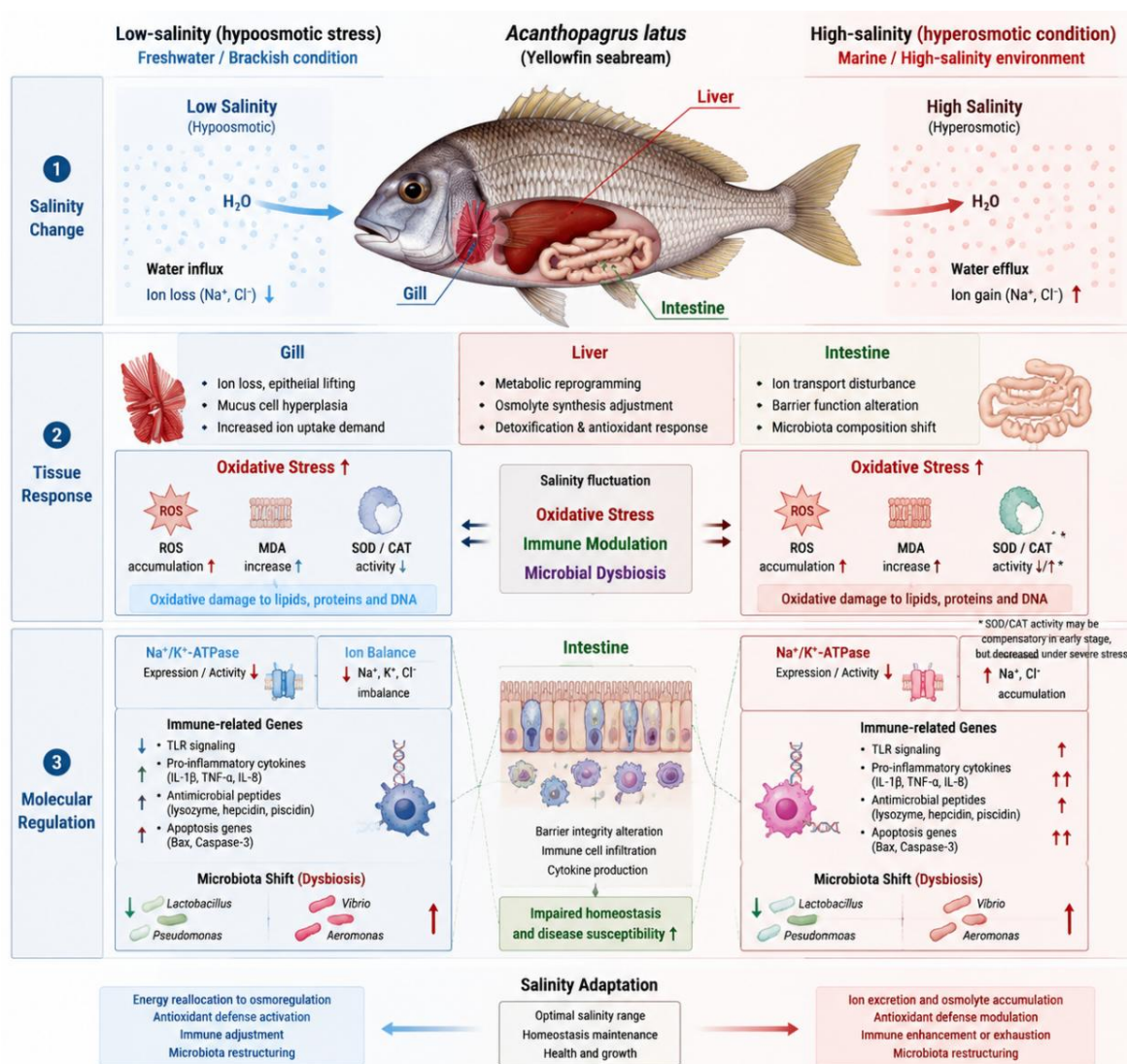


Figure 2 Mechanistic overview of salinity-induced oxidative stress, immune modulation, and microbiota alteration in yellowfin seabream

5 Molecular Regulatory Mechanisms of Salinity-Induced Health Responses in Yellowfin Seabream

5.1 Expression responses of osmoregulation-related genes

In yellowfin seabream, salinity-induced health responses begin with rapid remodeling of osmoregulatory gene expression in key epithelial tissues. Under hypoosmotic challenge, transcriptomic analysis showed that genes related to osmoregulation were strongly altered across gill, liver, and muscle, with the gill being the most sensitive tissue and showing enhanced Na^+/K^+ -ATPase activity to reduce ion loss. More broadly across euryhaline fishes, salinity acclimation consistently involves ion-transport and water-channel genes, and transcriptomic studies repeatedly identify transporters, osmoregulatory effectors, and stress-response genes as core components of adaptation (Mkulo et al., 2025). This general pattern is directly relevant to *Acanthopagrus latus*, because health maintenance under changing salinity depends on preserving hydromineral balance before secondary oxidative or immune damage develops.

Evidence from related euryhaline fishes helps clarify which genes are likely central to this regulation. In hybrid tilapia gills, salinity stress differentially regulated canonical osmoregulatory genes including CA, AQP1, SLC4A4/NBC1, CLCN2, and SLC12A2/NKCC1, indicating that ion exchange, bicarbonate transport, and water permeability are coordinated at the transcriptional level. In black porgy, another *Acanthopagrus* species, acute salinity transfer increased gill NKA transcripts under both freshwater and seawater challenge, while prolactin receptor expression rose specifically during freshwater adaptation, showing that branchial ion transport is tightly linked to endocrine signaling. Dynamic salinity regimes also appear to rely on especially labile *cfr* and *aqp3* regulation, as shown in tidally reared Mozambique tilapia, suggesting that fluctuating estuarine conditions may favor flexible local transcript control rather than fixed expression states (Seale, 2022).

5.2 Energy metabolism and stress response mechanisms

Salinity adaptation in yellowfin seabream is not only an ion-regulatory process but also an energy-allocation problem, because osmoregulation requires sustained metabolic support. Comparative work in teleosts shows that salinity stress consistently reorganizes metabolites linked to energy production and osmolyte synthesis, indicating that metabolic reprogramming is a basic requirement for osmotic compensation (Mkulo et al., 2025). In yellowfin seabream, hypoosmotic stress caused the liver to experience the strongest oxidative disturbance among examined tissues, with changes in SOD, CAT, and MDA indicating that the metabolic cost of acclimation is closely tied to redox imbalance. This means that salinity-induced health effects are shaped not only by whether fish can regulate ions, but by whether they can supply ATP and limit oxidative damage during that regulation.

Transcriptomic studies in other fishes provide a mechanistic framework for these changes. In spotted sea bass liver, salinity-responsive genes clustered in categories including energy metabolism, ion transport, signal transduction, immune response, and structural reorganization, and the liver was identified as a major source of carbohydrate metabolites for osmoregulatory organs. In spotted seabass exposed to salinity gradients, Na^+/K^+ -ATPase and MDA both rose and then fell over time, while most differentially expressed genes were enriched in energy metabolism, osmoregulation, signal transduction, and immune response, indicating a coordinated time-dependent stress program rather than a single static response (Hu et al., 2024). More detailed multi-omics work in *Pseudobagrus ussuriensis* further showed enrichment of glycolysis, oxidative phosphorylation, HIF-1, TNF, and Jak-STAT pathways under salinity stress, supporting the idea that metabolic reprogramming and stress signaling jointly determine whether acclimation remains adaptive or progresses toward injury (Liu et al., 2025).

5.3 Immune regulation and changes in disease susceptibility

Salinity variation also reshapes immune regulation in yellowfin seabream, and current evidence suggests that this is a central part of its health response rather than a secondary by-product. Under hypoosmotic stress, transcriptomic analysis showed that immune-related differentially expressed genes were widespread across tissues and that T cell-mediated immunity pathways were important in the response of *A. latus*. Intestinal analysis under freshwater exposure likewise revealed differential expression of genes involved in pathogen recognition, antimicrobial function, pro-inflammatory cytokines, apoptosis, and antioxidant defense, indicating that reduced salinity can simultaneously alter barrier defense and inflammatory signaling (Su et al., 2020). These results suggest that salinity stress changes how yellowfin seabream allocates resources between osmoregulation and host defense, which can influence disease vulnerability.

Changes in disease susceptibility are also likely mediated through microbiota and immune trade-offs. In yellowfin seabream intestine, brackish water favored *Lactobacillus* and *Pseudomonas*, whereas freshwater increased potentially pathogenic *Vibrio* and *Aeromonas*, implying that low salinity can shift the microbial environment toward higher infection risk. Comparative studies support this interpretation: in black-chinned tilapia from hypersaline habitats, genes linked to the immune system and heat-shock response were strongly downregulated, suggesting an energetic trade-off between acclimation and immune protection (Blondeau-Bidet et al., 2024). Similar links between low-salinity adaptation, energy metabolism, and disease resistance were observed in *Litopenaeus vannamei*, where the low-salt-tolerant family showed stronger immunity and higher resistance to *Vibrio parahaemolyticus*, supported

by enrichment of energy-metabolism and immune-regulation pathways. Overall, salinity-induced health responses in yellowfin seabream are regulated through three interacting molecular layers: osmoregulatory gene expression, metabolic and oxidative stress control, and immune-microbial regulation. The evidence indicates that health outcomes depend less on salinity tolerance in the narrow survival sense than on how effectively these regulatory systems remain coordinated under fluctuating environmental conditions.

6 Case Studies of Yellowfin Seabream Culture under Different Salinity Conditions

6.1 Case background: effects of salinity gradients on culture performance of yellowfin seabream

Case studies of yellowfin seabream culture under different salinity conditions consistently show that this species is broadly euryhaline, but culture performance varies markedly within that tolerance range. In a 56-day salinity-gradient trial, juveniles reared at 6‰, 12‰, 24‰, 35‰, and 48‰ showed improved growth when salinity increased from 6‰ to 12‰, whereas salinity above 24‰ suppressed growth, indicating that moderate brackish conditions were more favorable than full-strength or hypersaline seawater (Mozanzadeh et al., 2021). A separate acclimation study using 0.5, 3, 7, 15, 23, and 30 g/L reached a similar conclusion, with the highest growth rate and best feed conversion observed at 7 and 15 g/L and poorer performance at 23 and 30 g/L. Together, these studies provide a practical culture background for yellowfin seabream: the species survives over a wide salinity span, but production efficiency peaks within an intermediate salinity window rather than at salinity extremes.

This case background is strengthened by evidence that yellowfin seabream can withstand acute transfer across large salinity ranges, which helps explain its culture potential in estuarine and variable coastal systems. Juveniles transferred from 20 ppt to 34, 12, and 5 ppt acclimated within 48 h, and the main short-term changes were metabolic rather than ionic, showing that salinity stress was rapidly buffered at the whole-animal level. More generally, euryhaline fish maintain homeostasis under changing salinity through coordinated responses of the gill, intestine, and kidney, but rapid shifts beyond the optimal range still cause physiological stress even when survival is maintained (Mkulo et al., 2025). This means that field and farm salinity gradients should be evaluated not only by whether fish remain alive, but by whether salinity stays within the narrower range that supports efficient growth and stable health.

6.2 Case analysis: responses of growth performance and health status

The main growth-response pattern across case studies is that intermediate salinity improves production traits, whereas higher salinity reduces weight gain and feed efficiency. In juvenile yellowfin seabream, growth depression above 24‰ was accompanied by reduced feed utilization, showing that poorer performance at elevated salinity reflects both slower growth and weaker conversion of feed into biomass (Mozanzadeh et al., 2021). Another culture study found that fish reared at 23 and 30 g/L had lower body protein, fat, and moisture together with higher ash content than fish reared at lower salinity, indicating that salinity effects extend beyond growth rate to carcass composition and nutrient deposition. These findings show that salinity gradients shape not only how fast yellowfin seabream grows, but also how efficiently it uses feed and how body tissues are formed during culture.

Health responses in these case studies are similarly salinity-dependent and often precede visible mortality. Acute challenge experiments showed that cortisol, glucose, and lactate rose shortly after transfer and then returned toward basal levels within 24-48 h, indicating a transient but real physiological stress cost during acclimation. Longer-term salinity comparison in juvenile yellowfin seabream further showed that 10 ppt and 30 ppt conditions produced distinct gut microbial and transcriptomic states: brackish water enriched *Cetobacterium* and metabolism-related genes, whereas seawater enriched *Vibrio* and immune/redox pathways (Peng et al., 2025). In case-analysis terms, this suggests that a salinity regime can appear acceptable from a survival perspective while still shifting the fish toward higher immune activation and a less favorable intestinal microbial profile.

6.3 Case implications: optimal salinity regulation and aquaculture management strategies

The main management implication from these case studies is that yellowfin seabream culture should target a moderate brackish salinity range, especially during juvenile grow-out. Across direct growth trials, the best performance clustered around 7-15 g/L or near 12‰, while higher salinity consistently reduced growth or feed

conversion. This pattern aligns with broader aquaculture evidence that the most favorable salinity is often near the point where osmoregulatory costs are minimized and growth can receive a larger share of the energy budget (Mkulo et al., 2025). In practice, salinity regulation for yellowfin seabream should therefore be treated as a production lever rather than only a water-quality constraint.

A second implication is that salinity management should be integrated with acclimation strategy, nutrition, and life stage. Rapid changes caused by rainfall, estuarine mixing, or water exchange can trigger cellular stress responses involving energy reallocation and macromolecular protection, so gradual transfer remains important even in euryhaline species. Nutritional support can also modify tolerance: in black seabream, low-salinity performance improved when dietary cholesterol supported osmoregulation and reduced oxidative and inflammatory stress, while in yellowfin seabream other dietary additives have improved growth and haemato-immunological status under culture conditions. Overall, the case evidence indicates that optimal yellowfin seabream aquaculture depends on keeping salinity within a favorable intermediate range, avoiding abrupt fluctuations, and combining environmental control with nutritional strategies that stabilize health under osmotic challenge.

7 Environmental Regulation Strategies for Yellowfin Seabream Aquaculture under Salinity Variation

7.1 Salinity monitoring and dynamic regulation technologies

Effective salinity regulation in yellowfin seabream aquaculture depends first on continuous monitoring rather than periodic manual measurement. IoT-based pond systems can now track salinity in real time, issue threshold alarms, and support rapid corrective action, which reduces the likelihood that fish experience prolonged osmotic stress (Gulifardo et al., 2025). In automated pond-control trials, fuzzy logic systems maintained salinity within target ranges by activating freshwater pumps as salinity approached upper thresholds, thereby avoiding major deviations that would otherwise stress cultured animals. This type of dynamic control is especially relevant for euryhaline fish raised in estuarine or coastal systems where rainfall, evaporation, and tidal exchange can shift salinity over short time scales (Figure 3).

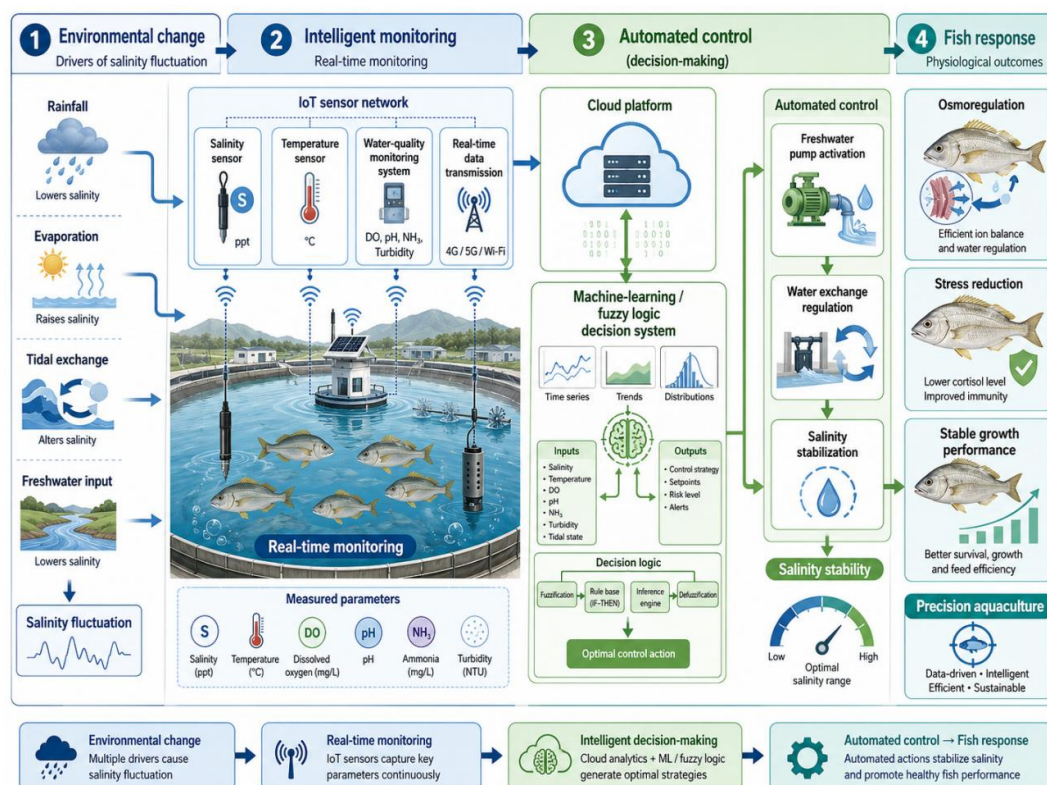


Figure 3 Environmental change-intelligent monitoring-automated control-fish response framework for salinity regulation in yellowfin seabream (*Acanthopagrus latus*) aquaculture systems

Dynamic regulation should also minimize the amplitude and rate of salinity change, because rapid shifts can impose physiological costs even in tolerant species. Machine-learning and sensor-integrated water-quality platforms now allow abnormal trends to be detected early and can automate interventions before water conditions become harmful. Pilot smart-aquaculture systems have shown that digital salinity controllers can stabilize estuarine ponds and accurately track real-time salinity shifts, supporting their use as practical management tools in variable environments (Prasetia et al., 2025). For yellowfin seabream, this means salinity management should aim not only to stay within a safe range, but also to maintain a stable trajectory that avoids repeated acute acclimation events.

7.2 Nutritional enhancement and health management strategies

Nutritional enhancement is a practical way to improve yellowfin seabream resilience when salinity cannot be held perfectly stable. Broad aquaculture evidence shows that dietary interventions can strengthen immunocompetence and stress resistance under environmental challenge, and that nutrient requirements often increase under stressful conditions. Functional nutrition is especially relevant under salinity fluctuation because vitamins, minerals, and amino acids influence mucosal integrity, antioxidant defense, cytokine activity, and immune-cell development, all of which are involved in salinity-linked health outcomes (Kari, 2025). These mechanisms are consistent with yellowfin seabream evidence showing that salinity shifts alter gut microbiota and activate either metabolic or immune-redox pathways depending on the rearing salinity.

More specific dietary strategies from related euryhaline fishes suggest how feeds could be optimized for yellowfin seabream culture. In black seabream, dietary cholesterol under low salinity improved ion reabsorption and osmoregulatory gene expression while reducing oxidative and inflammatory stress, indicating that membrane-related nutrients can directly support acclimation (Bao et al., 2022). In other salinity-stressed fishes, supplements such as myo-inositol and glutamine improved growth, antioxidant capacity, and ion-transport regulation, while selenium nanoparticles enhanced survival and immune performance during low-salinity stress and bacterial challenge. Therefore, health management in yellowfin seabream should combine salinity control with functional feeds targeted at osmoregulation, oxidative balance, and disease resistance rather than relying on environmental adjustment alone (Dildar et al., 2025).

7.3 Ecological aquaculture models and environmental adaptation strategies

Ecological aquaculture strategies under salinity variation should prioritize systems that match the natural adaptive capacity of yellowfin seabream. Because euryhaline species are inherently more suitable for variable-salinity production environments, they provide farmers with greater operational flexibility under climate-driven salinity instability. Recent work in juvenile yellowfin seabream also suggests that brackish-water culture can be advantageous, as 10 ppt conditions favored *Cetobacterium* enrichment and metabolic gene expression, whereas seawater conditions were associated with *Vibrio* enrichment and stronger immune-redox activation (Peng et al., 2025). This supports ecological models that use moderate brackish water as the baseline grow-out environment wherever local hydrology permits.

At the farm scale, environmental adaptation strategies should combine species selection, system diversification, and resilient infrastructure. Reviews of aquaculture under global change argue that cultivating euryhaline or native salinity-tolerant species is a key pathway for maintaining productivity in salinity-affected coastal and inland regions. More generally, farming euryhaline fish has been proposed as a climate-resilience strategy because these species can be reared successfully across different salinities without major loss of basic production capacity (Cusimano et al., 2025). For yellowfin seabream, an ecological aquaculture model should therefore integrate moderate-salinity water sourcing, real-time monitoring, gradual water exchange, and locally adapted production design so that environmental variability is buffered rather than simply endured. In yellowfin seabream aquaculture, the most effective environmental regulation strategy is to link real-time salinity control with targeted nutritional support and brackish-adapted ecological system design. This integrated approach is more consistent with the evidence than treating salinity, feeding, and health management as separate problems.

8 Future Research Directions and Perspectives

8.1 Applications of multi-omics technologies in salinity adaptation research

A key priority is to apply multi-omics technologies directly to yellowfin seabream tissues that mediate osmotic and health responses, especially gill, intestine, liver, and kidney. Recent omics-based reviews show that transcriptomics has already identified core ion transport, osmoregulation, and stress-response genes, while metabolomics has clarified shifts in energy production and osmolyte synthesis during salinity challenge (Mkulo et al., 2025). Multi-omics is especially valuable because it can connect these molecular changes to health-relevant outcomes such as antioxidant disruption, immune activation, and tissue injury, which single-layer datasets often cannot resolve. For yellowfin seabream, the next step is to build species-specific salinity-response atlases across organs, developmental stages, and exposure durations.

Future omics work should also become more granular and predictive. Metabolomics reviews now emphasize the value of LC-MS, GC-MS, NMR, spatial metabolomics, and machine-learning integration for identifying conserved osmotic-response patterns across fish species (Chen et al., 2026). Proteomic and metabolomic studies further show that salinity stress reorganizes pathways related to ion transport, energy synthesis, immunity, apoptosis, and cell-cycle control, especially when stress becomes extreme rather than moderate. Accordingly, future yellowfin seabream studies should move toward time-series multi-omics, single-cell or tissue-resolved profiling, and cross-platform integration with phenotypes such as growth, survival, and gut microbial stability so that biomarkers become usable for both diagnosis and selection (Raza et al., 2025).

8.2 Risk assessment of salinity fluctuations under climate change

Future risk assessment should treat salinity fluctuation as a dynamic climate hazard rather than a static water-quality variable. Climate change is expected to alter aquaculture through sea-level rise, saltwater intrusion, flooding, precipitation shifts, warming, and dissolved oxygen decline, all of which can reshape salinity regimes and fish health simultaneously. Because stress responses depend not only on absolute salinity but also on exposure rate, duration, and interaction with other drivers, yellowfin seabream risk models should explicitly incorporate compound-stressor scenarios instead of evaluating salinity in isolation. This is particularly important in coastal pond and estuarine systems where short-term hydrological events can rapidly move culture water outside optimal ranges.

A second research need is to connect environmental forecasting with biological vulnerability and socioeconomic consequences. Regional studies already show that climate-driven aquatic salinization can reduce habitat suitability and disproportionately affect poor communities that depend on fisheries and aquaculture. However, local outcomes are not uniform: in some transition zones, farmers have responded to changing salinity patterns through water-use shifts and diversification into mixed rice-shrimp-prawn-fish systems, improving production and livelihood security (Bhowmik et al., 2023). For yellowfin seabream aquaculture, future work should therefore combine salinity monitoring, hydrological modeling, early-warning systems, and farm-level adaptation trials to identify where this species can provide climate resilience and where salinity variability will exceed safe production thresholds (Froehlich et al., 2018).

8.3 Selective breeding and genetic improvement for salinity tolerance in yellowfin seabream

Selective breeding for salinity tolerance in yellowfin seabream should be developed as a genetically informed, polygenic program rather than a search for single major genes. Work in tilapia shows that salinity tolerance is a complex trait, but GWAS can still identify useful loci, including missense variants associated with more than twofold longer survival under high-salinity challenge (Huang et al., 2024). Reviews of aquaculture genomics also show that marker-assisted selection is helpful when robust QTL are available, whereas genomic selection is better suited to traits controlled by many loci of small effect. For yellowfin seabream, this means future breeding should combine accurate salinity phenotyping with dense genomic markers and validation across families, life stages, and farming environments.

The most promising long-term strategy is to integrate genome resources, selection models, and functional biology. In salinity-tolerant tilapia, genome improvement, QTL mapping, GWAS, and candidate-gene polymorphism

analysis are viewed as essential steps for accelerating molecular breeding (Yue et al., 2023). New genomic-selection work in spotted sea bass further shows that combining marker types can substantially improve prediction accuracy for tolerance traits, reaching an accuracy of 0.71 in the best-performing integrated model (Zhang et al., 2025). Yellowfin seabream breeding programs should therefore prioritize reference-genome quality, high-throughput salinity challenge phenotyping, and genomic prediction pipelines that can be updated with omics-derived biomarkers of osmoregulation and stress resilience, while also preserving growth and health traits needed for commercial culture. Overall, future research on yellowfin seabream should connect pan-omics biology, climate-resilient risk assessment, and genomic breeding into one framework. That integrated approach is the clearest path to defining optimal salinity management and improving health and productivity under increasingly variable culture conditions.

9 Conclusions

Salinity variation is one of the most important environmental factors influencing the growth performance of yellowfin seabream. As a euryhaline marine fish, this species has a certain capacity to tolerate a relatively wide salinity range, but its growth response is not uniform under all conditions. When salinity remains within an appropriate physiological range, yellowfin seabream can maintain stable feeding activity, efficient nutrient assimilation, and normal metabolic function, thereby supporting satisfactory growth rate and body weight gain. In contrast, exposure to excessively low, high, or rapidly fluctuating salinity often increases the energetic cost of osmoregulation, causing more metabolic resources to be diverted from somatic growth toward physiological adjustment and survival maintenance. Overall, the growth performance of yellowfin seabream tends to depend not only on the absolute salinity level but also on the duration, amplitude, and frequency of salinity change. Moderate and relatively stable salinity conditions are generally more favorable for feed utilization efficiency, protein deposition, and body composition balance, whereas persistent salinity stress can suppress appetite, reduce feed conversion efficiency, and impair normal growth trajectories. Therefore, salinity should be recognized as a central regulator of production performance in yellowfin seabream aquaculture, and growth optimization requires maintaining environmental salinity within a biologically suitable and dynamically manageable range.

Beyond growth, salinity variation has comprehensive effects on the physiological health of yellowfin seabream. Changes in salinity can alter hematological characteristics, ionic balance, endocrine responses, antioxidant capacity, and immune status, reflecting the broad systemic nature of salinity adaptation. Under manageable salinity conditions, yellowfin seabream can activate osmoregulatory and metabolic adjustment mechanisms that help preserve internal homeostasis. However, when salinity stress exceeds the adaptive threshold of the fish, disturbances begin to appear in blood biochemical indicators, oxidative stress regulation, tissue integrity, and cellular function, indicating that health impairment often accompanies environmental instability. The health consequences of salinity stress are also closely linked to the intensity and duration of exposure. Short-term salinity shifts may trigger compensatory responses that are initially protective, but long-term or repeated stress can weaken antioxidant defenses, increase susceptibility to inflammation or infection, and damage key organs such as the gills, liver, kidney, and intestine. At the molecular level, these outcomes are associated with changes in the expression of genes related to ion transport, energy metabolism, stress signaling, and immune regulation. Taken together, the available evidence indicates that salinity variation affects yellowfin seabream health through integrated physiological, biochemical, histological, and molecular pathways, making health assessment essential when evaluating the biological effects of salinity in culture systems.

From an aquaculture perspective, effective salinity management is essential for improving both productivity and animal welfare in yellowfin seabream farming. Maintaining salinity within an appropriate range, avoiding abrupt fluctuations, and adjusting culture conditions according to developmental stage and environmental context can help reduce physiological stress and support stable growth and health outcomes. In practice, salinity regulation should be combined with water quality monitoring, nutritional support, and health management strategies so that fish can better cope with environmental variation. This integrated approach is particularly important in coastal and estuarine farming areas, where rainfall, evaporation, tidal exchange, and freshwater input can cause pronounced salinity

instability. Future applications in yellowfin seabream aquaculture should move beyond simple salinity control toward more precise and adaptive management frameworks. The use of real-time monitoring technologies, automated environmental regulation systems, and data-driven culture models could improve the prediction and mitigation of salinity stress under commercial conditions. At the same time, selective breeding for salinity tolerance, together with molecular and multi-omics research on adaptive mechanisms, may provide new opportunities to develop more resilient stocks. In the context of climate change and increasing environmental variability, advancing salinity management from passive response to proactive regulation will be a key direction for sustainable yellowfin seabream aquaculture.

Acknowledgments

We extend our sincere gratitude to the anonymous reviewers for their valuable and insightful comments, which have greatly strengthened this paper.

Conflict of Interest Disclosure

The authors affirm that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

References

- Ahmed H., Bakry K.A., Abdeen A., El bahgy H.E.K., Abdo M., Imbrea F., Fericean L., Elshemy M.A., Ibrahim S.F., Shukry M., Baloza S.H., and Emeish W.F.A., 2023, The involvement of antioxidant, stress, and immune-related genes in the responsive mechanisms of common carp (*Cyprinus carpio*) to hypersalinity exposure, *Frontiers in Marine Science*, 10: 1195016.
<https://doi.org/10.3389/fmars.2023.1195016>
- AlKatrani L., 2022, A preliminary study on the effects of different salinities on some hormones level in serum of yellow fin seabream *Acanthopagrus latus* fingerlings, *Mesopotamian Journal of Marine Sciences*, 31: 109-118.
<https://doi.org/10.58629/mjms.v3i2.96>
- Bao Y., Shen Y., Li X., Wu Z., Jiao L., Li J., Zhou Q.C., and Jin M., 2022, A new insight into the underlying adaptive strategies of euryhaline marine fish to low salinity environment: through cholesterol nutrition to regulate physiological responses, *Frontiers in Nutrition*, 9: 855369.
<https://doi.org/10.3389/fnut.2022.855369>
- Bhowmik B.C., Rima N.N., Gosh K., Hossain M., Murray F., Little D., and Mamun A.A., 2023, Salinity extrusion and resilience of coastal aquaculture to the climatic changes in the southwest region of Bangladesh, *Heliyon*, 9(3): e13935.
<https://doi.org/10.1016/j.heliyon.2023.e13935>
- Blondeau-Bidet E., Tine M., Gonzalez A.A., Guinand B., and Lorin-Nebel C., 2024, Coping with salinity extremes: gill transcriptome profiling in the black-chinned tilapia (*Sarotherodon melanocheilus*), *The Science of the Total Environment*, 929: 172620.
<https://doi.org/10.1016/j.scitotenv.2024.172620>
- Chen X., Tang Y., Du X., Giffard-Mena I., and Cao Q., 2026, Metabolomic insights into fish osmoregulation: Unveiling adaptive mechanisms to salinity change, *Comparative Biochemistry and Physiology Part D: Genomics and Proteomics*, 2026: 101742.
<https://doi.org/10.1016/j.cbd.2025.101742>
- Cusimano G., Cueto P.S., Lladó S., Paolacci S., Chiang J.C., Panasiak N.E., Ghemis R., Bosch M., Parras-Moltó M., Kleinegris D., Nagel F., Deguara S., Robinson F., and Bardóc T., 2025, Effect of water salinity and dietary supplementation with *Microchloropsis gaditana* on growth, health, quality and microbiota of Barramundi *Lates calcarifer*, *Open Research Europe*, 5: 58.
<https://doi.org/10.12688/openreseurope.18715.1>
- Dildar T., Cui W., Ikhwanuddin M., and H., 2025, Aquatic organisms in response to salinity stress: ecological impacts, adaptive mechanisms, and resilience strategies, *Biology*, 14(6): 667.
<https://doi.org/10.3390/biology14060667>
- Evans T.G., and Kültz D., 2020, The cellular stress response in fish exposed to salinity fluctuations, *Journal of Experimental Zoology Part A: Ecological and Integrative Physiology*, 333(6): 421-435.
<https://doi.org/10.1002/jez.2350>
- Gulifardo A.B.E., Balane B.J.D., Ebor M.T., Serrano M.R., Ellazar E.P., Nicolas A.V., and Maaño R.C., 2025, iPond: an internet of things-based water quality monitoring system for fishpond, *IOP Conference Series: Earth and Environmental Science*, 1446(1): 012005.
<https://doi.org/10.1088/1755-1315/1446/1/012005>
- Hassan H., Ali Q., Ahmed A.E., Gabol K., Swelum A., Masood Z., Mushtaq S., S. S., Gul Y., Rizwan S., Zulfiqar T., and Siddique M.A., 2022, Growth performance and survivability of the Asian seabass *Lates calcarifer* (Bloch, 1790) reared under hyper-saline, hypo-saline and freshwater environments in a closed aquaculture system, *Brazilian Journal of Biology*, 84: e254161.
<https://doi.org/10.1590/1519-6984.254161>

- Huang D., Qin H., Zhu Z., Liang X., and Xia J.H., 2024, Genome-wide association studies in a F1 tilapia population reveal novel genetic loci associated with salinity tolerance, *Aquaculture*, 588: 740913.
<https://doi.org/10.1016/j.aquaculture.2024.740913>
- Kari A.Z., 2025, Nutritional immunomodulation in aquaculture: functional nutrients, stress resilience, and sustainable health strategies, *Aquaculture International*, 33(6): 441.
<https://doi.org/10.1007/s10499-025-02122-5>
- Lin G., Zheng M., Gao D., Li S., Fang W., Huang J., Xie J., Liu J., Liu Y., Li Z., and Lu J., 2020, Hypoosmotic stress induced tissue-specific immune responses of yellowfin seabream (*Acanthopagrus latus*) revealed by transcriptomic analysis, *Fish and Shellfish Immunology*, 99: 285-294.
<https://doi.org/10.1016/j.fsi.2020.02.028>
- Liu Y., Gu L., Zhao J., Liu M., Wang K., Zhou Q., Cao Y., Hu R., Wang W., and Liu Q., 2025, Comprehensive multi-omics and biochemical analysis to elucidate the molecular response mechanisms of gill and kidney tissues under acute salinity stress in *Pseudobagrus ussuriensis*, *BMC Genomics*, 26(1): 590.
<https://doi.org/10.1186/s12864-025-11773-w>
- Lu J., Gao D., Sims Y., Fang W., Collins J., Torrance J., Lin G., Xie J., Liu J., and Howe K., 2022, Chromosome-level genome assembly of *Acanthopagrus latus* provides insights into salinity stress adaptation of Sparidae, *Marine Biotechnology*, 24: 655-660.
<https://doi.org/10.1007/s10126-022-10119-x>
- Mkulo E. M., Iddrisu L., Yohana M. A., Zheng A., Zhong J., Jin M., Danso F., Wang L., Zhang H., Tang B., Zhou H., Amoah K., Huang J., Wang B., and Wang Z., 2025, Exploring salinity adaptation in teleost fish, focusing on omics perspectives on osmoregulation and gut microbiota, *Frontiers in Marine Science*, 12: 1559871.
<https://doi.org/10.3389/fmars.2025.1559871>
- Mozanzadeh M. T., Safari O., Oosooli R., Mehrjooyan S., Najafabadi M., Hoseini S., Saghabi H., and Monem J., 2021, The effect of salinity on growth performance, digestive and antioxidant enzymes, humoral immunity and stress indices in two euryhaline fish species: Yellowfin seabream (*Acanthopagrus latus*) and Asian seabass (*Lates calcarifer*), *Aquaculture*, 534: 736329.
<https://doi.org/10.1016/j.aquaculture.2020.736329>
- Okomoda V. T., Isah S. Y., Solomon S. G., and Ikhwanuddin M., 2024, Salinity tolerance in *Clarias gariepinus* (Burchell, 1822): insight on blood parameter variations and gill histological changes, *Fish Physiology and Biochemistry*, 50(2): 605-616.
<https://doi.org/10.1007/s10695-023-01293-3>
- Peng C., Xue H., Zhang J., Zhang J., Dai J., Zhang Y., and Hu S., 2025, Salinity modulates gut microbiota and host transcriptome dynamics in juvenile euryhaline fish yellowfin seabream (*Acanthopagrus latus*), *Aquaculture Reports*, 44: 103075.
<https://doi.org/10.1016/j.aqrep.2025.103075>
- Praselia A., Salim G., Sartika L., Mujiyanto M., Ransangan J., Jose A. S. E., Hartinah S., and Hartati R., 2025, Smart automation of salinity and turbidity for sustainable aquaculture of *Harodon nehereus*, *Jurnal Ilmiah Perikanan dan Kelautan*, 18(1): 80.
<https://doi.org/10.20473/jipk.v18i1.78793>
- Raza A., Zaman Q. U., Shabala S., Tester M., Munns R., Hu Z., and Varshney R. K., 2025, Genomics-assisted breeding for designing salinity-smart future crops, *Plant Biotechnology Journal*, 23(8): 3119-3151.
<https://doi.org/10.1111/pbi.70104>
- Seale A., 2022, Endocrine and osmotic responses to tidally-changing salinities in Mozambique tilapia, *Oreochromis mossambicus*, *The FASEB Journal*, 36(S1): R3248.
<https://doi.org/10.1096/fasebj.2022.36.s1.r3248>
- Seale A., Cao K., Chang R.J.A., Goodearly T.R., Malintha G., Merlo R.S., Peterson T.L., and Reighard J.R., 2024, Salinity tolerance of fishes: experimental approaches and implications for aquaculture production, *Reviews in Aquaculture*, 16(3): 1351-1373.
<https://doi.org/10.1111/raq.12900>
- Su H., Fan J., Zhong Z., Tian Y., and Zhu H., 2025, A TMT-based proteomic analysis of osmoregulation in the gills of *Oreochromis mossambicus* exposed to three osmotic stresses, *International Journal of Molecular Sciences*, 26(6): 2791.
<https://doi.org/10.3390/ijms26062791>
- Su H., Zhu H., Liu Z., and Gao F., 2020, Transcriptomic response to three osmotic stresses in gills of hybrid tilapia (*Oreochromis mossambicus* female $\times$ *O. urolepis hornorum* male), *BMC Genomics*, 21(1): 110.
<https://doi.org/10.1186/s12864-020-6512-5>
- Tang G.-D., He Z., Liu Y., Xiao Y., Bi S., Sun Y., Liang J., Wu P., Wang T., Ye J., and Li C.-H., 2023, *Acanthopagrus latus* migration patterns and habitat use in Wanshan Islands, Pearl River Estuary, determined using otolith microchemical analysis, *Frontiers in Marine Science*, 10: 1104528.
<https://doi.org/10.3389/fmars.2023.1104528>
- Yue G., K. and Xia J., 2023, Status of conventional and molecular breeding of salinity-tolerant tilapia, *Reviews in Aquaculture*, 16(1): 271-286.
<https://doi.org/10.1111/raq.12838>
- Zhang Y., Zhang C., Liu C., Wen H., Qi X., Zhang K., Wang H., Cui K., Wang L., Sun D., and Li Y., 2025, Deciphering the optimal genomic selection (GS) strategy of alkalinity tolerance trait in spotted sea bass (*Lateolabrax maculatus*), *Genomics*, 2025: 111190.
<https://doi.org/10.1016/j.ygeno.2025.111190>

- Zhao Y.-B., Liu L., Huang Z., and Li Z.-B., 2025, Adaptation of the yellowfin seabream (*Acanthopagrus latus*) in the southeast coast of China to four environmental factors based on SNP loci analysis, *Acta Hydrobiologica Sinica*, 50(1): 1-10.
<https://doi.org/10.3724/1000-3207.2025.2025.0206>
- Zhou K., Chen Z., Qin J., Huang Y., Du X., Zhang C., Pan X., and Lin Y., 2024, Effects of salinity on muscle nutrition, fatty acid composition, and substance anabolic metabolism of blue tilapia *Oreochromis aureus*, *Journal of Applied Ichthyology*, 2024(1): 5549406.
<https://doi.org/10.1155/2024/5549406>



Disclaimer/Publisher's Image caption

The statements, opinions, and data contained in all publications are solely those of the individual authors and contributors and do not represent the views of the publishing house and/or its editors. The publisher and/or its editors disclaim all responsibility for any harm or damage to persons or property that may result from the application of ideas, methods, instructions, or products discussed in the content. Publisher remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.