

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.