

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