

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.