

reveal genetic structure differences among geographic populations, between wild and cultured populations, and between parents and offspring (Figure 1) (Vaini et al., 2021; Yang et al., 2022).

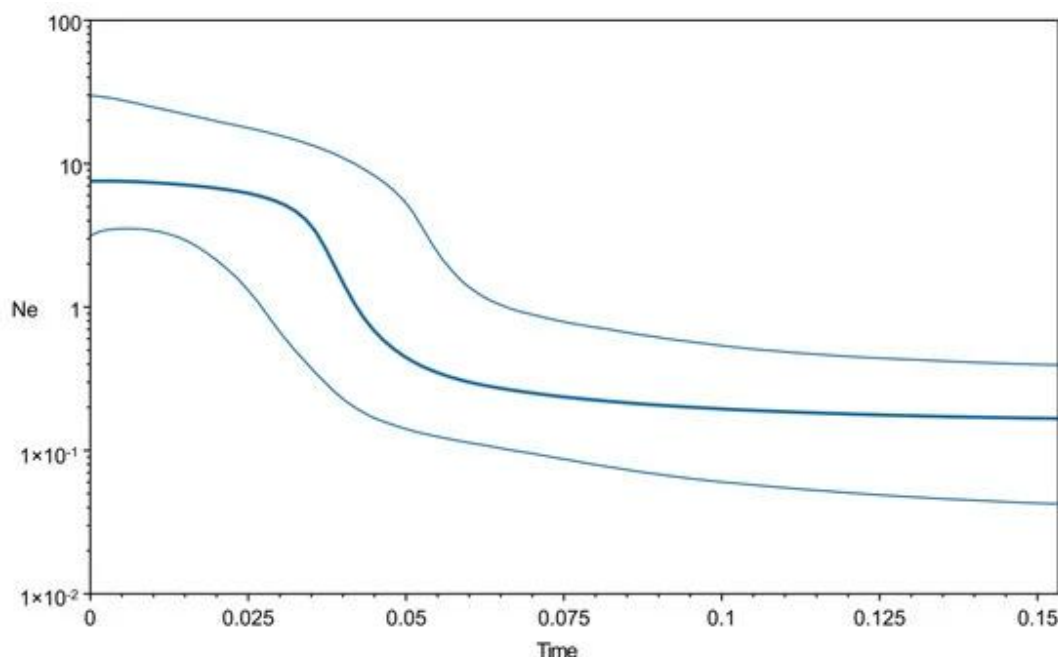


Figure 1 Bayesian skyline plot of the effective population sizes through time for *Epinephelus awoara* (Adopted from Yang et al., 2022)

Image caption: The y-axis is the product of effective population size ( $N_e$ ) and generation length in a log scale while the x-axis is the time scale before present in units of million years ago (Adopted from Yang et al., 2022)

### 3.2 Population genetic structure and evolutionary mechanisms

Population genetic structure refers to the distribution patterns of genotypes and allele frequencies within and among populations and is a key aspect of genetic diversity research. In groupers, varying degrees of genetic differentiation may exist among geographic populations, among cultured populations from different hatcheries, and even among different families within the same farming system. Such differentiation can be quantified and visualized using methods such as  $F_{ST}$ , genetic distance, analysis of molecular variance (AMOVA), PCA, and clustering analysis, thereby revealing phylogenetic relationships, levels of gene flow, and potential boundaries of genetic units (Vaini et al., 2021; Yang et al., 2022). Therefore, population genetic structure analysis is not only fundamental for understanding patterns of population differentiation but also provides an important basis for germplasm conservation, broodstock management, and breeding utilization.

From the perspective of natural populations, the genetic structure of groupers results from the combined effects of gene flow, genetic drift, natural selection, and historical population dynamics. Traditional views suggest that marine fishes, due to their pelagic larval stages, should exhibit high connectivity and genetic homogeneity. However, extensive empirical studies have demonstrated that grouper populations are not completely randomly mixed. Studies on Nassau grouper, yellow grouper, orange-spotted grouper, and brown grouper indicate that their population structures are often influenced by straits, marginal seas, island barriers, ocean current systems, and dependence on specific spawning grounds, leading to significant regional differentiation (Vaini et al., 2021; Yang et al., 2022; Chen et al., 2025). In addition, Pleistocene glaciations, sea-level fluctuations, and repeated isolation-connection events in marginal seas have shaped the present-day genetic patterns of groupers over longer timescales. In other words, the observed population genetic structure reflects not only contemporary ecological processes but also the combined effects of historical geological events and modern ecological dynamics.

In aquaculture systems, anthropogenic factors play an even more significant role in shaping population genetic structure. Artificial breeding typically relies on a limited number of broodstock, and the effective population size