

economic traits can impose directional selection on specific genomic regions, thereby altering population structure. Although introducing new broodstock or hybrid breeding may partially increase genetic diversity, these practices may also blur the boundaries between wild and cultured populations and increase the risk of genetic contamination. Therefore, enhanced genetic monitoring and structural assessment are necessary.

6.3 Analysis of genetic bottlenecks and inbreeding effects

A genetic bottleneck refers to the loss of genetic diversity resulting from a sharp reduction in population size, while inbreeding effects arise under conditions of small population size or closed breeding systems. In grouper aquaculture, these issues are relatively common, particularly during artificial seed production and juvenile propagation (Hsu et al., 2023). Without effective management, genetic bottlenecks and inbreeding can reduce population adaptability and breeding potential, negatively impacting industry development.

Under aquaculture conditions, genetic bottlenecks often occur during the initial stages of artificial breeding. When broodstock numbers are limited or derived from a single source, offspring inherit only a restricted portion of genetic variation, leading to rapid allele loss. Studies have shown that offspring populations of kelp grouper and tomato grouper exhibit bottleneck signals, closely associated with the contributions of a small number of broodstock (Hsu et al., 2023). Inbreeding effects manifest as an increased probability of homozygosity for deleterious recessive alleles, often resulting in reduced growth, lower survival rates, and decreased disease resistance in production systems.

It is noteworthy that genetic bottlenecks and inbreeding are not limited to cultured populations but are also observed in some wild populations. For example, yellow grouper shows high haplotype diversity but low nucleotide diversity, indicating historical population contraction (Yang et al., 2022), while brown grouper exhibits low effective population sizes globally (Vaini et al., 2021). To mitigate these issues, it is necessary to expand broodstock sources, optimize mating designs, and establish pedigree management systems, combined with molecular marker-based kinship analysis and population renewal strategies. Furthermore, strengthening habitat protection and resource management for wild populations is essential for maintaining the long-term genetic stability of grouper germplasm resources.

7 Existing Issues and Future Development Trends

7.1 Current limitations in research

Although significant progress has been made in recent years in grouper genetic diversity research—particularly in molecular marker development, population structure analysis, and germplasm evaluation—there are still notable limitations overall. First, in terms of sampling and study design, most research focuses on a limited number of economically important species or specific key aquaculture regions. Sample sizes are often relatively small and geographic coverage is insufficient, making it difficult to comprehensively reveal large-scale spatial genetic patterns and their temporal dynamics in grouper germplasm resources (Hassanien and Al-Rashada, 2020; Tavakoli-Kolour et al., 2022; Yang et al., 2022). This is particularly problematic for grouper species with strong connectivity across marine regions and complex historical population dynamics, where limited sampling may fail to accurately identify true genetic boundaries and evolutionary units.

In terms of methodology and analytical frameworks, there is a lack of standardization across studies regarding marker types, number of loci, and evaluation indices, resulting in limited comparability among findings. Some studies rely on a single marker system, such as mtDNA or a small number of SSR loci, which can provide preliminary insights but are insufficient for integrating multiple layers of information, including neutral variation, adaptive variation, and selection signals. This limitation reduces the ability to resolve fine-scale population structure and local adaptive differentiation (Hassanien and Al-Rashada, 2020; Saha et al., 2021; Tavakoli-Kolour et al., 2022). In addition, inconsistencies in statistical models, parameter settings, and quality control procedures further affect the robustness and reproducibility of results.