This pattern—"high variation in wild populations and gradual drift in cultured populations"—is consistent with general trends observed in multiple grouper studies, indicating that long-term artificial selection, limited broodstock usage, and patterns of germplasm exchange among hatcheries have significantly influenced the genetic structure of cultured populations (Chen et al., 2025). Without timely intervention, this trend may lead to further inbreeding accumulation, narrowing of the genetic base, and germplasm degradation, ultimately reducing production performance and future breeding potential.

Based on these findings, several measures should be implemented in aquaculture practice to protect and enhance genetic diversity. First, broodstock sources should be expanded by establishing base breeding populations from multiple genetically diverse and well-documented populations, while avoiding indiscriminate mixing of highly divergent management units to prevent disruption of local adaptation or new genetic instability (Yang et al., 2022). Second, standardized breeding management systems should be established, including pedigree recording, controlled reuse of broodstock, balanced family contributions, and rotational mating strategies to reduce inbreeding and maintain effective population size (Weng et al., 2021). In addition, molecular marker monitoring should be incorporated into routine germplasm management to continuously track key parameters such as allelic richness, He, FIS, and effective population size, and to detect genetic bottlenecks and germplasm degradation signals in a timely manner (Wenne, 2023).

Conservation of wild grouper resources is essential for maintaining overall germplasm quality. Studies have shown that although many wild populations still retain relatively high genetic diversity, some regional populations exhibit signs of historical contraction, low effective population size, and significant geographic differentiation (Vaini et al., 2021; Yang et al., 2022; Chen et al., 2025). Therefore, it is necessary to strengthen the protection of key spawning grounds, juvenile habitats, and locally unique populations, while restricting intensive fishing and habitat destruction. In stock enhancement programs, genetic data should be used to select appropriate source populations to avoid genetic homogenization or dilution of local genotypes in wild populations. Where feasible, long-term conservation strategies such as germplasm reserves, live conservation populations, cryopreserved sperm banks, and DNA repositories should be established to preserve important genetic resources. Ultimately, a dynamic management framework integrating "wild resource conservation—cultured germplasm optimization—genetic monitoring feedback—re-conservation" should be developed. Through this integrated cycle of conservation, utilization, and re-conservation, it is possible to maintain evolutionary potential and future breeding resources while ensuring production performance, thereby supporting the high-quality and sustainable development of the marine aquaculture industry (Hassanien and Al-Rashada, 2020; Weng et al., 2021).

5 Methods for Genetic Diversity Analysis in Groupers

5.1 Molecular marker technologies

Molecular marker technologies based on DNA variation are among the most widely used and informative approaches in grouper genetic diversity studies. Their core principle is to detect genetic variation in the nuclear or mitochondrial genome to reveal population genetic structure, diversity levels, kinship relationships, and germplasm origins (Hassanien and Al-Rashada, 2020). Compared with traditional phenotypic traits, molecular markers directly target genetic material and are less influenced by environmental factors, thus offering clear advantages in population identification, broodstock management, inbreeding monitoring, population differentiation analysis, and molecular breeding. Commonly used techniques include microsatellite markers (SSR), ISSR, single nucleotide polymorphisms (SNPs), and mitochondrial DNA markers. Each type differs in resolution, cost, and application scenarios, collectively forming the technical foundation for genetic diversity analysis in groupers.

Microsatellite markers (simple sequence repeats, SSR) are typical codominant markers characterized by high polymorphism, abundant information content, high resolution, and well-established protocols, and they have long been core tools in grouper population genetic studies (Hassanien and Al-Rashada, 2020). By analyzing allele number, frequency distribution, heterozygosity, and polymorphism information content at SSR loci, researchers