Beyond individual-level genotyping, the development of environmental DNA (eDNA) and metabarcoding technologies offers efficient and non-invasive approaches for wild resource surveys and population monitoring. Compared with traditional capture-based methods, eDNA can identify target species and haplotype information from DNA traces in water samples, making it particularly suitable for continuous monitoring in restoration areas, protected zones, and critical habitats of wild populations (Li, 2022; Ai et al., 2025). In terms of germplasm conservation, the establishment of standardized germplasm banks and high-throughput cryopreservation systems also holds great promise. By developing live conservation populations, cryopreserved sperm banks, DNA repositories, and integrated database platforms, it is possible to systematically preserve allelic diversity and provide long-term support for resource restoration, broodstock renewal, and breeding innovation (Li, 2022).

In the future, grouper genetic resource management will increasingly rely on bioinformatics, big data analytics, artificial intelligence-assisted phenotyping, and genome-based decision support systems. By integrating genomic, transcriptomic, phenotypic, and environmental data, researchers can more comprehensively elucidate the genetic mechanisms underlying important economic traits, thereby supporting molecular-assisted breeding and genomic selection (Yang et al., 2021; Wu et al., 2024). At the same time, the development of national or regional aquatic genetic resource information systems that integrate genetic monitoring, germplasm conservation, breeding records, and risk warning mechanisms is expected to significantly enhance the standardization and intelligence of germplasm management (Sonesson et al., 2023; Wenne, 2023). Overall, future grouper genetic diversity assessment will move toward "genome-wide analysis, dynamic monitoring, data platform integration, and intelligent management."

8 Conclusions and Recommendations

Studies on the genetic diversity of groupers indicate that most wild populations still maintain moderate to high levels of genetic variation, although significant differences exist among species and regions. For example, yellow grouper and brown grouper exhibit high haplotype or microsatellite diversity, while also showing clear population structure and, in some cases, historical declines in effective population size. These patterns are largely influenced by marine environmental barriers, hermaphroditic reproductive traits, and historical population fluctuations. Research on orange-spotted grouper and giant grouper consistently shows that cultured populations exhibit reduced allelic richness, lower heterozygosity, and significant genetic differentiation compared to wild populations, mainly due to founder effects, genetic drift, and artificial selection. Overall, in the aquaculture sector, the management of aquatic genetic resources (AqGR) has lagged behind production development. Many cultured populations lack systematic genetic evaluation, and genetic monitoring has not yet been routinely implemented. Meanwhile, rapid advances in molecular and genomic technologies—such as microsatellites, SNPs, reduced-representation sequencing, and whole-genome resequencing—have made it possible to assess genetic diversity, monitor inbreeding, and conduct molecular-assisted breeding even in non-model aquaculture species. Existing evidence suggests that cultured grouper germplasm is facing ongoing risks of genetic deterioration, but also has the potential for sustainable management through the application of advanced technologies.

The conservation of grouper germplasm resources should be based on systematic genetic evaluation, with genetic management incorporated into seed production systems. For major cultured species such as orange-spotted grouper and giant grouper, molecular markers (e.g., microsatellites or SNPs) should be regularly used at broodstock, seed, and grow-out stages to monitor allelic richness, heterozygosity, FST, and effective population size, with wild populations serving as references. Broodstock populations should be maintained at sufficiently large sizes with high genetic diversity and, where feasible, derived from multiple genetically compatible wild populations, while avoiding indiscriminate mixing of highly divergent management units to preserve local adaptation. In seed production, molecular marker-based parentage and kinship analyses should be applied to balance family contributions, reduce inbreeding, and prevent unintended domestication effects in stock enhancement programs. At the policy and management level, it is necessary to strengthen capacity for aquatic genetic resource management, promote cost-effective genotyping technologies, incorporate genetic risk assessment into species introduction and stock enhancement planning, and integrate these efforts with marine