Species misidentification and unclear sample origins remain significant issues. Groupers are highly diverse and morphologically similar, and samples from markets, fisheries, or hatcheries often involve mixed species or inconsistent naming. Without molecular-level species identification, genetic structure and diversity assessments may be based on incorrect taxonomic assumptions, leading to biased conclusions (Hassanien and Al-Rashada, 2020; Tavakoli-Kolour et al., 2022). Meanwhile, genetic monitoring of cultured populations lacks systematic and continuous implementation. Most studies are based on single-time sampling and static analyses, making it difficult to detect ongoing processes such as inbreeding accumulation, allele loss, and genetic drift in a timely manner (Sonesson et al., 2023; Ybanez and Gonzales, 2023). Overall, current research on grouper genetic diversity remains largely descriptive, with insufficient integration of dynamic processes, environmental drivers, and anthropogenic effects.

7.2 Challenges in germplasm conservation and utilization

Grouper germplasm conservation and utilization are currently facing dual pressures from the decline of wild resources and the rapid expansion of aquaculture. Declines in wild populations have become a major issue in many regions. In areas such as the South China Sea and the Persian Gulf, overfishing, habitat degradation, and marine environmental changes have led to reduced population sizes and habitat deterioration. Additionally, groupers generally have relatively slow growth rates, late sexual maturity, and, in some species, spawning aggregation behavior. These life-history traits increase their vulnerability to genetic diversity loss and resource depletion (Tavakoli-Kolour et al., 2022; Yang et al., 2022; Ai et al., 2025). The decline of wild populations not only weakens the stability of natural germplasm reservoirs but also limits access to valuable genetic resources and locally adapted genetic units.

Within aquaculture systems, germplasm management remains insufficiently standardized, and genetic risk management often lags behind breeding and industry expansion. Many cultured strains and hybrid combinations are developed primarily for growth performance, stress resistance, and economic returns, while systematic evaluations of their genetic background, long-term stability, and potential impacts on wild populations are still lacking (Yang et al., 2021; Yang et al., 2023; Wu et al., 2024). Particularly with the widespread use of hybrid groupers, the absence of germplasm purity identification, pedigree management, and risk warning systems may lead to disturbances in wild population genetic structures through introduction, stock enhancement, or escape. At the same time, stock enhancement programs lacking proper genetic planning may increase genetic homogenization due to limited source populations or mismatches with local wild populations.

From a management perspective, national-level systems, information platforms, and commercial frameworks for aquatic genetic resources (AqGR) remain relatively underdeveloped. Many regions lack clear regulations for the introduction of cultured species, the spread of exotic species, hybrid management, and genetic risk assessment, making it difficult to achieve a balance between utilization and conservation (Sonesson et al., 2023). Furthermore, ex situ conservation systems—such as germplasm banks, live conservation populations, and cryopreservation platforms—are still in early stages of development, facing challenges in scale, quality control, and integration into long-term conservation strategies (Li, 2022). Therefore, achieving efficient utilization while maintaining genetic diversity remains a key issue in both research and industry practice.

7.3 Prospects for emerging technologies in genetic diversity assessment

With the rapid advancement of biotechnology, sequencing technologies, and data science, new technologies offer unprecedented opportunities for grouper genetic diversity assessment and germplasm management. First, continuous improvements in whole-genome resequencing, chromosome-level genome assembly, and high-density SNP genotyping enable researchers to analyze genetic variation, selection signals, population structure, and quantitative trait loci (QTLs) at the genome-wide level, significantly enhancing the resolution and functional interpretation of genetic diversity assessments (Yang et al., 2021; Yang et al., 2023; Wu et al., 2024). Meanwhile, SNP genotyping platforms based on multiplex PCR capture or targeted enrichment provide cost-effective, high-throughput solutions for breeding and genetic monitoring (Shan et al., 2022; Wu et al., 2024).