

genomic data in elucidating the mechanisms of economically important traits, identifying candidate functional genes, and interpreting selection signals.

## 6 Current Status of Genetic Diversity Research in Groupers

### 6.1 Comparison of genetic diversity among different grouper species

At present, based on microsatellite markers, mitochondrial DNA, and other molecular marker technologies, researchers have systematically evaluated the genetic diversity of multiple grouper species (*Epinephelus* spp. and related taxa). Overall, most grouper species exhibit moderate to high levels of genetic variation; however, significant differences exist among species. These differences are closely related to their evolutionary history, distribution range, ecological niches, and population dynamics (Hassanien and Al-Rashada, 2020). Therefore, comparative studies of genetic diversity among different grouper species not only help to elucidate their evolutionary divergence but also provide important references for germplasm conservation and the selection of superior breeding stocks. Existing studies suggest that species with wider distribution ranges and more complex ecological environments generally possess higher genetic diversity.

For example, yellow grouper (*Epinephelus awoara*) exhibits high haplotype diversity ( $h = 0.968$ ) and a rich number of microsatellite alleles (13-20 alleles per locus), indicating strong genetic variation potential (Yang et al., 2022). Giant grouper (*E. lanceolatus*) shows an average of approximately 5.9 alleles per locus and expected heterozygosity ( $H_e$ ) ranging from 0.62 to 0.80, suggesting a relatively high level of nuclear genetic diversity suitable for fine-scale population analysis and molecular breeding studies. Although brown grouper (*E. marginatus*) maintains relatively high heterozygosity across multiple regions, its effective population size is relatively low, indicating potential risks to its genetic stability (Vaini et al., 2021).

In contrast, some grouper species with narrower ecological niches or more restricted distributions tend to exhibit lower levels of genetic diversity and are more prone to pronounced population differentiation. In certain island or localized populations, limited gene flow can lead to the accumulation of genetic drift and the formation of unique lineages (Hassanien and Al-Rashada, 2020; Yang et al., 2022). In addition, different marker systems may vary in their ability to detect genetic variation; for example, studies on *Plectropomus* species have reported discrepancies in diversity estimates across different technical platforms. With the increasing study of hybrid groupers, their offspring often show relatively high diversity in some indices; however, their long-term stability and genetic security still require further evaluation.

### 6.2 Genetic differences between wild and cultured populations

Wild grouper populations generally exhibit higher genetic diversity, as they have long been subjected to natural environmental conditions, including ocean currents, habitat heterogeneity, and natural selection (Yang et al., 2022). Gene flow among wild populations helps maintain genetic connectivity, and although geographic differentiation may occur at large spatial scales, they collectively form a relatively stable genetic resource pool. Therefore, wild populations are not only critical for conservation but also serve as key genetic sources for artificial breeding and broodstock renewal.

In contrast, cultured populations typically show lower genetic diversity, a conclusion consistently supported by multiple studies. Research on giant grouper in the South China Sea indicates that cultured populations have significantly lower allelic richness and heterozygosity compared to wild populations. At the same time, analyses such as FST, AMOVA, and STRUCTURE reveal significant genetic differentiation between the two groups. Similarly, in orange-spotted grouper, clear genetic differences exist between cultured populations and multiple wild populations, while variation among wild populations is relatively small (Wang et al., 2011), indicating that genetic changes occur more rapidly within aquaculture systems.

The decline in genetic diversity in cultured populations is mainly attributed to founder effects, genetic drift, and the accumulation of inbreeding. In aquaculture, limited broodstock numbers and repeated use reduce effective population size and lead to unequal family contributions (Hsu et al., 2023). In addition, artificial selection for