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## CHAPTER-10

### RECENT ADVANCES IN MOLECULAR MARKERS DEVELOPMENT AND THEIR APPLICATIONS IN FISHERIES AND AQUACULTURE

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#### Introduction

All fishes are produced to undergo mutations because of the regular cellular activity or interactions with the environment,

leading to genetic difference (polymorphism). The difference in the genome level of a species improves the capability of the species to acclimatize to changing the environment and is vital for the overall fitness and survival of the species. In combination with other evolutionary forces like genetic variation and natural selection, genetic drift rises between individuals leading to distinction at the level of species, population, and higher order taxonomic groups. Molecular genetic markers are influential tools to detect genetic infrequency of individuals, populations or species. These markers have transformed the analytical power, necessary to explore the genetic diversity (Hillis et al., 1996)<sup>[1]</sup>. The conclusion from genetic diversity data has diverse application in research on evolution, conservation, and management of natural resources and genetic improvement programmes (Liu et al., 2004)<sup>[2]</sup>. The progress of DNA-based genetic markers discovery has had an innovatory impact on animal and fish genetics. It is theoretically possible to detect and exploit genetic variation in the whole genome with the help of DNA markers. Genetic markers popularly used in the aquaculture field includes protein based marker like allozymes, DNA bases markers like mitochondrial DNA, RAPD, AFLP, RFLP, microsatellite, SNP, and expressed sequence tag markers. Currently, the advancement and ease of marker discovery, the applications of DNA based marker are rapidly progressed in fisheries researches. The markers are used to construct high-resolution genetic linkage maps for different aquaculture species, detect the rate of inbreeding, genetic variability, identification of species and strain, and parentage assignments in fishes. Well-designed studies using these genetic markers will certainly accelerate the identification of genes involved in quantitative trait loci (QTL) for marker-