

Review Article

Importance of Marker Assisted Selection in Fish Breeding in India: Challenges and Opportunities

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Abstract

The important economical traits like body growth, resistance to diseases, meat quality, etc. highly influence the profitability of the food animals including fishes. The main target of every selective breeding programme is to produce improve offspring for these traits. However, improvement of performance traits through traditional phenotype-based selection needs several generations to optimise these characters. Other problems associated with the traditional breeding programme is the maintenance of each generation and complexity of the measure qualitative trait such as meat quality. Marker-Assisted Selection (MAS) can be the best alternative to solve these problems. Marker-Assisted Selection (MAS) is a type of indirect method of selection of better performing breeding individuals. MAS depends on identifying the link between a genetic marker and Quantitative traits loci (QTL). The distance between marker and target traits determines the association of the marker with the QTL. After identifying the markers linked to QTL, they can be used in the selective breeding programme to select the brooders having better genetic potential for the targeted trait. Improvement of performance traits through MAS is fast and more accurate and allows us to understand the genetic mechanism affecting performance traits.

INTRODUCTION

The desirable phenotypic variations in the performance traits of fishes are used to increase the aquacultural yield, improve incomes of farmers and enhances food security through selective breeding by choosing better-performed individuals. However, phenotype-based selection needed considerable time to optimise the traits, so researchers are now moving from phenotype based selection to genotype-based selection. The lacking of a molecular marker is the main limiting factor for the realization of genotype based selection potentials in fishes. However, with the advent of DNA-based genetic markers in the late 1970s and now the ease of the marker discovery through the next generation sequencing allowed the researchers to identify large numbers of markers spreads throughout the genome of any species of interest. The markers are used to detect linkage with the traits of interest, thus allowing MAS finally to become a reality. It opens a new field of academic research, including the milestone paper by [1]. In aquaculture, genetic mapping has been completed for tilapia, tiger shrimp, kuruma prawn, rainbow trout, catfishes and atlantic salmon. Now genetic map needs to be developed for the other essential species for successful development of aquaculture industry by increasing overall production through MAS. The traits, difficult and expensive to measure or showing

low heritability and recessive traits, can easily be optimised using MAS.

However, lack of the resources such as dense linkage maps, needed to locate QTL accurately in fishes is one of the major problem in aquaculture. Recently, expressed sequence tag (EST) databases based sequencing approach has been used for developing molecular markers such as simple sequence repeats (microsatellites) and single nucleotide polymorphisms (SNPs). In aquaculture, SNPs are mostly used for genomic studies and identification of diagnostic markers for various diseases [2]. Marker-assisted selection method (MAS) or genome-wide marker-assisted selection method (G-MAS) are not widely used in aquaculture, but nowadays its use is increasing due to its ease of use and quicker than traditional phenotype-based selection. Now it becomes a fertile field of research for the aquaculture researchers to discover novel genetic marker that can be used to link with the QTLs in selective breeding programmes.

Most of the genetic improvement in fish and shellfish species to date has been made through the use of traditional selective breeding [3]. Well-designed breeding programmers have shown substantial response to selection for body weight, e.g. Atlantic salmon, 10 to 14 percent [4], reported rates of genetic

gain 8 percent for indirect selection for body weight at sea in rainbowtrout but it is 13 percent for direct selection [5]. Recently MAS become very popular method of indirect selection for production of the genetically improved offspring's in aquaculture breeding programme. As most of the performance traits such as growth or disease resistance are controlled by multiple genes and therefore inherited as quantitative traits, analysis of their associated quantitative trait loci (QTL) is an essential part of aquaculture genomics [6]. QTLs are largely unknown genes that affect performance traits (such as growth rate and disease resistance) and these are important to breeders. Relative chromosomal positions of QTL in a genome can be identified in a two-step process that begins by constructing a genetic linkage map. Genetic linkage maps are made by assigning (mapping out) polymorphic DNA markers (such as microsatellites, SNP or AFLPs) to chromosome configurations based on their segregation relationships. SNPs and other markers that are linked to QTLs form the basis of marker assistance selection (MAS) in a selective breeding program for improving aquaculture production.

Importance of MAS in selective breeding programme:

The rate of the genetic gain through MAS can increase when there is a continuous identification of new QTL for the targeted traits. The extra genetic gain through the MAS may decrease very quickly in successive generation of selection for the same QTL and also the rate of identification of new QTL is hard to predict. The genetic gain due to MAS for a targeted QTL is higher when the characteristics measured after the selection. The frequency of the favourable QTL allele can be quickly increased in a population using marker assisted selection method during the first generations compared to traditional selection based on BLUP (Best linear unbiased prediction). The information generated from the detected QTL in the selection requires developing some selection criteria to connect this molecular information with phenotypic information. MAS can be efficiently used to identify the major QTLs for a trait and for a phenotypic which is expensive to measure. According to Yue [7], in more than 20 aquaculture fish species, QTL for traits like cold and salinity, sex determination, growth and disease resistance have been mapped. Such studies can provide necessary information about patterns and the rate of evolutionary changes besides may provide tools for marker assisted selection [8]. Mapping typically results in differing crosses and segregation pattern analysis in the offspring of hybrids between the divergent crosses. The applied goal of mapping understood so far is to identify the position of specific phenotypic traits, which could be helpful in breeding programs. Mapping genes and QTLs is of fundamental and applied interest in aquaculture species. Yue [9] mentioned polymorphic markers, genotyping platforms, reference families and software programs are prerequisite for constructing a linkage map of any species. The purpose of QTL mapping is to assist in selective breeding by understanding the effect and quantity of genes determining a trait [10]. QTL analysis for important traits like thermal tolerance, spawning time, embryonic development, growth traits, stress, salinity tolerance, infectious hematopoietic necrosis and bacterial cold-water disease have been conducted for more than 20 aquaculture species including finfish, mussels and crustaceans. QTL mapping is the practical application of marker-assisted selection in aquaculture [11]. Among the 20

species studied so far, tilapia and rainbow trout are among most important freshwater food fish species where salmon is the major cultured marine fish species [12].

Advantages of marker-assisted selection

MAS is profitable for the aquaculturist over conventional selection methods when the traits show low heritability. It helps to discover the existing genetic diversity in breeding populations and can be used to improve desirable characters in aquaculture species. Improvement of performance traits through traditional selection integrated with molecular tools is fast and more accurate and allows us to understand the genetic mechanism affecting performance traits. The dramatic development of molecular genetics laid the groundwork for genomics that has introduced a new generation of molecular markers for use in the genetic improvement of farm animals. These markers provide more accurate genetic information and better understanding of the animal genetic resources [13]. Molecular markers have been used in QTL mapping for better genetic management in aquaculture. It is beneficial for sex-limited traits such as sperm production, egg production or traits that are a poor predictor of breeding value like fertility. The traits which are difficult or expensive to measure (disease resistance), expressed late in life is very difficult to optimize using conventional breeding programme. Selection programme needs several progenies to optimise traits and in some case the progeny testing scheme requires a long generation interval and also very costly. There the MAS is very useful tool to reduce generation interval through early selection, even before maturity of the fish and to select those traits which are restricted to only one sex.

Limitation of marker-assisted selection

The main restriction in MAS is the increasing sample collection cost for genotyping and lack of complete genotype information of the fishes. There are very limited study has been conducted on MAS in fisheries in India. Genotyping the whole population is also difficult in commercial fish populations. To decrease genotyping costs, researcher are concern on the identification of the most informative individuals based on phenotypic information, segregation analysis or combining the phenotypic and genotypic information in breeding. There is a limited number of genotypes studied for a performance traits and also lack of confidence of users to associated this gene which the molecular marker leads to lower the accuracy of QTL detection for fishes.

In case fish there is a lack of the complete genotype information in the population used in MAS schemes and lack of markers for the species make it difficult to link a QTL with a molecular marker. The selection of the marker information is not entirely reliable because of the possibilities of over estimation of QTL effects in QTL position in the fish population. The inconsistency is also a major problem in QTL estimation in fish because the QTL effect is not expressed similarly over the years or when it is used in a different population or stock [14]. The main targeted traits in aquaculture for MAS are body growth, disease resistance, meat quality, feed efficiency and maturation.

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