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MARKER-ASSISTED SELECTION IN FISH: A REVIEW

ABSTRACT

The important economical traits like body growth, resistance to diseases, meat quality, etc. highly influence the profitability of food animals including fishes. The main target of every selective breeding programme is to produce improved traits offspring's. However, improvement of performance traits through traditional phenotype-based selection needs several generations to optimise these characters. Marker-Assisted Selection (MAS) is a type of indirect method of selection of better performing breeding individuals. MAS is beneficial when the traits are difficult, expensive to measure and has both low heritability and recessive traits. MAS facilitates the exploitation of existing genetic diversity in breeding populations and can be used to improve desirable traits in livestock. 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.

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Keywords: Marker-Assisted Selection, Quantitative traits loci, genetic diversity, trait

1.0 INTRODUCTION

Marker-Assisted Selection (MAS) is a type of biotechnology that uses molecular genetic markers as a criterion for selecting desired traits (Ashraf, 2012). Marker Assisted Selection (MAS) is an indirect selection process where a trait of interest is selected not based on the trait itself but on a marker linked to it (Ribaut and Ragot 2007).

34 MAS is considered a “revolutionary” approach to traditional tree breeding as it allows
35 breeders to select individuals based on their genotypes, rather than being restricted to
36 phenotypic characteristics (Boopathi *et al.*, 2013).

37 Sax (1923) was the first to show how genetic factors influencing quantitative traits can be
38 identified using markers.

39 Recently MAS became a very popular method of indirect selection for production of
40 the genetically improved **in aquaculture breeding programme offspring's**. Most of the
41 performance traits including growth or disease resistance are controlled by multiple genes
42 and are therefore inherited as quantitative traits, analysis of their associated quantitative trait
43 loci (QTL) is an essential part of aquaculture genomics (Liu and Cordes, 2004). QTLs are
44 largely unknown genes that affect performance traits (such as growth rate and disease
45 resistance) and these are important to breeders.

46 MAS in a breeding context involves scoring indirectly for the presence or absence of
47 a desired phenotype or phenotypic component based on the sequences or banding patterns of
48 molecular markers located in or near the genes controlling the phenotype. The sequence
49 polymorphism or banding pattern of the molecular marker is indicative of the presence or
50 absence of a specific gene or chromosomal segment that is known to carry a desired allele
51 (Brumlop and Finckh, 2011).

52 Marker-assisted selection method (MAS) or genome-wide marker-assisted selection
53 method (G-MAS) was not widely used in aquaculture, but nowadays its use is increasing due
54 to its ease of use and quicker than traditional phenotype-based selection. Now it becomes a
55 fertile field of research for the aquaculture researchers to discover novel genetic marker that
56 can be used to link with the QTLs in selective breeding programmes (Hauser *et al.*, 2011;
57 Dichmont *et al.*, 2012; Abdul-Muneer, 2014).

58 In order to manage individual species effectively, identification of different species
59 from a mixed catch becomes important. DNA markers are widely being accepted not only to
60 obtain information about gene flow and allele frequencies in aquaculture practices but also to
61 identify hybrids. The majority of the markers, which are used in inter- and intra-specific
62 disparity, include Random Amplified Polymorphic DNA (RAPD) for species and sub-species
63 identification done in tilapia (Bardakci and Skibinski, 1994), and iso-enzyme used in
64 intraspecific variations in Sparidae species (Alarcón and Alvarez, 1999). Similarly, Nijman *et al.*,
65 (2003) reported the use of mtDNA markers as an important tool in rapid detection of
66 hybridization between species and subspecies of livestock.

67 Markers tend not to have any biological effect, but rather can be thought of as notable and
68 constant points of reference within the genome (Guimaraes, *et al.*, 2007). Markers can be
69 found within the desired gene or, more commonly, linked to a gene determining a trait of
70 interest (Brumlop and Finckh, 2011; Guimaraes *et al.*, 2007). Unlike genetic engineering,
71 MAS does not alter the original DNA (Vogel and Van Aken, 2009); instead it uses genetic
72 marker to identify naturally-occurring genetic variations among individuals, with the intent of
73 selecting those with the best potential to meet desired criteria and objectives.

74 Marker Assisted Selection (MAS) provides several other benefits to breeders, in that
75 it can select for genes that demonstrate low heritability, have recessive alleles, and are
76 difficult, expensive, or time exhaustive to determine phenotypically (Boopathi, 2013a;
77 Brumlop and Finckh, 2011; Xu and Crouch, 2008). MAS also allows for gene pyramiding or
78 combining multiple genes within the same breeding line, while having fewer unintentional
79 losses and fewer selection cycles (Boopathi, 2013a; Xu and Crouch, 2008).
80 Furthermore, MAS may be viewed by the public with more support than genetic engineering
81 as breeders are not manually manipulating the genes, and thus all offspring inheritance occurs
82 naturally (Vogel and Van Aken, 2009). It is also believed that genetic markers may be
83 important in the assessment, conservation and use of diversity in germplasm and varieties
84 (Brumlop and Finckh, 2011).

85 Molecular marker maps have been constructed for a number of aquaculture species,
86 e.g. tilapia, *Clarias*, giant tiger prawn, kuruma prawn, Japanese flounder and Atlantic salmon,
87 although their density is generally low (Nichols *et al.*, 2003). As many preferred traits are not
88 observed until maturity, MAS eliminates this waiting period by allowing for the early
89 selection of desired genotypes at the seedling stage (Yanchuk *et al.*, 2002).

90 The desirable phenotypic variations in the performance traits of fishes are used to
91 increase the aquacultural yield, improve incomes of farmers and enhances food security
92 through selective breeding by choosing better-performed individuals. However, phenotype-
93 based selection needed considerable time to optimise the traits, so researchers are now
94 moving from phenotype based selection to genotype-based selection. The absence of a
95 molecular marker is the main limiting factor for the realization of genotype based selection
96 potentials in fishes. However, with the advent of DNA-based genetic markers in the late
97 1970s and now the ease of the marker discovery through the next generation sequencing
98 allowed researchers to identify large numbers of markers spreads throughout the genome of
99 any species of interest. The markers are used to detect linkage with the traits of interest, thus

100 allowing MAS finally to become a reality (Peterson *et al.*, 1990). This paper aims to provide
101 information regarding the technical aspect of MAS and the current application in fisheries
102 and Aquaculture in other to increase high quality production within a period of time.

103 **2.0 Marker Assisted Selection**

104 Incorporation of marker information into breeding programs in aiding identification
105 and selection of superior individuals has been widely studied (Bernardo, 1994; Han *et al.*,
106 1997; Xie and Xu, 1998; Romagosa *et al.*, 1999; Ayoub *et al.*, 2003; Jordan *et al.*, 2003).

107 Molecular markers in aquaculture and fisheries have been used for over 50 years
108 (Ryman and Utter, 1987; Liu and Cordes, 2004) and their use has steadily increased over the
109 last two decades (Park and Moran, 1994; Chauhan and Rajiv, 2010; Dichmont *et al.*, 2012;
110 Abdul-Muneer, 2014).

111 An important factor in MAS is the accuracy of estimating the genetic effects related to
112 the trait of interest. In contrast to genetic engineering (GE), MAS does not alter the original
113 DNA. Rather, it identifies whether the desired trait(s) are being expressed, so that individuals
114 with the best potential can be selected (Andersson, 2001).

115 Molecular marker analysis allows the identification of genome segments, so called
116 Quantitative Trait Loci (QTL), contributing to the genetic variance of a quantitative trait and
117 thus to select superior genotypes as these loci (Cannai *et al.*, 2003). Allelic variation in
118 genetic markers can be linked to the variation in traits of economic interest, and thus the
119 marker provides DNA level information on the inheritance of the traits.

120 The practical use of markers in selection can be roughly divided into three classes:

- 121 1) Removing genetic disorders,
- 122 2) Marker breeding value-selection, and
- 123 3) Genomic selection.

124 **2.1 MAS versus Phenotypic Selection**

125 Marker-Assisted Selection (MAS) will probably never replace Phenotypic Selection
126 (PS) entirely. There is no general pattern by which it can be predicted whether MAS or PS
127 will be more useful. Empirical comparisons of MAS and PS for increasing gain from
128 selection have been made in several studies. The outcomes of these studies are conflicting. In
129 some **studies**, MAS is reported to be more effective/efficient than PS (Yousef and Juvik
130 2001; Abalo *et al.*, 2009) while other studies considered the two methods equal (Van Berloo
131 and Stam 1999; Willcox *et al.*, 2002; Hoeck *et al.*, 2003; Moreau *et al.*, 2004). In a third
132 group of studies PS proved to be more effective/efficient than MAS (Davies *et al.*, 2006;

133 Wilde *et al.*, 2007) and in other comparisons the effectiveness/efficiency of MAS and PS
134 varied within the same study, depending on the populations or on the trait selected for
135 (FlintGarcia *et al.*, 2003b; Robbins and Staub 2009).

136 **2.2 Limitations of MAS**

- 137 • Cost
- 138 • Requirement of technical skill
- 139 • Automated techniques for maximum benefit

140 **2.3 Advantages of MAS**

141 In addition to the cost and time savings described above, for a number of breeding
142 scenarios, MAS methods are likely to offer significant advantages compared with
143 conventional selection methods. These scenarios assume the availability of markers for
144 multiple traits and take into consideration the advantages of MAS under optimum situations
145 (Dreher *et al.*, 2002; Dudley, 1993).

- 146 1. Gene stacking for a single trait: MAS offers potential savings compared with
147 conventional selection when it allows breeders to identify the presence of multiple
148 genes/alleles related to a single trait, and the alleles do not exert individually
149 detectable effects on the expression of the trait.
- 150 2. Early detection: MAS offers potential savings compared with conventional selection
151 when it allows alleles for desirable traits to be detected early, well before the trait is
152 expressed and can be detected phenotypically. This benefit can be particularly
153 important in species that grow slowly.
- 154 3. Heritability of traits: Up to a point, gains from MAS increase with decreasing
155 heritability. However, due to the difficulties encountered in QTL detection, the gains
156 are likely to decline beyond a certain threshold heritability estimate.

157 **2.4 Disadvantages of MAS**

158 Perhaps the greatest disadvantage of MAS is the time and financial **investment**
159 **required to develop** markers that are widely applicable for traits of agronomic importance.
160 Often a marker developed in one or a few related genotypes will not work for
161 other genotypes in a breeding scheme due to allelic effects. Furthermore, development of
162 markers, particularly for QTL, is complicated by epistatic interactions and the critical need
163 for good quality phenotypic data.

164 **2.5 Quantitative Trait Loci**

165 In fish, several QTL studies have been published; in salmonids (Jackson *et al.*, 1998;
166 Johansen 1999; Robinson *et al.*, 1999; Sakamoto *et al.*, 1999; Marfyaniuk 2001, Ozaki *et al.*,
167 2001 Somorger 2001. Tao and Baiding 2003), in catfish (Liu *et al.*, 2003), in tilapia (Cnaani
168 *et al.*, 2003) and in silver barb (Hussain *et al.*, 2002).

169 Marker Assisted Selection (MAS) is followed by two steps, detection of molecular markers
170 associated with quantitative trait locus (QTL) and application of those markers.

171 The position of the chromosome that controls the economical important trait is termed as
172 QTL.

173 The concepts for detecting QTL were developed more than 90 years ago (Sax, 1923). In
174 aquaculture species, much effort has been applied for QTL mapping. QTLs are mapped by
175 linkage disequilibrium with molecular markers exhibiting Mendelian segregation.
176 Economically important traits are controlled by the single or group of gene.

177 The basic concept of QTL studies is to know the number and location of loci
178 associated with phenotypic traits (Mackay, 2001; Mauricio, 2001; Burt and Hocking, 2002;
179 Erickson *et al.*, 2004). Thus, candidate gene or molecular markers, resulted by QTL mapping,
180 could be used in MAS (Groenen *et al.*, 2000). QTL detection is an ongoing effort in
181 aquaculture species. More than 37 important traits have been located in about 20 aquaculture
182 species.

183 QTL mapping is the practical application of marker-assisted selection in aquaculture
184 (Al-Samarai, 2015). With rapid advancement of molecular technology, it is now possible to
185 use molecular marker information to map major quantitative trait loci (QTLs) on
186 chromosomes (Paterson *et al.*, 1988,1991; Hilbert *et al.*, 1991; Jacob *et al.*, 1991; Stuber *et al.*,
187 1992). Once QTL for a trait are identified, individuals can be selected for breeding on the
188 basis of marker alleles that segregate with favourable phenotypes (Lande and Thompson,
189 1990). This strategy, known as marker-assisted selection (MAS), is particularly useful for
190 traits that cannot be measured on selection candidates directly, notably disease resistance or
191 meat quality traits (Sonesson, 2007a).

192 **2.5.1 QTL Detection in Fish**

193 A number of genetic maps have been developed specifically to locate QTL in several
194 fish species. The first of such map was produced in Zebrafish *Danio rerio* (Postlethwait
195 *et al.*, 1994; Shimoda *et al.*, 1999), which is a non-aquacultural species. Among
196 cultivable fish groups low-density maps have been developed for salmonids (Sakamoto *et al.*,
197 2000; Ghabi 2001) for catfish (Liu *et al.*, 2003; Poompuang and Na-Nakorn 2004) for tilapia

198 (Kocher *et al.*, 1998; Cnaani *et al.*, 2003), for Japanese flounder (Sanchez *et al.*, 2003), for
 199 red sea beam (Sakamoto *et al.*, 2003), for Oyster (Yu and Geso 2003), and for shrimp
 200 ([Http://shrimppmap.tag.csiro.au](http://shrimppmap.tag.csiro.au)).

201 **2.5.2 QTL Mapping in Fish**

202 Although in fish several studies have confirmed the existence of significant genetic
 203 variation for quantitative traits at commercial importance (Kause *et al.*, 2003) and have
 204 recognized the potential of MAS for their genetic improvement (Flint and Mott, 2001). Thus
 205 far, very few QTL for production traits have been identified in fish (Sonesson, 2003). Much
 206 effort is devoted to QTL mapping for growth, feed conversion efficiencies, disease resistance,
 207 fecundity, and spawning time (Dunham *et al.*, 2001).

208 Several QTL studies have been published in rainbow trout for temperature tolerance
 209 (Jackson *et al.*, 1998). Danzmann *et al.*, 1998, Perry 2001), spawning time (Sakamoto *et al.*,
 210 1999; fish back *et al.* 2000, O' Malley 2001); growth (Martynicik 2001), disease resistance
 211 (Ozaki *et al.*, 2001), and fitness traits (Somorjai 2001). Other notable QTL studies published
 212 in aquaculture fish species include: in tilapia for temperature and salinity tolerance
 213 (Streadman and Kocher 2002; Cnaan *et al.*, 2003), in catfish for feed conversion efficiency
 214 and bacterial septicaemia resistance (Liu 2003), in guppy for growth (Nakajima and
 215 Taniguchi 2002), in Atlantic salmon for infectious anaemia resistance (Moen *et al.*, 2003 and
 216 in Arctic charr for growth rates and fitness traits (Johansen 1999, Somorjai 2001).

217 In salmonids, QTL have been found related to body weight and size (Martyniuk *et al.*,
 218 2003; O'Malley *et al.*, 2003; Reid *et al.*, 2005), for colouration pattern (Streelman, Albertson
 219 and Kocher, 2003) and for one form of albinism (Nakamura *et al.*, 2001). Zimmerman *et al.*,
 220 (2005) found QTL for pyloric caeca number, a trait related to feed conversion efficiency.

221 **Table 1: QTL studies in selected aquaculture species**

Species	Traits	Reference
Arctic charr	Body weight and sexual maturation; Salinity tolerance	Küttner <i>et al.</i> , 2011
Asian seabass	Resistance against viral nervous necrosis disease Growth-related trait Omega-3 fatty acids	Wang <i>et al.</i> , 2006 Xia <i>et al.</i> , 2014

Atlantic salmon	Growth traits and flesh colour Resistance against IPN Late sexual maturation	Baranski <i>et al.</i> , 2010; <i>Tsai et al.</i> , 2014; <i>Moen et al.</i> , 2009 ; <i>Houston et al.</i> , 2008; 2010
Catfish	Columnaris disease resistance ESC disease resistance Hypoxia tolerance Heat stress Head size	<i>Gutierrez et al.</i> , 2014 <i>Geng et al.</i> , 2015 <i>Wang et al.</i> , 2013; <i>Zhou et al.</i> , 2017 <i>Wang et al.</i> , 2016; <i>Jin et al.</i> , 2016 <i>Geng et al.</i> , 2016
Common carp	Common carp Morphometric traits Swimming ability	<i>Zhang et al.</i> , 2011 <i>Boulton et al.</i> , 2011 <i>Laghari et al.</i> , 2014
Eastern oyster	Disease resistance	<i>Yu and Guo</i> , 2006
European seabass	Growth, body weight Morphometric traits and stress Response	<i>Louro et al.</i> , 2016 <i>Massault et al.</i> , 2010
Pacific white shrimp	Growth parameters	<i>Andriantahina et al.</i> , 2013
Giant tiger prawn	Disease resistance and sex determination	<i>Robinson et al.</i> , 2014
Japanese flounder	<i>Vibrio anguillarum</i> resistance	<i>Wang et al.</i> , 2014
Pacific oyster	Growth Resistance against summer mortality Viability	<i>Guo et al.</i> , 2012 <i>Sauvage et al.</i> , 2010 <i>Plough and Hedgecock</i> , 2011 <i>Plough et al.</i> , 2016
Gilthead seabream	Skeletal deformities Sex determination and body growth	<i>Negrín-Báez et al.</i> , 2015 <i>Loukovitis et al.</i> , 2011 <i>Massault et al.</i> , 2011

Rainbow trout	Growth related traits	Kocmarek <i>et al.</i> , 2015; Wringe <i>et al.</i> , 2010; Leder <i>et al.</i> , 2006.
Tilapia	Growth traits Sex	Liu <i>et al.</i> , 2014; Wang <i>et al.</i> , 2015 Palaikostas <i>et al.</i> , 2015

222

223 2.5.3 QTL analysis

224 2.5.3.1. QTL for growth traits

225 Growth is one of the most important economic traits of all aquaculture species. Up to
 226 2012, QTL analyses have been conducted in more than 20 aquatic species (Yue *et al.*, 2014),
 227 and growth was the most popular trait studied. Wang *et al.*, (2006) used 380
 228 F1 Asian seabass to identify five major QTLs and 27 potential QTLs. Of them, three major
 229 QTLs for body weight, length, and body length were located at a similar linkage group 2
 230 (LG2) position with the nearby Lca287 microsatellite and accounted for 28.8%, 58.9%, and
 231 59.7% of
 232 the phenotypic variations. The other two major QTLs for body weight were located at another
 233 LG2 position. These five major QTLs have been confirmed in two other Asian
 234 seabass populations (Wang *et al.*, 2008). Further QTL fine mapping of the Asian seabass
 235 growth trait identified three **candidate** “growth genes” (CATHEPSIN D, KCTD15, and
 236 CSMD2) affecting body weight, body length, and total length (Wang *et al.*, 2011). The
 237 function of the *cathepsin D* gene in humans involves cell proliferation and cell growth;
 238 therefore, *cathepsin D* may also be a major “growth gene” in Asian seabass. O’Malley *et al.*,
 239 (O’Maller *et al.*, 2008) identified QTLs for body weight in rainbow trout on 10 different LGs.

240 Wringe *et al.* (2010) used additional backcrossed families and SSR markers to
 241 confirm **the O’Malley *et al.*(2003),’s results** and found several major candidate growth genes
 242 (e.g., *GH2* and *Pax7*). Reid *et al.*, 2004 identified a QTL for body weight in two LGs (AS8
 243 and 11) of Atlantic salmon, and reported that it was homologous to the growth QTL in
 244 rainbow trout. Houston *et al.*, (2009) identified QTLs for body weight in Linkage group 1
 245 (LG1) and LG5 of Atlantic salmon. Gutierrez *et al.*, (2012) further used a 6.5 K Single
 246 Nucleotide Polymorphisms (SNP) chip to identify QTLs in six LGs at the genomic level.
 247 Cnaani *et al.* (2004) identified a QTL for tilapia growth on LG23, which is the linkage group
 248 with the genetic sex-determining region. Song *et al.* (2012) used 1487 SSRs to produce a

249 high-density genetic linkage map and successfully identified a QTL affecting body weight in
250 LG14 of Japanese flounder.

251 Some reports have used a candidate gene approach to identify growth-related genes
252 and molecular markers in fish. Tao and Boulding (2003) found polymorphisms in the growth
253 hormone gene (*GH*) that were significantly associated with growth rate of Arctic charr
254 (*Salvelinus alpinus*). Li *et al.*, (2009) reported an SNP in the insulin-like growth factor-
255 (IGF)1 gene 5' untranslated region (UTR) of largemouth bass (*Micropterus salmoides*). Sun *et*
256 *al.* (2012) reported that two SNPs in exon 3 of the myostatin (*MSTN*) gene were significantly
257 related to body weight and Fulton's factor in common carp. Liu *et al.* (2012) also found that a
258 SNP in the *MSTN* 3' UTR was very significantly associated with total length, body length,
259 and body weight of bighead carp.

260 **2.5.3.2. QTL for feed conversion rate**

261 Food Conversion Ratio (FCR) is one of the most important economic traits in fish, as
262 fish with a better FCR increase profits.

263 Liu (2005) used Amplified Fragment Length polymorphisms (AFLP) markers to
264 construct a catfish genetic map and found a QTL associated with FCR. Zimmerman *et al.*
265 (2005) revealed three QTLs for the number of pyloric caeca in three LGs of rainbow trout,
266 and this is an important index associated with FCR.

267 Food Conversion Ratio (FCR) studies have also been reported in common carp from
268 the Heilongjiang Fisheries Research Institute of the Chinese Academy of Fishery Sciences
269 (Wang, 2012).

270 **2.5.3.3. QTL for sex determination**

271 Sex phenotype and sex determination in fish have specific evolutionary status and
272 diversity. Males and females of some species have significant differences in growth rate or
273 commercial value; therefore, **mono sex fish** culture is a promising strategy. The sex-
274 determining (SD) loci and QTLs have been studied in a limited number of fish, such as tilapia
275 (Lee *et al.*, 2004) rainbow trout (Alfaqih *et al.*, 2009) and salmonids (Davidson *et al.*, 2009).
276 Previous studies have demonstrated that sex QTLs are located on LG1, 2, 3, 6, and 23 of
277 tilapia (Cnaani *et al.*, 2004; Lee *et al.*, 2004; Cnaani *et al.*, 2008) Eshel *et al.* (2011) reported
278 a major candidate sex QTL that is considered the sex determining region in tilapia. Fifty-one
279 genes in this region have been annotated, and 10 have been confirmed.

280 The anti-Müllerian hormone gene is the most differentially expressed gene in male
281 and female tilapia. Sun *et al.*, (2014) recently published several sex-specific markers, and one

282 is tightly linked with the sex-determining region discovered by Eshel *et al.*, (2011) The sex-
283 determining locus in rainbow trout is located on the LG of RT10, and this locus also
284 significantly affects thermo-resistance and body length. The sex-determining regions in Artic
285 charr (Moghadam *et al.*, 2007) brown trout (Gharbi *et al.*, 2006) and Atlantic salmon (Gilbey
286 *et al.*, 2004) are located on the LGs of AC4, BT28, and AS1, respectively.

287 Woram *et al.*, (2003) compared LGs of sex-determining loci in four salmonids and
288 found that although the nucleotide sequences flanking the sex-determining loci were well-
289 conserved, the SD LGs were diverse, suggesting that the regions underwent different
290 recombination events.

291 Loukovitis *et al.*, (2011) located growth and sex-determining QTLs in gilthead sea
292 bream and showed that these two traits have similar genetic control in LG21. Martínez *et al.*,
293 (2009) located a sex QTL on LG5 of turbot and proposed a ZZ/ZW sex-determining
294 mechanism. Viñas *et al.*, (2012) also found a major sex QTL on turbot LG5. These findings
295 suggest that the sex-determining genes may occur on turbot LG5. Song *et al.*, (2012) used
296 high-density genetic maps to locate seven sex QTLs on the half-smooth tongue sole LG1f,
297 LG14f, and LG1m.

298 Additional study by Chen *et al.* (2014) provided insight into ZW sex chromosome
299 evolution and identified sex-determining genes, such as *dmrt1* and *neurl3*.

300 **2.5.4 Factors affecting QTL analyses**

301 The power of mapping QTL can be influenced by a number of factors, such as genetic
302 properties of QTL, experimental design, environmental effects, marker density and
303 informativeness, genotyping errors and precision of trait measurement. Details about how
304 these factors influence the power of QTL mapping can be found in some very good reviews
305 (Crosses 2001; Flint and Mott 2001; Doerge 2002).

306 **2.5.5 Methods of Detecting QTL**

307 Basically, three methods are frequently used for mapping QTL and estimating their
308 effects, namely Single-Marker Association Analysis (SMAA), Simple Interval Mapping
309 (SIM) and Composite Interval Mapping (CIM) (Crosses 2001; Flint and Mott 2001; Doerge
310 2002).

311 **2.6 Current Status of Applications of MAS in Fish**

312 Molecular marker maps have been constructed for a number of aquaculture species,
313 e.g. tilapia, catfish, giant tiger prawn, kuruma prawn, Japanese flounder and Atlantic salmon,
314 although their density is generally low. Density is high for the rainbow trout, where the map

315 published in 2003 has over 1300 markers spread throughout the genome – the vast majority
316 are AFLPs but it also includes over 200 microsatellite markers (Nichols *et al.*, 2003). Some
317 QTLs of interest have been detected (e.g. for cold and salinity tolerance in tilapia and for
318 specific diseases in rainbow trout and salmon).

319 **Conclusion:**

320 In a recent review of MAS in fish breeding schemes, Sonesson (2003) suggested that
321 MAS would be especially valuable for traits that are impossible to record on the candidates
322 for selection such as disease resistance, fillet quality, feed efficiency and sexual maturation,
323 and concluded that MAS is not used in fish breeding schemes today and that the lack of dense
324 molecular maps is the limiting factor. Marker Assisted Selection (MAS) has become a
325 valuable tool in selecting organisms for desirable traits. MAS is expected to increase genetic
326 gain compared to traditional breeding programs and reduce the cost of progeny testing by
327 early selection. The application of MAS in breeding programmes depends on the knowledge
328 of breeders about variable marker information.

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