MARKER ASSISTED SELECTION FOR RESISTANCE AGAINST VIRAL NERVOUS NECROSIS IN EUROPEAN SEABASS (*Dicentrarchus labrax*)

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Introduction

Contagious diseases are a major threat in aquaculture due to losses caused by high mortalities and the reduced growth of surviving fish. Viral nervous necrosis (VNN) is an infectious disease caused by nervous necrosis virus (NNV, red-spotted grouper nervous necrosis virus, RGNNV in European sea bass) which is considered a serious concern for European seabass producers, with fry and juveniles being highly susceptible. The outbreak of VNN may cause up to 100% mortalities at larval and around 20% mortalities at advanced juvenile stages[1, 2]. Moreover, the surviving fish present poor growth rate and ultimately high economic losses for the producers.

Selection and breeding for resistance against infectious diseases is highly effective tool to prevent and/or diminish disease outbreaks. Currently available advanced selection methods with the application of genomic/marker(s) information could pace up response to selection. The genetic variation for resistance against VNN obtained from the challenge tested population was presented previously [3]. The aim of current study was to further look into the genomic architecture of the trait and explore potential of marker assisted and/or genomic selection and obtain realized validation of QTL effects.

Material and Methods

This study comprises of a resource population belonging to multiple year classes (YC2016, YC2017, and YC2019) derived from the Nireus SA's breeding nucleus of European seabass. Families from each of these year classes were gone through the challenge test against VNN, and the subset of the families and individuals from year classes YC2016 and YC2017 including 30 (~27 individuals/family) and 92 (~8 individuals/family) families, respectively were genotyped. Additionally, 536 breeding candidates from multiple year-classes (YC2011-2016) pre-selected according to selection criteria defined in the commercial seabass nucleus work and linked to YC2016 and YC2017 through pedigree were genotyped. The tested individuals and the candidates from YC2016 and YC2017 were genotyped using SNPs based ~57K Affymetrix Axiom array (DlabCHIP) [4]. The detection of QTL was performed using survival phenotype and the genotype information on YC2016 and YC2017 whereas validation of QTL effects was performed using genotype information on candidates (YC2011-2016) and the phenotype of descendent year class, YC2019. For the purpose of validation, additional specific crosses were made in YC2019 using QTL information to produce resistant ("RR", homozygous for favorable allele), moderate ("Rr", heterozygous) and susceptible ("rr", homozygous for alternative allele) families.

Analyses: Genome wide association analysis was performed using following linear mixed animal model implemented in GCTA program with "--mlma-loco" function [5].

$$y=\mu+Xb+Ma+Zu+e$$

Where is the vector of phenotypes (0 dead or 1 alive); is the overall mean; is an incidence matrix for fixed effects and is a vector of fixed effect of year class; is the incidence matrix for SNP containing marker genotypes coded as , is the allele substitution effect of SNP, is a design matrix to relate the records to genetic values and is a vector of random additive genetic effects, it is assumed that , where is the genetic variance and is a genomic relationship matrix computed using VanRaden's method 1. The is the vector of random residual effects with .

Moreover, the accuracy of genomic prediction was evaluated using different models (GBLUP and Bayesian) to assess and compare the potential of genomic and/or marker assisted selection.

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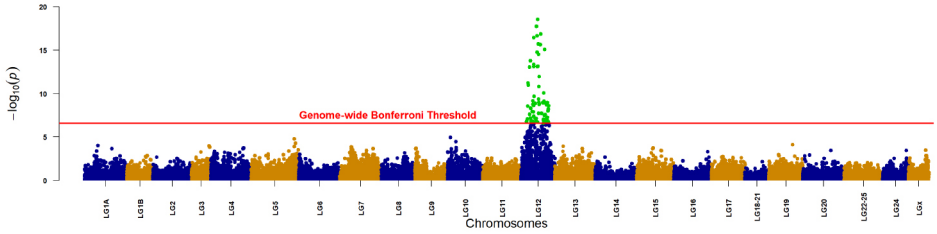

Figure. 1: Manhattan plot presenting association of SNPs with the trait.

Results and Discussion

The GWAS analysis revealed a strong signal of QTL at LG12 with 72 SNPs presenting significant association to the trait with P-value crossing genome-wide Bonferroni corrected threshold (Figure 1) The proportion of the genetic variance explained by the highest significant SNP was ~33% of the total genetic variance. Multiple genes were identified within the QTL region with *REEP1* gene located immediately at the upstream of the highest significant SNP which seems to be more pronounced with functions involving nervous system. The mean accuracy of prediction for resistance against VNN obtained using different genomic models (GBLUP and Bayesian) was 0.72 with Bayesian models worked either better or equally well as GBLUP.

The validation results for survival of "RR", "Rr" and "rr" families which were specifically produced using QTL information on parents revealed >30% higher survival of "RR" over "rr" families and 7% higher survival over "Rr" families.

In conclusion, the tested realized effect of QTL showed >30% higher survival of families carrying homozygous favorable genotype over families containing homozygous unfavorable genotype. Hence, marker assisted selection using QTL information has a shown strong potential for improving resistance against VNN.

Acknowledgement

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