GENETIC VARIATION, GWAS, AND PREDICTABILITY FOR SURVIVAL AGAINST IPNV STRAINS IN RAINBOW TROUT

M. L. Aslam [*a], S. Valdemarsson [b], A. A. Berge [b], T. Bue [b], B. Gjerde [a]

[a] Nofima, AS, Ås, Norway; [b] Osland Stamfisk AS, Osland brygge, 5962 Bjordal
E-mail addresses:
luqman.aslam@nofima.no

Introduction

Contagious diseases are a major threat in aquaculture due to losses caused by high mortalities and the reduced growth of surviving fish. Infectious pancreatic necrosis (IPN) is one of the highly contagious diseases of farmed salmonid fish caused by *Aquabirnavirus*. The disease often causes high levels of morbidity and mortality (30–80%, [1]), and ultimately huge economic loses. Juvenile fish and post-smolts during the months following seawater transfer appear to be the most susceptible phases of production cycle. The clinical symptoms of disease outbreak include swollen abdomen and eyes, darkening of the skin, necrosis of the pancreas and spiral swimming [2]. The survivors can become healthy carriers that may infect susceptible animals either by vertical and/or horizontal means. Although a large proportion of rainbow trout are vaccinated against IPN-virus, the protective effect is uncertain. Host genetic make-up plays significant role for survival against infectious pancreatic necrosis virus (IPNV) with some families survive better than the others. Genetically improved resistance against IPNV is a highly valuable tool to improve survival and to reduce losses due to IPN. The aim of current study was to compute genetic variation for survival against IPNV, further look into the genomic architecture of the trait and explore potential for marker assisted and/or genomic selection.

Material and Methods

The population used in current study originated from the breeding nucleus (year class 2021) of Osland Stamfisk AS, comprising 98 full-sib families. Population was created as crosses among 61 sires and 75 dams, with an average family size of 23 sibs per family (N=3 to 47). Challenge test for survival to IPNV was performed at fry stage with immersion method using two different strains of infectious pancreatic necrosis virus: rainbow trout specific strain of IPNV (IPNV-RT) and Atlantic salmon specific strain of IPNV (IPNV-AS). The IPNV strain was obtained from a rainbow trout farm during field outbreak, and IPNV-AS strain was a previously available isolate. The fry were challenged in two tanks, where one tank (E-4, IPNV-RT) had fry from all 98 families, while the other (E-5, IPNV-AS) had fry from 25 full-sib families. The challenge test model had been previously established and optimized by VESO Vikan, where the concentration of IPNV-RT virus in tank E-4 was set to 6.8 x 10^7 $TCID_{50}$ per ml while IPNV-AS virus in tank E-5 had a concentration of 1 x 10^8 $TCID_{50}$ per ml. Survival phenotype was recorded during the challenge test and all the surviving and dead fish were tissue sampled for genotyping to construct pedigree and for the later genomic analyses.

Analyses: Estimation of genetic parameters, genome-wide association analysis (GWAS), and predictions of estimated breeding values (EBVs) were performed using a linear mixed model(s). Estimates of genetic parameters were computed using ASREML v4.2 applying genomic or pedigree information, and the GWAS analysis was performed with GCTA using "--mlma-loco" function [3]. Moreover, the power of predictability was evaluated using cross validation scheme with different models (PBLUP, GBLUP and Bayesian) to assess and compare the potential of genomic and/or marker assisted selection over classical pedigree information.

The applied model and components are explained below,

$$\boldsymbol{y} = \mu + \boldsymbol{Zu} + \boldsymbol{e}$$

Where y is the vector of phenotypes (0 dead or 1 alive); μ is the overall mean; $\boldsymbol{Z}$ is a design matrix to relate the records to genetic values and u is a vector of random additive genetic effects, it is assumed that $u \sim (0, \sigma_g^2[\mathrm{A/G})$, where σ_g^2 is the genetic variance, $\boldsymbol{A}$ is the relationship matrix obtained using pedigree information, $\boldsymbol{G}$ is a genomic relationship matrix computed using VanRaden's method 1. The $\boldsymbol{e}$ is the vector of random residual effects with $e \sim N(0, I\sigma_e^2)$.

(Continued on next page)

Results and Discussion

The obtained heritability estimates for survival to IPNV-RT were 0.33±0.12 and 0.27±0.03 using pedigree vs. genomic information, respectively. These estimates for survival to IPNV-AS were 0.16±0.04 and 0.20±0.06 with pedigree and genomic information, respectively. However, the estimates derived for survival to IPNV-AS are indicative estimates because these are obtained from small set of families (n=25). The bivariate animal model revealed strong genetic correlation for survival to IPNV-RT and IPNV-AS with estimates of 0.85±12. As, genetic correlation was high and therefore general survival as a single trait was also used to obtain estimates. The general survival showed heritability of 0.25±0.03.

The accuracy of predictions and GWAS analyses were performed for each trait separately. However, GWAS and predictability results obtained through general survival are described as follows. The GWAS analysis revealed a strong signal of QTL at chromosome 1 comprising 23 SNPs presenting significant association to the survival 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 up to ~27% of the total genetic variance. The genomic Bayesian models performed the best in terms of predictability with ~21% improvement in predictability compared to PBLUP model.

In conclusion, survival to IPNV-RT and IPNV-AS in current population revealed significant genetic variation with one major QTL contributing significant proportion of genetic variation while remaining contribution possibly coming from many other loci. The prediction using genomics-based Bayesian models outperforms the predictions using PBLUP model.

Acknowledgement

The results of produced in current study are a part of FutureEUAqua project funded by the H2020 program Sustainable European aquaculture 4.0: nutrition and breeding (GA nr. 817737).

References

1. Zhu L, Wang X, Wang K, Yang Q, He J, Qin Z, Geng Y, Ouyang P, Huang X: Outbreak of infectious pancreatic necrosis virus (IPNV) in farmed rainbow trout in China. Acta Tropica 2017, 170:63-69.
2. Dopazo CP: The Infectious Pancreatic Necrosis Virus (IPNV) and its Virulence Determinants: What is Known and What Should be Known. Pathogens 2020, 9(2):94.
3. Yang J, S.H. Lee, M.E. Goddard, P.M. Visscher: GCTA: A tool for genome-wide complex trait analysis. Am J Hum Genet 2011, 88:76-82.

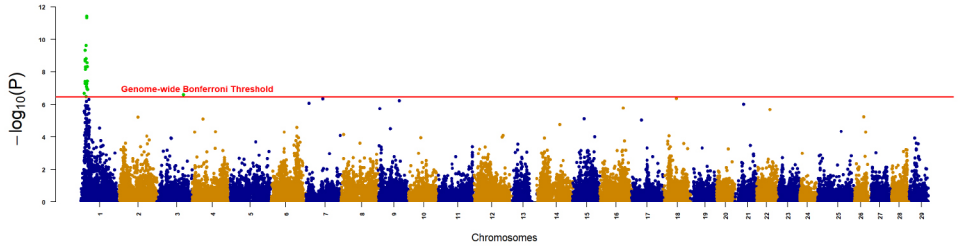

Figure. 1: Manhattan plot presenting association of SNPs with the survival trait.