Genetic enhancement of striped catfish (*Pangasianodon hypophthalmus*) using quantitative genetic and genomic approaches

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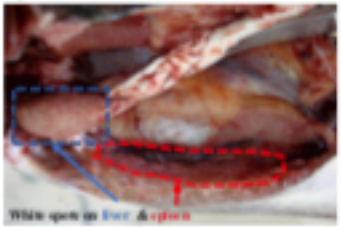
1. OBJECTIVES

Diseases caused by *Edwardsiella ictaluri* bacteria (known as Bacillary Necrosis of Pangasius, BNP) have caused significant economic losses in catfish farming. Genetic selection provides a cost-effective option to develop disease resistance lines of catfish to sustain the aquaculture sector.



Main aims of the study were:

a) To understand genetic inheritance of disease resistance traits in striped catfish;
b) To understand population structure of striped catfish to strengthen genetic variation for disease resistance selection;
c) To examine genetic architecture of the disease at molecular genetic and genomic levels

2. METHODS

Pathogens: Bacterial isolates were identified and tested for their virulence and susceptibility by biochemical and challenge tests.

Testing Animal: approximately 190 full- and half-sib families in G0 and G1 were available for both challenge and growth out tests

Traits recording: disease resistance, infectivity, symptoms, survival at harvest and body weight with over 5,000 observations each generation

Genomic analysis: 12 individual per family of low (20) and high (20) resistance to disease were available

Genotype imputation: we use low density sequencing and imputing to missing genotype using siblings and parental genotypes.

Methodology: Multi-trait deep learning approach, with Bayesian and Single step genomic framework

Striped catfish (*Pangasianodon hypophthalmus*) is the most important freshwater fish for aquaculture in Mekong Delta of Vietnam

Breeding scheme to improve disease resistance in striped catfish

Striped catfish accounted 2 – 4% of total GDP; total value of 1.8 billion SU Sin 2017.

3. STATISTIC ANALYSIS

The mathematical equation used to analyse the disease resistance (1) and growth traits at harvest (2) were:

(1) $y_{ijk} = \mu + \beta_1 \times$ tagged weight$_i$ + tank$_j$ + fish$_k$ + e_{ijk}

(2) $y_{ijk} = \mu +$ batched state + $\beta_1 \times$ age$_{ijk}$ + fish$_j$ + class$_k$ + e_{ijk}

The variance components obtained from bivariate model were used to calculate heritability, genetic correlation for traits studied.

4. RESULTS

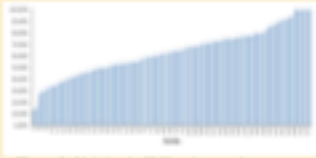
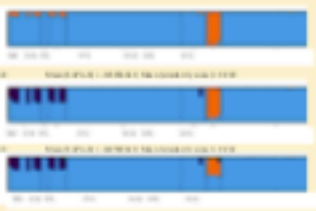


Figure 1: Variation in BNP resistance phenotypes among 177 families studied

Trait	σ_a^2	σ_c^2	σ_e^2	σ^2 / σ_a^2	σ^2 / σ_e^2
Resistance (survival)					
linear model	0.08	-	0.17	0.25	0.04 ± 0.02
high model	0.76	-	1.00	1.76	0.02 ± 0.02
poisson model	0.28	-	1.00	1.28	0.02 ± 0.02
Resistance (healthy)					
linear model	0.03	-	0.0017	0.0103	0.15 ± 0.02
high model	-	-	-	-	-
poisson model	-	-	-	-	-
Disease survival					
linear model	0.08	-	0.04	0.04	0.14 ± 0.02
high model	0.47	-	1.00	1.47	0.02 ± 0.02
poisson model	0.17	-	1.00	1.17	0.02 ± 0.02
Harvest weight	17000	10117	30100	60070	0.17 ± 0.10

σ_a^2 = additive genetic variance; σ_c^2 = common environmental effect variance; σ_e^2 = residuals variance; σ^2 = phenotypic variance; σ^2 = variability; σ^2 = common environmental effect of separately rearing; σ^2 = standard error.

Figure 2: Variance components, heritability (σ^2) and common full-sib effects (σ^2) for BNP resistance and growth traits in striped catfish (estimated using different statistical models).



MAIN FINDINGS SO FAR

We reported genetic parameters for BNP resistance in striped catfish that are of practical significance for this species. Our main findings included heritability for BNP resistance, genetic correlations between BNP resistance and growth performance. There is abundant genetic variation in BNP resistance in Tra catfish with the heritability estimate ranging from 0.10 to 0.43, indicating that there are great prospects to improve this trait through genetic selection. The genetic correlations of BNP resistance with growth traits were moderate and positive (0.25 – 0.29), giving possibilities for improving both traits simultaneously. We also found one wild population from Thailand which had distinct genetic characteristic and is valuable genetic resource for genetic improving program.

GENOMIC STUDIES

Future genomic studies have three main aims: i) to identify genes or SNP associated with BNP disease; ii) increase the accuracy of breeding value estimation; and iii) to build up a linkage map in striped catfish.

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