



Genomic evaluation for harvest and residual carcass weight in channel catfish using single-step genomic BLUP

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Introduction

- Harvest weight: 0.8 to 1 kg
- Sexual maturity between 2 and 3 years old
- Spawning season in the Spring/Summer
- About 20,000 eggs/year
- Channel catfish (Ictalurus punctatus)
- Blue catfish (Ictalurus furcatus)
- Hybrid



Breeding program

- USDA Warmwater Aquaculture Research Unit
- Pedigree based evaluation since 2006 (Harvest weight and carcass yield)
- Genotypes available early 2017

Genomic selection

- Increases accuracy
- Reduces generation interval
- Explore within family variation

Objectives

- Investigate feasibility of implementing genomic selection by using ssGBLUP
- Identify major SNP associated with harvest weight and residual carcass weight

Material and Methods

<u>Data</u>

- USDA-ARS Warmwater Aquaculture Research Unit
- Records from 2008 to 2015
- Pedigree information: 36,365 animals
- Harvest weight (HW): 27,160 records (h²= 0.27)
- Residual carcass weight (RCW)*: 6,020 records (h²= 0.34)
- * Carcass weight adjusted to a common body weight

Genotypes

- 55k panel developed by the USDA Warmwater Aquaculture Research Unit
- 2,911 genotyped animals
 2,826 with harvest weight records
 969 with carcass weight records
- 54k SNP after quality control

Single-step GBLUP (ssGBLUP)

- Includes all animals
- Combines genotypes, phenotypes and pedigree
- Integrated genomic/pedigree relationship matrix (H)

$$\begin{bmatrix} X'X & X'Z \\ Z'X & Z'Z + H^{-1}\lambda \end{bmatrix} \begin{bmatrix} \beta \\ a \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \end{bmatrix}$$

$$\mathbf{H}^{-1} = \mathbf{A}^{-1} + \begin{bmatrix} 0 & 0 \\ 0 & \mathbf{G}^{-1} - \mathbf{A}_{22}^{-1} \end{bmatrix}$$

- A = pedigree relationship matrix
- A₂₂ = pedigree relationship matrix for genotyped animals
- G = genomic relationship matrix

•
$$\lambda = \frac{\sigma_e^2}{\sigma_a^2}$$

Validation Study

Validation

- Method to compare traditional and genomic evaluation
- ✓ Adjusted phenotypes based on complete data (\hat{Y})
- ✓ 5-fold cross validation
- ✓ 10-fold cross validation
- Genotyped animals randomly divided in 5/10 mutually exclusive groups
- 5 replicates



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• BLUP and ssGBLUP performed using BLUPF90 family of programs

✓ Predictive ability: ability to predict future performance $cor((G)EBV, \hat{Y})$

✓Accuracy: $acc = \frac{predictive ability}{\sqrt{h^2}}$

✓ Inflation: b1<1.0

$$\hat{Y}c = b_0 + b_1 \times (G)EBV$$

✓ Updated variance components

Results 5-Folds Cross Validation

Predictive Ability



Accuracy





Is it important to genotype processed fish?

- Remove phenotypes only for genotyped animals
- New validation data set
- Calculate predictive ability and accuracy
- Compare BLUP and ssGBLUP

Predictive Ability for RCW



Accuracy for RCW



Weighted ssGBLUP Study

Weighted ssGBLUP

• Iterative process

1.
$$D = I$$

2. $G = \frac{ZDZ'}{2\Sigma p_i(1-p_i)}$

- 3. GEBV from ssGBLUP
- 4. $\hat{u} = \delta DZ'G^{-1}\hat{a}$
- 5. $d_i = \hat{u}_i^2 2p_i(1-p_i)$
- 6. Iterate from 2

- G = genomic relationship matrix
- $\lambda = \frac{\sigma_e^2}{\sigma_a^2}$ • $\delta = \frac{\sigma_u^2}{\sigma_a^2}$
 - D = diagonal matrix for SNP weights
- Z = matrix of SNP markers centered for current allele frequencies
- u = SNP effect
- d_i = Weight for SNP markers
- p_i = allele frequency

Variance explained by 20 adjacents SNP



• 2.2% at most

Variance explained by 20 adjacents SNP



• 3.3% at most

• Genomic information improved ability to predict future performance

• Estimated variance components for training data sets reduced inflation

• It is important to genotype processed fish for carcass traits

• No major SNP were found in both traits, indicating the need of using all the markers available for evaluation purposes

Acknowledgements





Thank you!

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