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

Data

• USDA-ARS Warmwater Aquaculture Research Unit
• Records from 2008 to 2015

• Pedigree information: 36,365 animals
• Harvest weight (HW): 27,160 records ($h^2 = 0.27$)
• Residual carcass weight (RCW)*: 6,020 records ($h^2 = 0.34$)

* 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)

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

\[
H^{-1} = A^{-1} + 
\begin{bmatrix}
0 & 0 \\
0 & G^{-1} - A_{22}^{-1}
\end{bmatrix}
\]

- A = pedigree relationship matrix
- \(A_{22}\) = 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
• BLUP and ssGBLUP performed using BLUPF90 family of programs

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

✓ Accuracy:
\[ \text{acc} = \frac{\text{predictive ability}}{\sqrt{h^2}} \]

✓ Inflation: b1<1.0
\[ \hat{Y}c = b_0 + b_1 \times (G)EBV \]

✓ Updated variance components
Results
5-Folds Cross Validation
Predictive Ability

- Harvest Weight
  - Same Var. Components: 0.29
  - Updated Var. Components: 0.29

- Harvest Weight
  - Same Var. Components: 0.37
  - Updated Var. Components: 0.37

- Residual Carcass Weight
  - Same Var. Components: 0.24
  - Updated Var. Components: 0.24

- Residual Carcass Weight
  - Same Var. Components: 0.31
  - Updated Var. Components: 0.31

Legend:
- BLUP
- ssGBLUP
Accuracy

- Harvest Weight
  - Same Var. Components: 0.55
  - Updated Var. Components: 0.64
- Harvest Weight
  - BLUP (Updated Var. Components): 0.80
- Residual Carcass Weight
  - Same Var. Components: 0.42
- Residual Carcass Weight
  - Updated Var. Components: 0.43

Comparison between BLUP and ssGBLUP for different weight components.
The graph shows the inflation of Harvest Weight and Residual Carcass Weight for both Same Var. Components and Updated Var. Components, using BLUP (blue) and ssGBLUP (orange) methods.

- Harvest Weight:
  - Same Var. Components: 0.87 (BLUP), 0.92 (ssGBLUP)
  - Updated Var. Components: 0.97 (BLUP), 1.00 (ssGBLUP)

- Residual Carcass Weight:
  - Same Var. Components: 0.80 (BLUP), 0.91 (ssGBLUP)
  - Updated Var. Components: 0.89 (BLUP), 0.94 (ssGBLUP)
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

<table>
<thead>
<tr>
<th>5-Fold Cross Validation</th>
<th>No phenotypes for genotyped animals</th>
</tr>
</thead>
<tbody>
<tr>
<td>BLUP</td>
<td>ssGBLUP</td>
</tr>
<tr>
<td>0.24</td>
<td>0.22</td>
</tr>
<tr>
<td>0.31</td>
<td>0.24</td>
</tr>
</tbody>
</table>

No phenotypes for genotyped animals
Accuracy for RCW

5-Fold Cross Validation

- BLUP: 0.42
- ssGBLUP: 0.53

No phenotypes for genotyped animals

- BLUP: 0.38
- ssGBLUP: 0.41
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
• \( \lambda = \frac{\sigma^2_e}{\sigma^2_a} \)
• \( \delta = \frac{\sigma^2_u}{\sigma^2_a} \)
• \( D = \) 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

Proportion of variance explained

SNPs

• 2.2% at most
• 3.3% at most
Conclusions

• 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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