

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

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## 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)

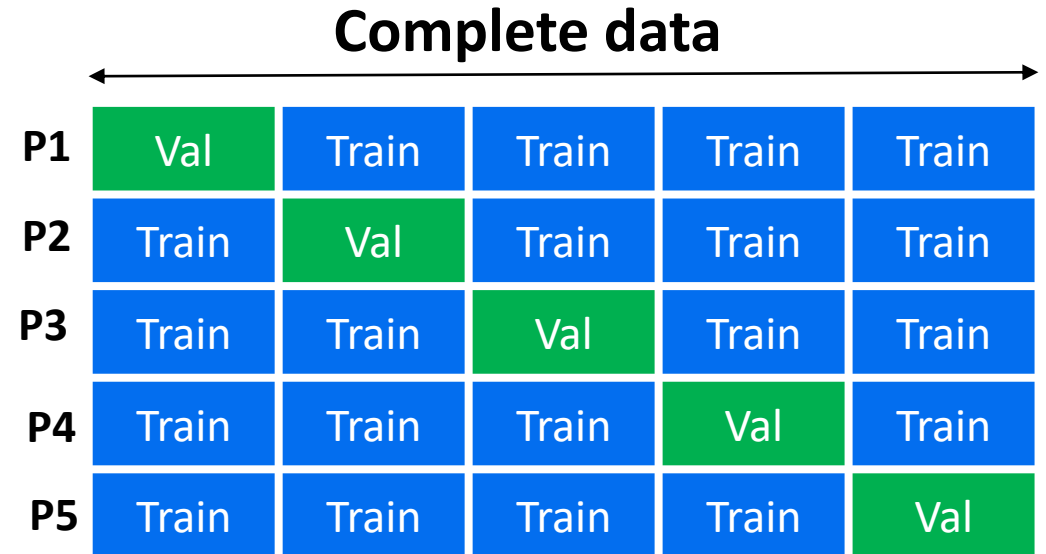
$$\begin{bmatrix} X'X & X'Z \\ Z'X & Z'Z + H^{-1}\lambda \end{bmatrix} \begin{bmatrix} \beta \\ a \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \end{bmatrix}$$

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

- A = pedigree relationship matrix
- $A_{22}$  = pedigree relationship matrix for genotyped animals
- G = genomic relationship matrix
- $\lambda = \sigma_e^2 / \sigma_a^2$

## 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

$$\text{cor}((G)EBV, \hat{Y})$$

- ✓ Inflation:  $b_1 < 1.0$

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

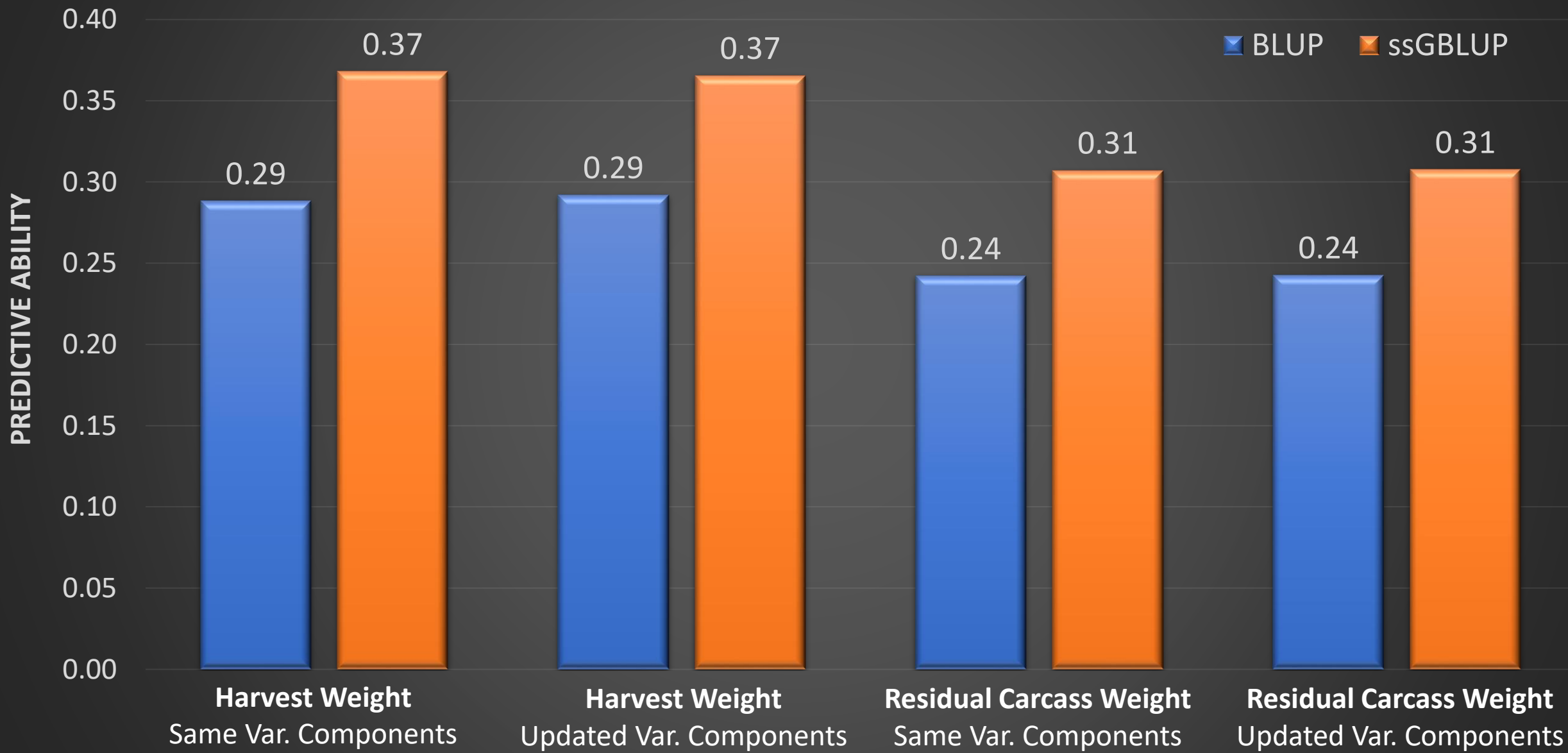
- ✓ Updated variance components



# Results

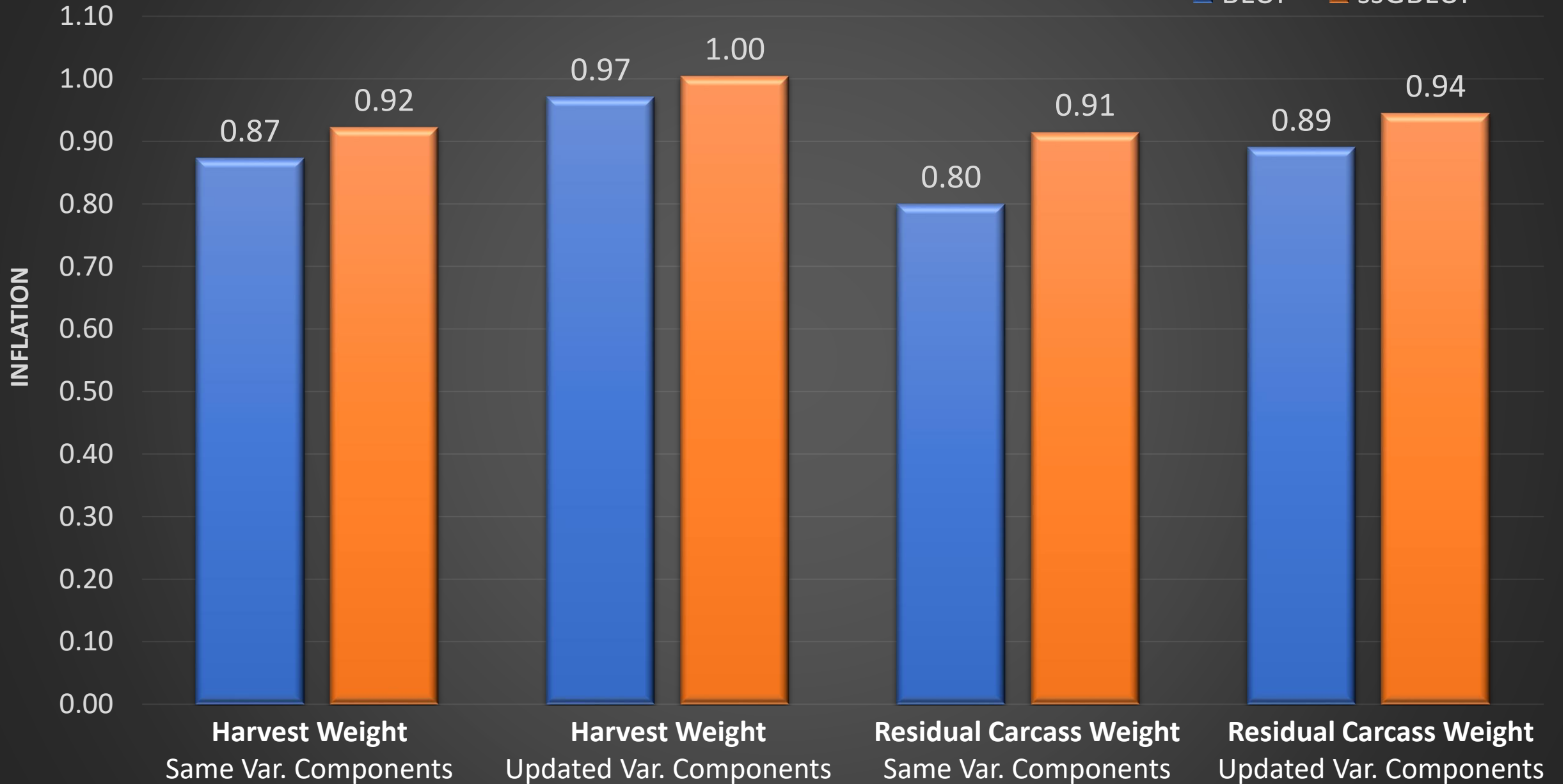
## 5-Folds Cross Validation

# Predictive Ability



# Inflation

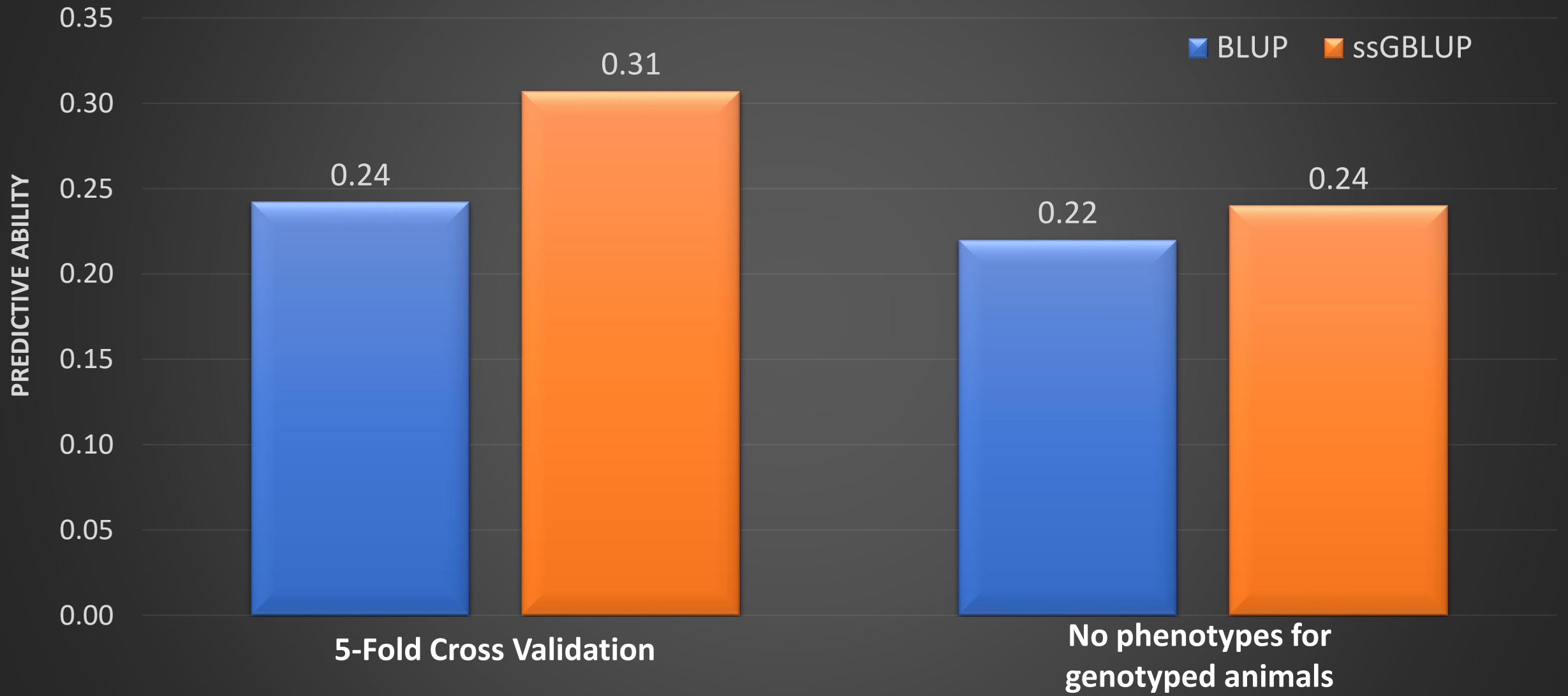
BLUP ssGBLUP



## Is it important to genotype processed fish?

- Remove phenotypes only for genotyped animals
- New validation data set

# Predictive Ability for RCW



## Weighted ssGBLUP

- Iterative process

1.  $D = I$

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

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

- $\lambda = \sigma_e^2 / \sigma_a^2$

- $\delta = \sigma_u^2 / \sigma_a^2$

- $D$  = diagonal matrix for SNP weights

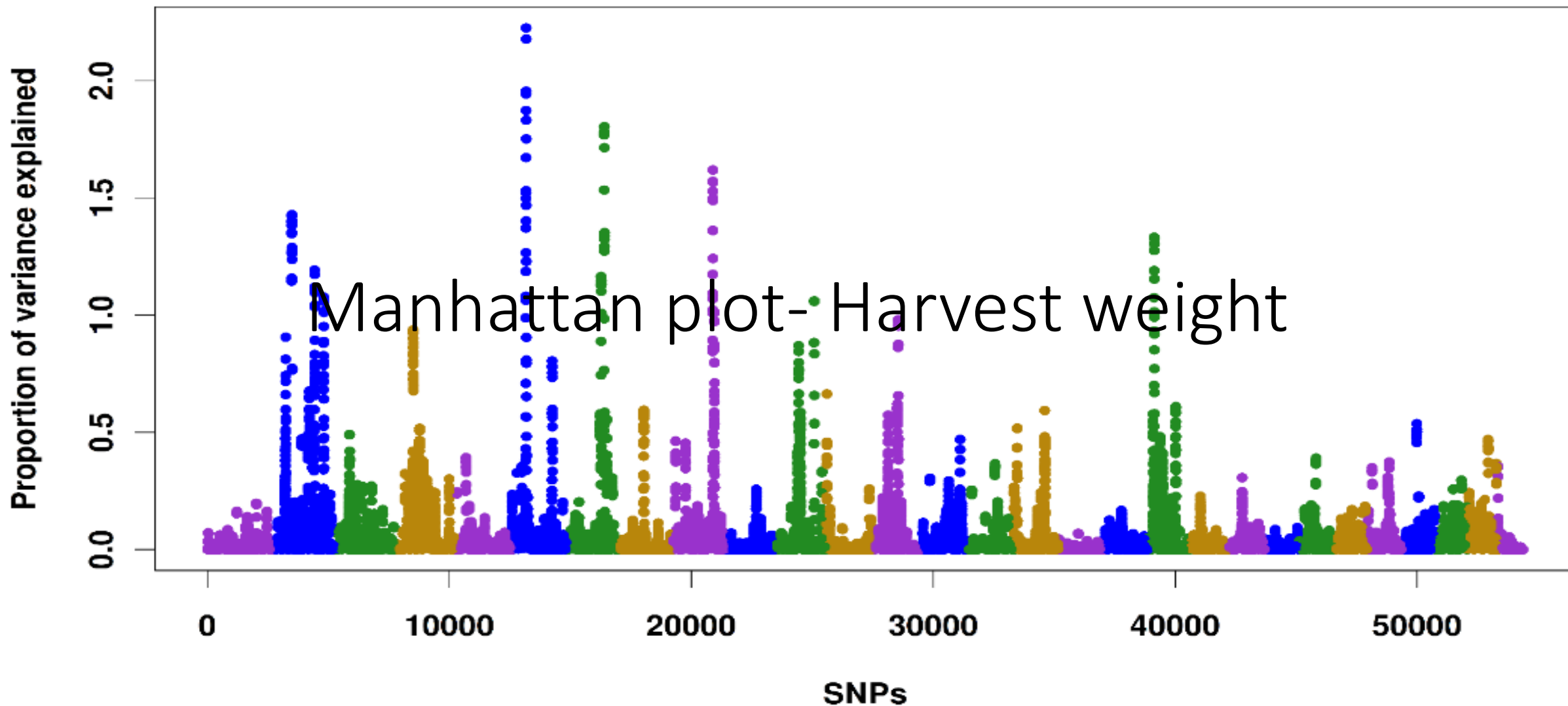
- $Z$  = matrix of SNP markers centered for current allele frequencies

- $u$  = SNP effect

- $d_i$  = Weight for SNP markers

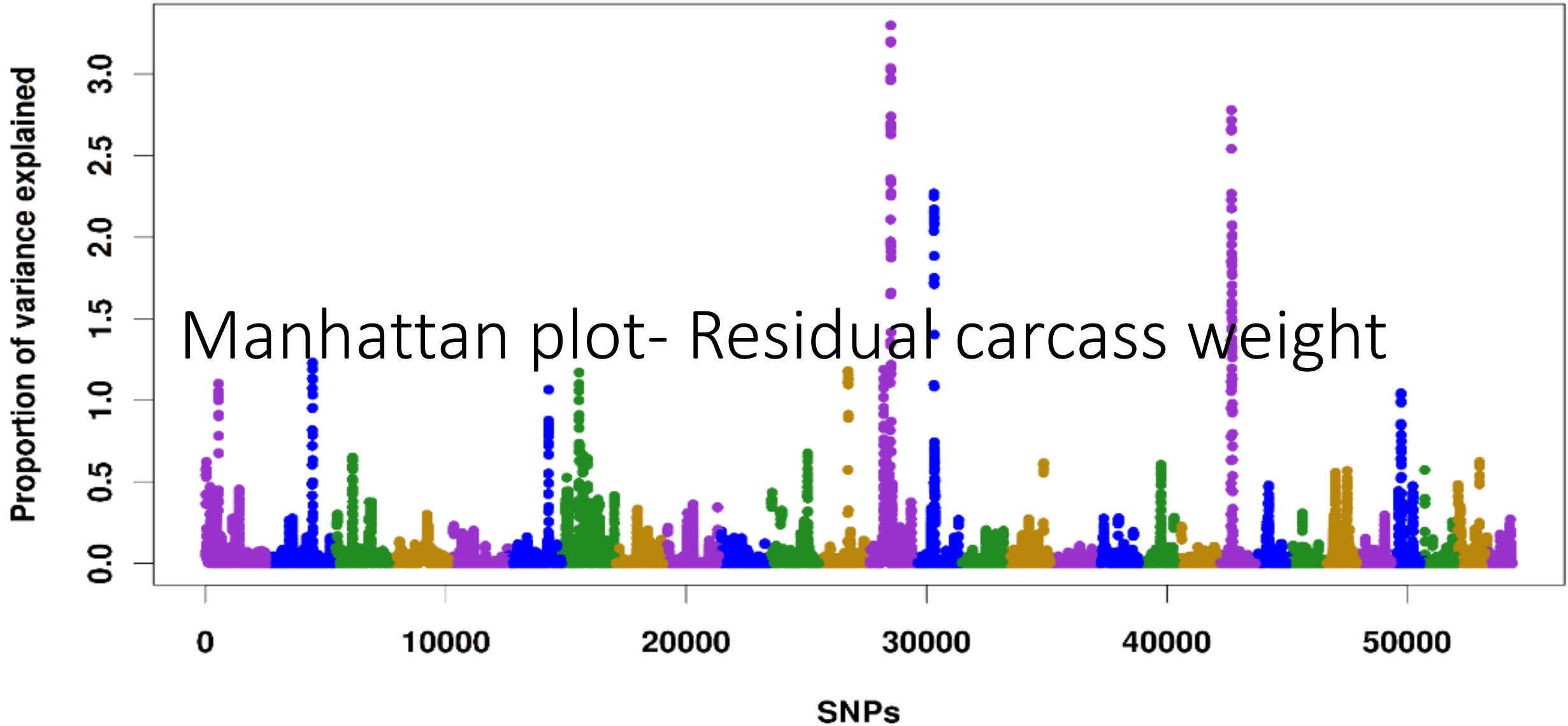
- $p_i$  = allele frequency

### Variance explained by 20 adjacent SNP



- 2.2% at most

# Variance explained by 20 adjacent SNPs



- 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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