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

<u>Objectives</u>

- 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

<u>Genotypes</u>

- 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
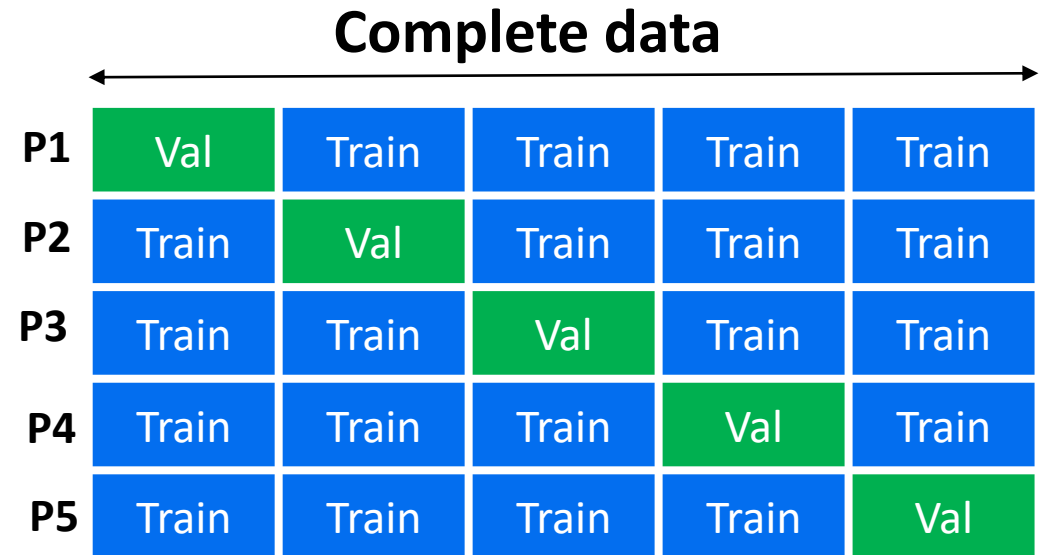- Integrated genomic/pedigree relationship matrix (H)

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

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

- 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

Complete data

P1 Val	Train	Train	Train	Train
P2 Train	Val	Train	Train	Train
P3 Train	Train	Val	Train	Train
P4 Train	Train	Train	Val	Train
P5 Train	Train	Train	Train	Val

- BLUP and ssGBLUP performed using BLUPF90 family of programs

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

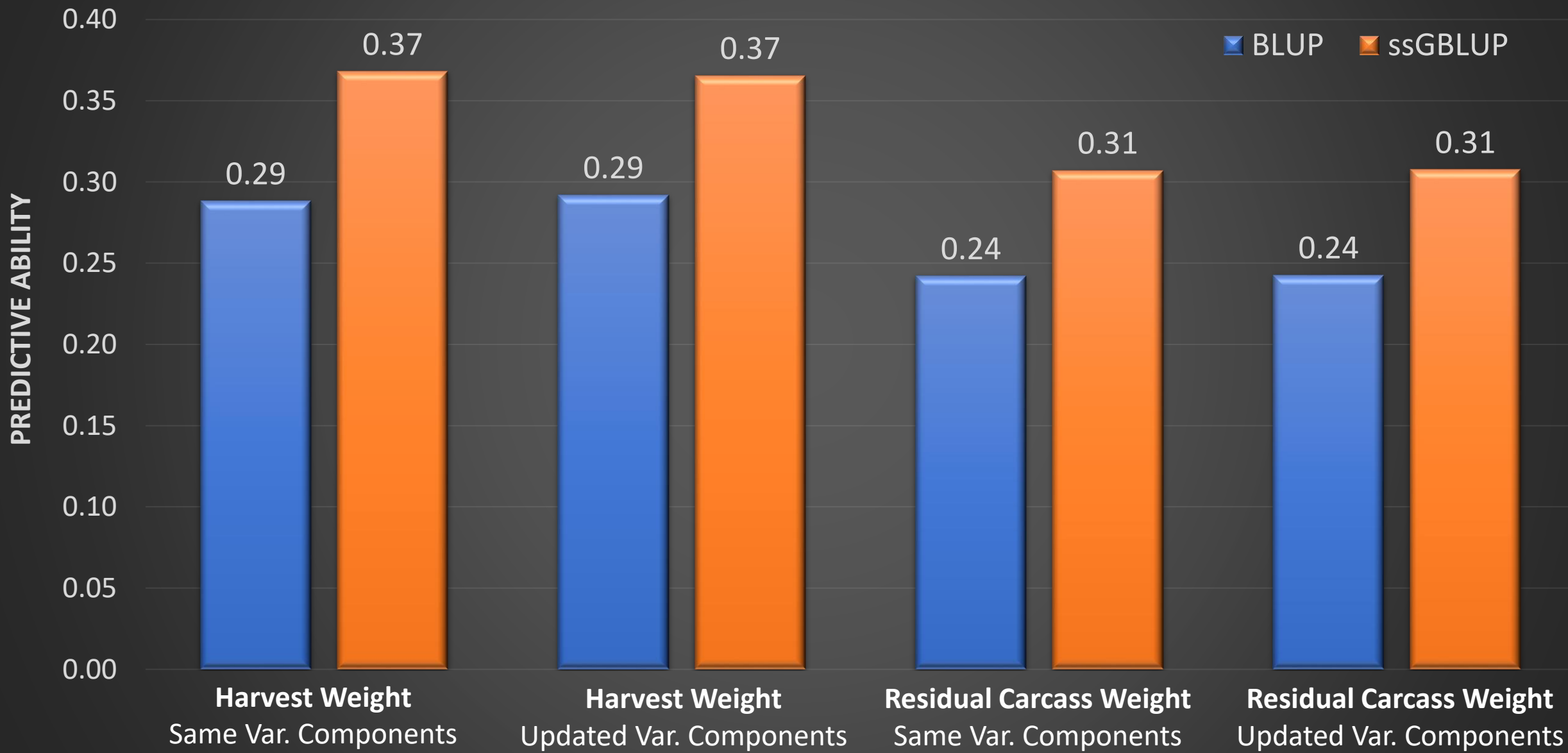✓ Inflation: b1<1.0

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

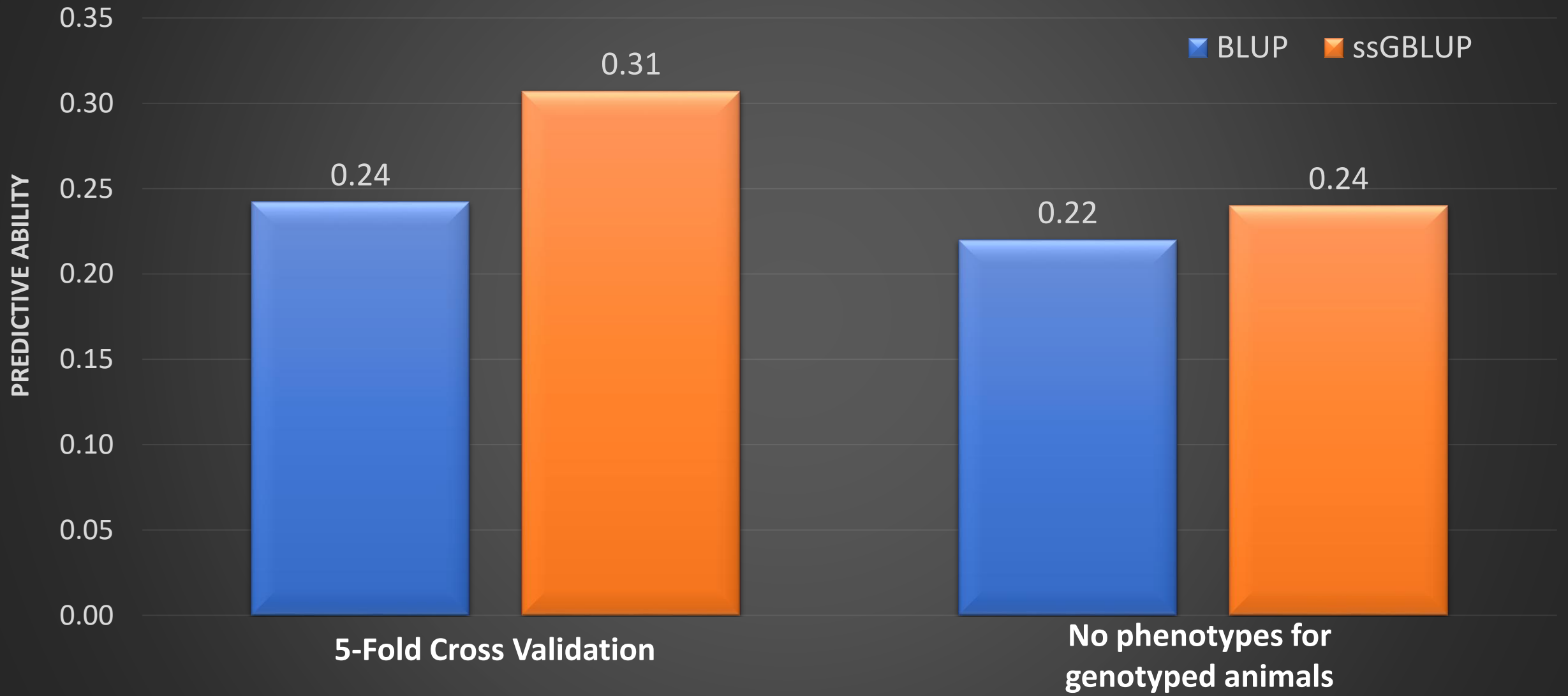✓ Updated variance components

Results
5-Folds Cross Validation

Inflation
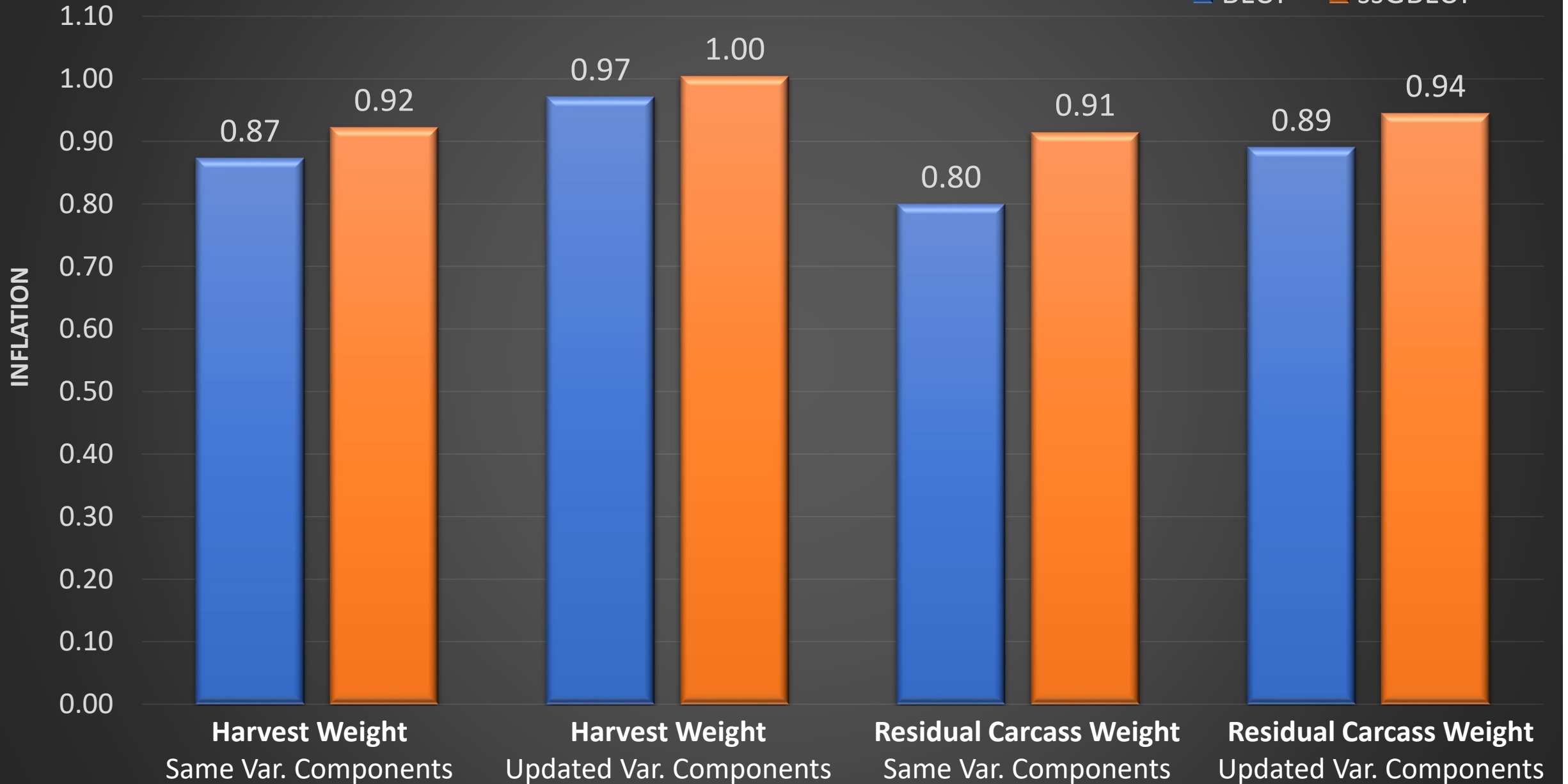
Is it important to genotype processed fish?

- Remove phenotypes only for genotyped animals

- New validation data set

Predictive Ability for RCW

Weighted ssGBLUP

- Iterative process

1. D = I

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

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
- $\lambda = \sigma_e^2 / \sigma_a^2$
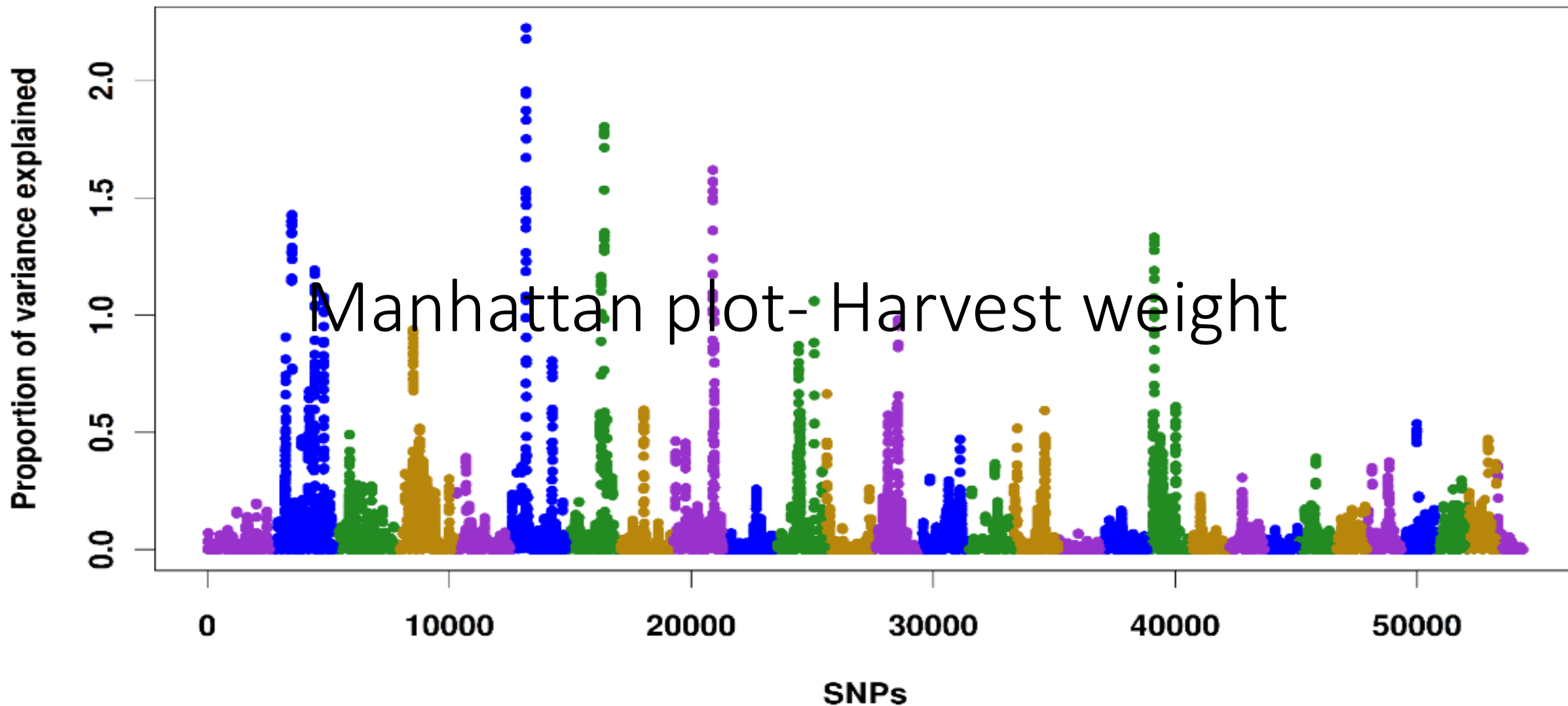- $\delta = \sigma_u^2 / \sigma_a^2$
- D = diagonal matrix for SNP weights
- Z = matrix of SNP markers centered for current allele frequencies
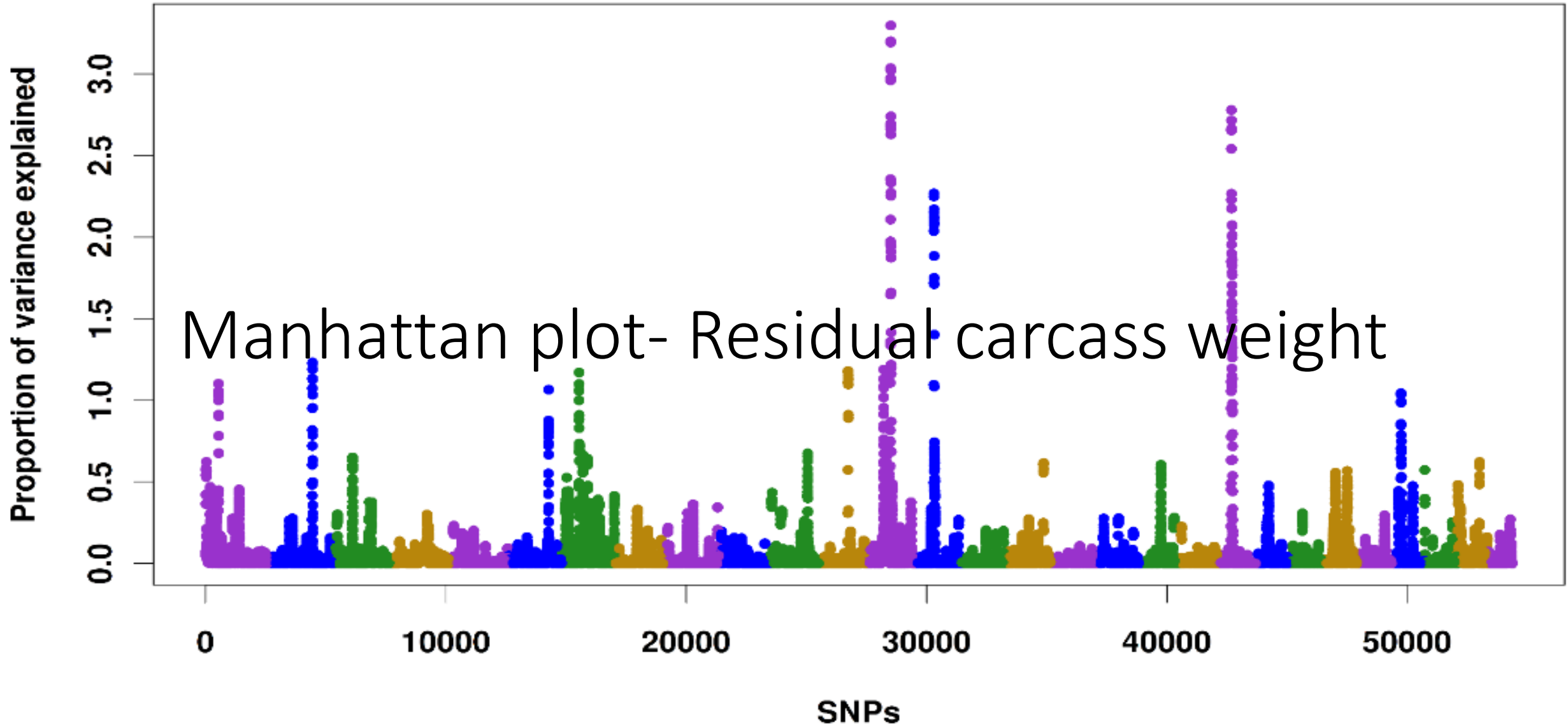- u = SNP effect
- d_i = Weight for SNP markers
- p_i = allele frequency

Variance explained by 20 adjacents SNP

Manhattan plot- Harvest weight

- 2.2% at most

16

Variance explained by 20 adjacents SNP

Manhattan plot- Residual carcass weight

- 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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