



PLANT & ANIMAL
GENOME



GWAS for Detecting QTL Associated with Columnaris Disease in Two Rainbow Trout Breeding Populations

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Introduction

- **Parasites and disease - (NASS, 2017)**
- ***Columnaris* disease - CD (*Flavobacterium columnare*)**
 - ✓ Affects both cultured and wild freshwater fish of all ages
 - ✓ High mortality
 - ✓ Economic loss
 - ✓ Horizontal transmission



<https://columbusaudubon.org/invasive-species-rainbow-trout/>



LaFrentz et al., 2012 Declercq et al., 2013

Introduction

- **Control of infectious diseases**

- **Antibiotic**

- **Vaccine**

- High cost of vaccines

- Efficiency not clear in rainbow trout

- **Genetic Selection**

- ✓ Traditional genetic improvement

- ✓ Genomic information

- ✓ More accurate genomic evaluation

- ✓ QTLs

Objectives

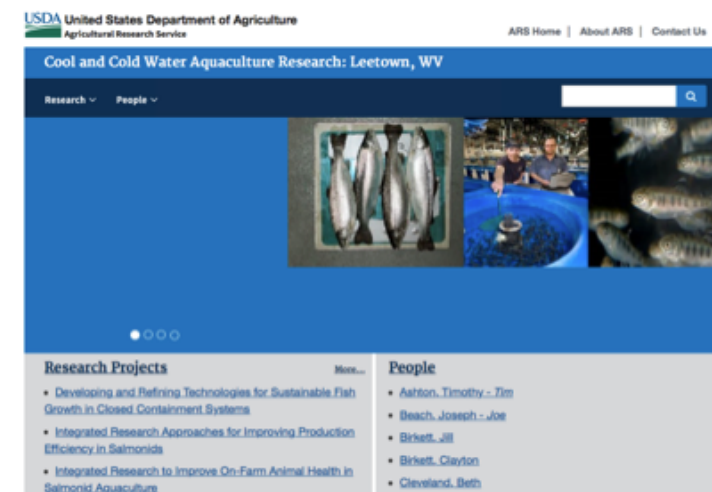
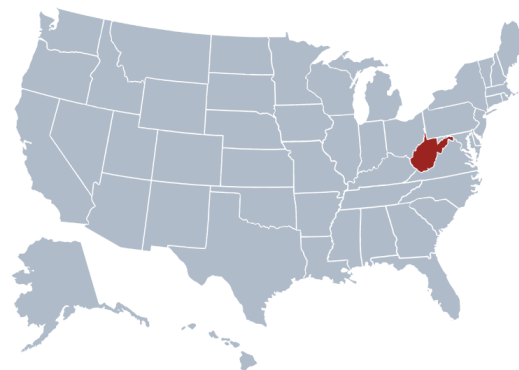
- Explore, understand and compare the genetic architecture of CD resistance in two rainbow trout breeding populations
- Prospect genomic regions that explain large proportion of the additive genetic variance of CD resistance



Material and Methods

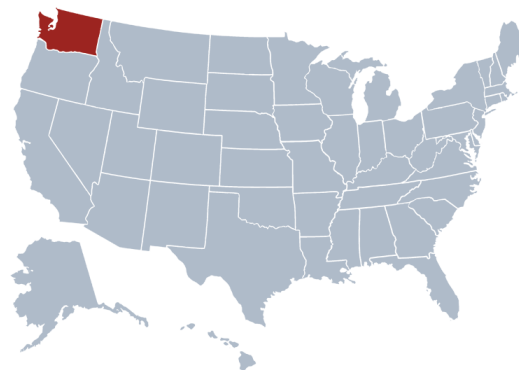
- National Center of Cool and Cold Water Aquaculture (NCCCWA)

- Leetown, West Virginia



- Troutlodge, Inc. (TLUM)

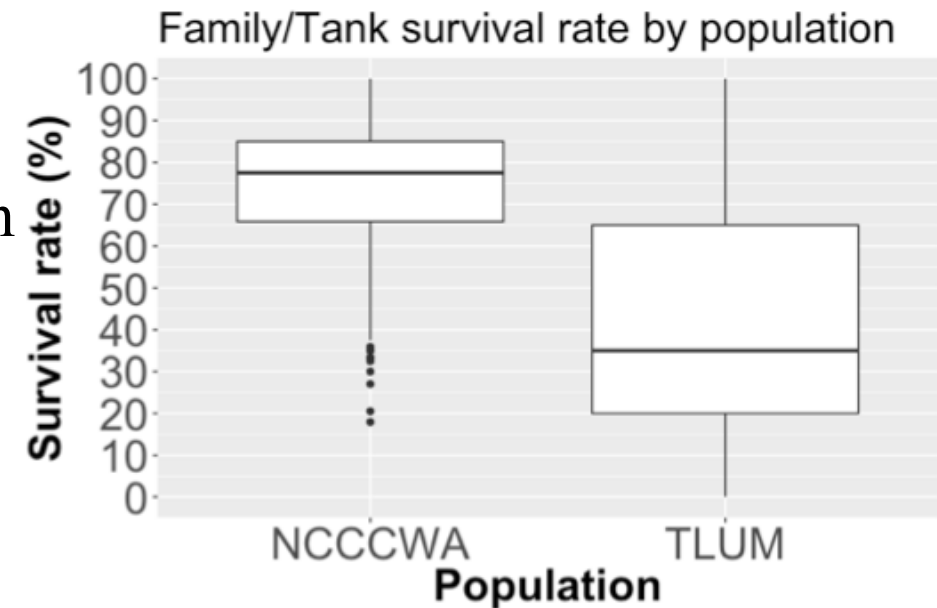
- Sumner, WA



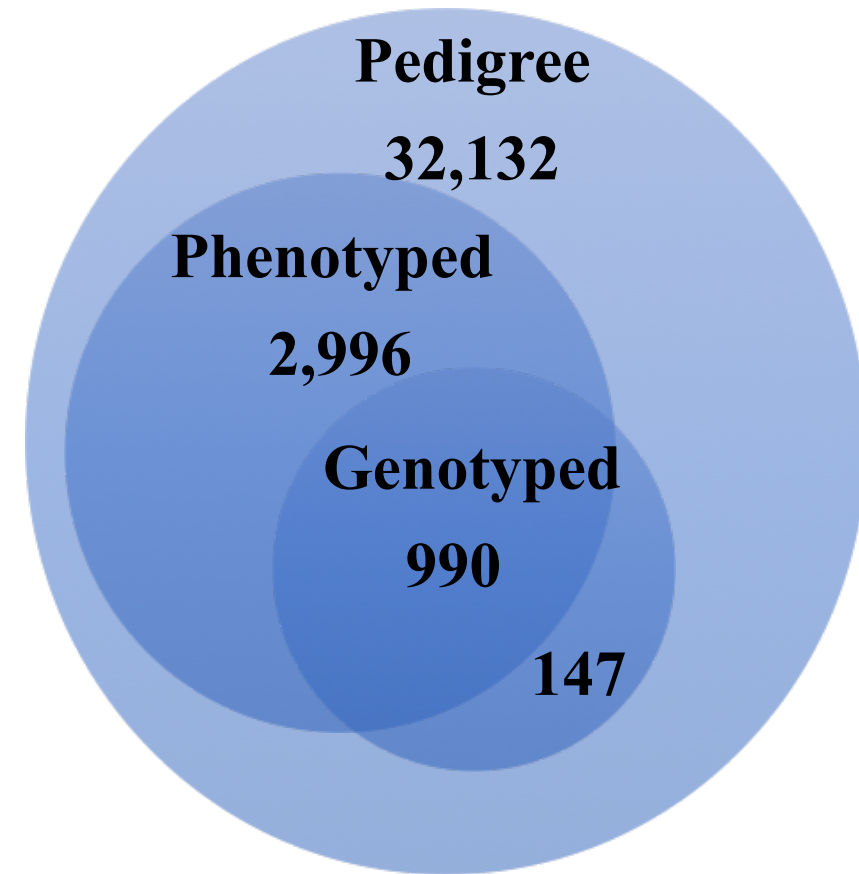
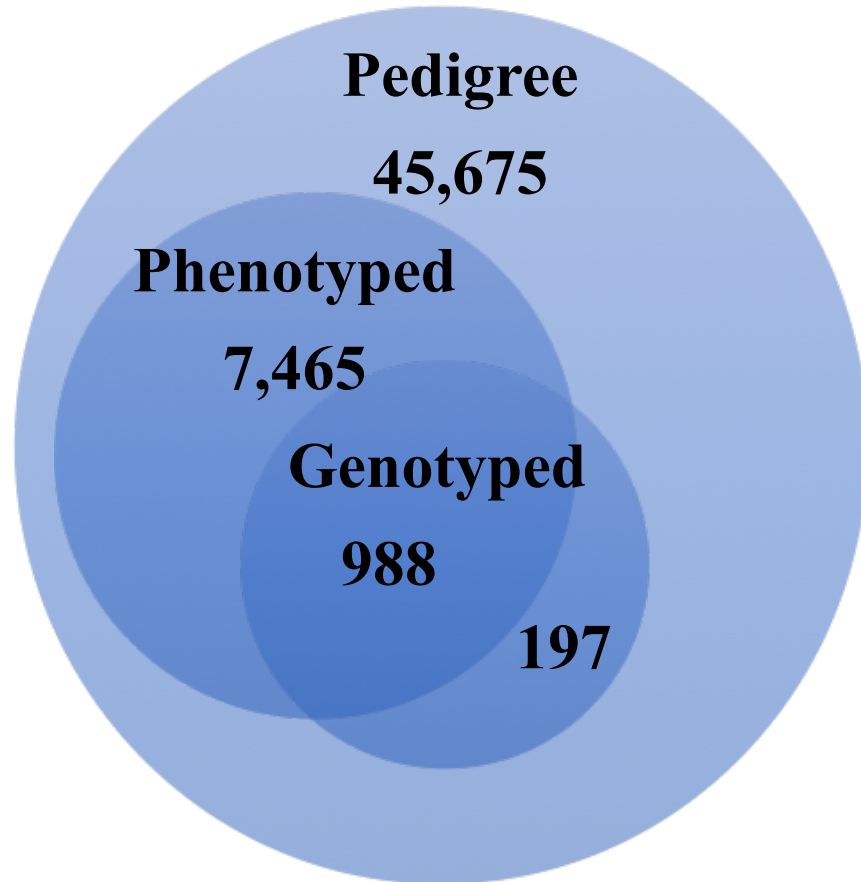
Material and Methods

Disease resistance phenotypes

- Disease challenges were conducted at the USDA, ARS, NCCCWA
- Bath challenge
- *F. Columnaris* strain CSF298-10 (Evenhuis *et al.*, 2014)
- Binary survival status (STATUS)
 - 1= fish died during the 21 d post-challenge evaluation
 - 2= fish was alive on day 22 post-challenge



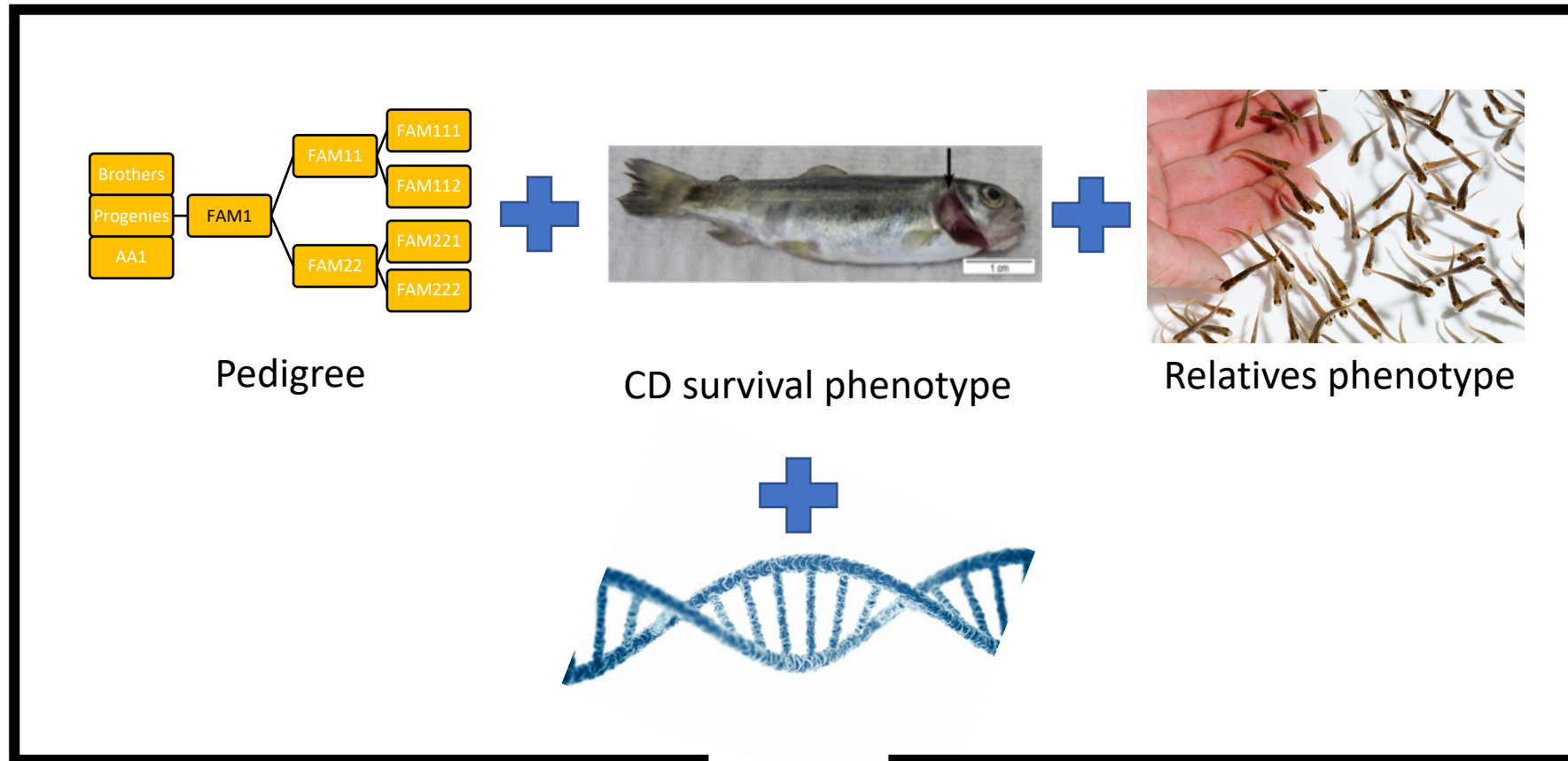
Data



Genotypes

- Genotypes for 57k SNP (Affymetrix Axiom®)

Weighted Single Step Genome Wide Association- WssGWAS



Genomic estimated breeding value (GEBV)

Weighted Single Step Genome Wide Association- WssGWAS

1) SNP/Sample quality control

- allele freq > 0.05
- call rate SNP > 0.90
- call rate sample > 0.90



35,900 SNPs
1,185 fish



33,980 SNPs
1,136 fish

Weighted Single Step Genome Wide Association- WssGWAS

1) SNP/Sample quality control

2) Compute genomic estimated breeding value (GEBV) using ssGBLUP:

➤ Aguilar et al., 2010:

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

$$\mathbf{G} = \frac{\mathbf{Z}\mathbf{Z}'}{2 \sum p_i(1 - p_i)}$$

Weighted Single Step Genome Wide Association- WssGWAS

➤ Threshold model:

$$\mathbf{I} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\mathbf{a} + \mathbf{W}\mathbf{f} + \mathbf{e}$$

\mathbf{I} is the vector of underlying distribution of CD resistance

$\boldsymbol{\beta}$ is the vector of systematic effects (system and row)


\mathbf{a} is the vector of random additive direct genetic effects

\mathbf{f} is a vector of random tank/family effect

\mathbf{e} is the vector of random residuals

\mathbf{X} , \mathbf{Z} , and \mathbf{W} are the incidence matrices for the effects contained in $\boldsymbol{\beta}$, \mathbf{a} , and \mathbf{f} , respectively

Weighted Single Step Genome Wide Association- WssGWAS

- 1) SNP/Sample quality control
 - 2) Compute genomic estimated breeding value (GEBV) using ssGBLUP:
 - 3) Compute SNP effects based on GEBV
 - 4) Calculate SNP weight (W)
 - 5) Use the weights to construct the genomic relationship matrix as:
- 

$$\mathbf{G}^* = \frac{\mathbf{Z}\mathbf{W}\mathbf{Z}'}{2 \sum p_i(1 - p_i)}$$

Weighted Single Step Genome Wide Association- WssGWAS

- Percentage of variance explained by 1Mb length size moving windows

$$\frac{\text{Var}(a_i)}{\sigma_a^2} \times 100\% = \frac{\text{Var}(\sum_{j=i}^x Z_j \hat{u}_j)}{\sigma_a^2} \times 100\%$$

a_i is genetic value of the i^{th} region

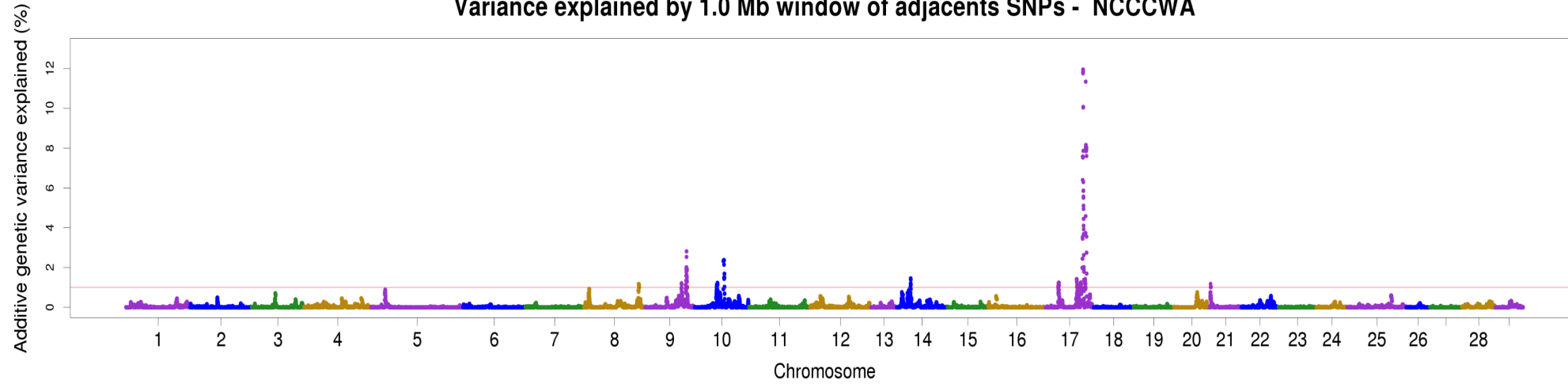
σ_a^2 is the total genetic variance

Z_j is vector of SNP content of the j -th SNP for all individuals

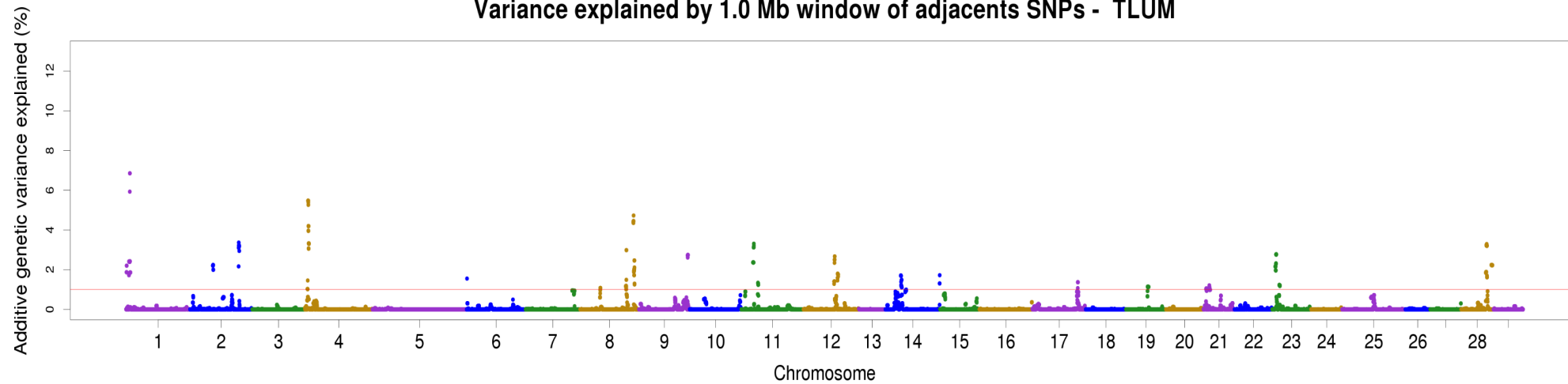
\hat{u}_j is marker effect of the j -th within the i -th region

Results

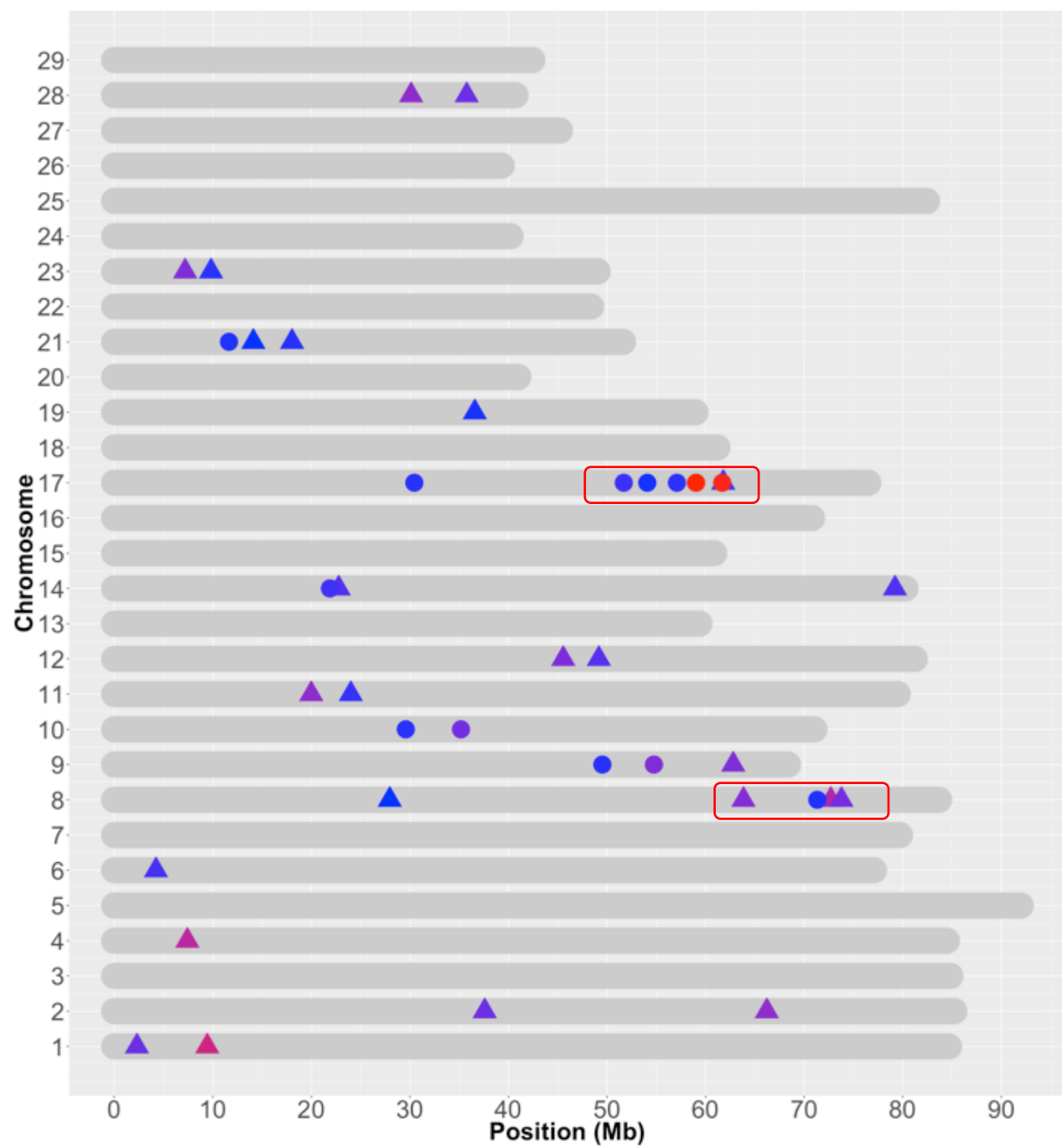
Variance explained by 1.0 Mb window of adjacent SNPs - NCCCWA



Variance explained by 1.0 Mb window of adjacent SNPs - TLUM



Var explained by 1Mb SNP Window (%) ■ 3 ■ 6 ■ 9 Population ● NCCCWA ▲ TLUM



SNP Windows that explained more than **1%** of the additive genetic variance.



A total of 13 associated windows located on six chromosomes



A total of 25 associated windows located on 13 chromosomes

Discussion

- Selective pressure for different purposes might have contributed to detecting different genomic regions associated with CD resistance in the two populations.
- BCWD and CD resistance can be simultaneously improved, genetic correlation between these traits 0.35 ± 0.25 (Evenhuis et al., 2015)
- CD resistance $h^2=0.18\pm0.07$, $h^2=0.35\pm0.09$ for USDA's and TLUM's population, respectively.
- Genes possibly fixed due to genetic selection
- Small population is hard to estimate the SNP effect precisely
- Overlapping windows

Conclusion

- Columnaris disease has a polygenic architecture
 - small/moderate effect QTLs were detected
- The SNP windows found to be associated with CD do not explain a proportion of variance large enough for choosing marker assisted selection (MAS) instead of genome-wide selection (GS)
- Few overlapping windows regions should not be used for selection decisions across populations



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