Genomic selection in American chestnut backcross populations

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Selection against blight susceptibility in seed orchards

Artificially inoculate stems at age two with slightly pathogenic strain of *C. parasitica*

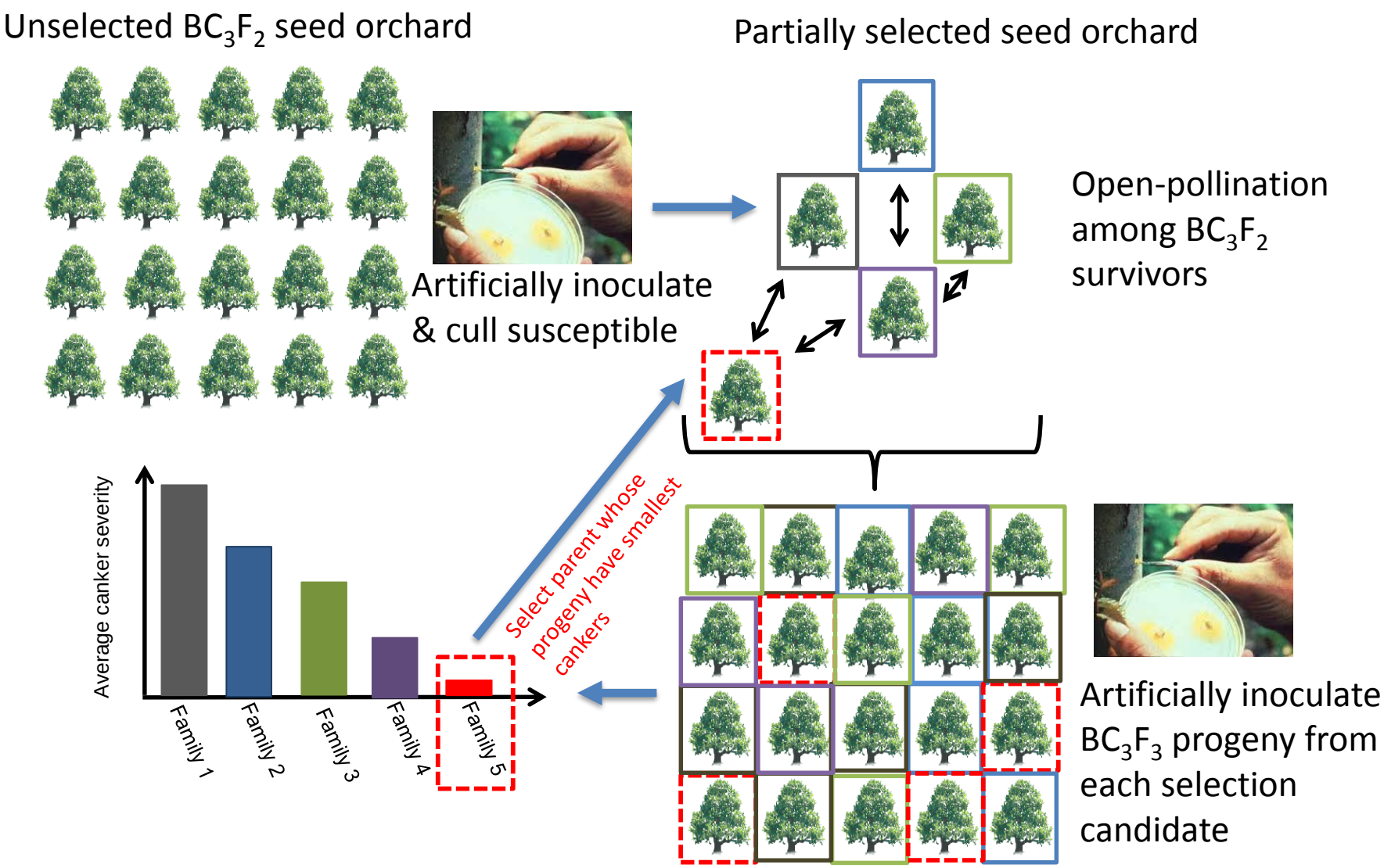
= **Genes** + Environment

Progress of selection in Meadowview seed orchards

	Clapper	Graves
N (%) trees planted	36,000 (100%)	25,000 (85%)
N trees remaining	3297	2244

Steve Hoy (PA Chapter) helped with removal of 2600 BC3-F2s from Meadowview seed orchards in 2017

Progeny testing has begun on BC_3F_2 trees that remain after initial culling



Progeny testing is too slow to finish selection for blight resistance

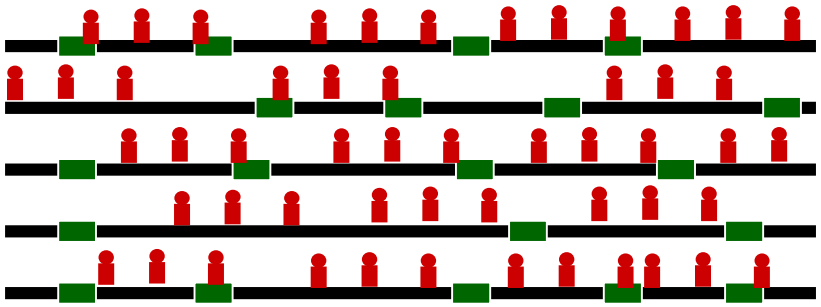
Meadowview breeding program

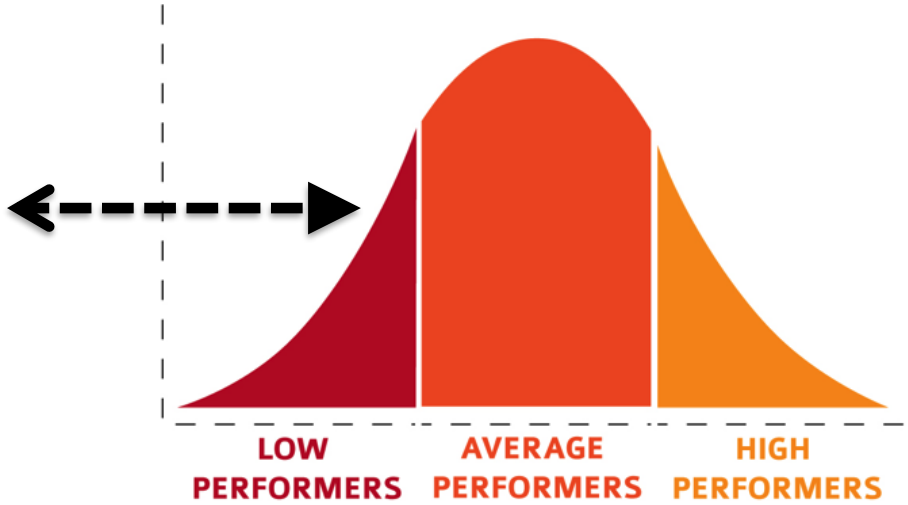
	Clapper	Graves
Number BC_3F_2 trees remaining	3200	2200
N BC_3F_2 parents progeny tested 2009-2017	300	300
N BC_3F_2 to select	300	300

N trees remaining after selection based on canker size >> N trees progeny tested

Genomic selection alleviates the need to progeny test all trees that remain after phenotypic selection

Variation in disease resistance in BC_3F_2 populations



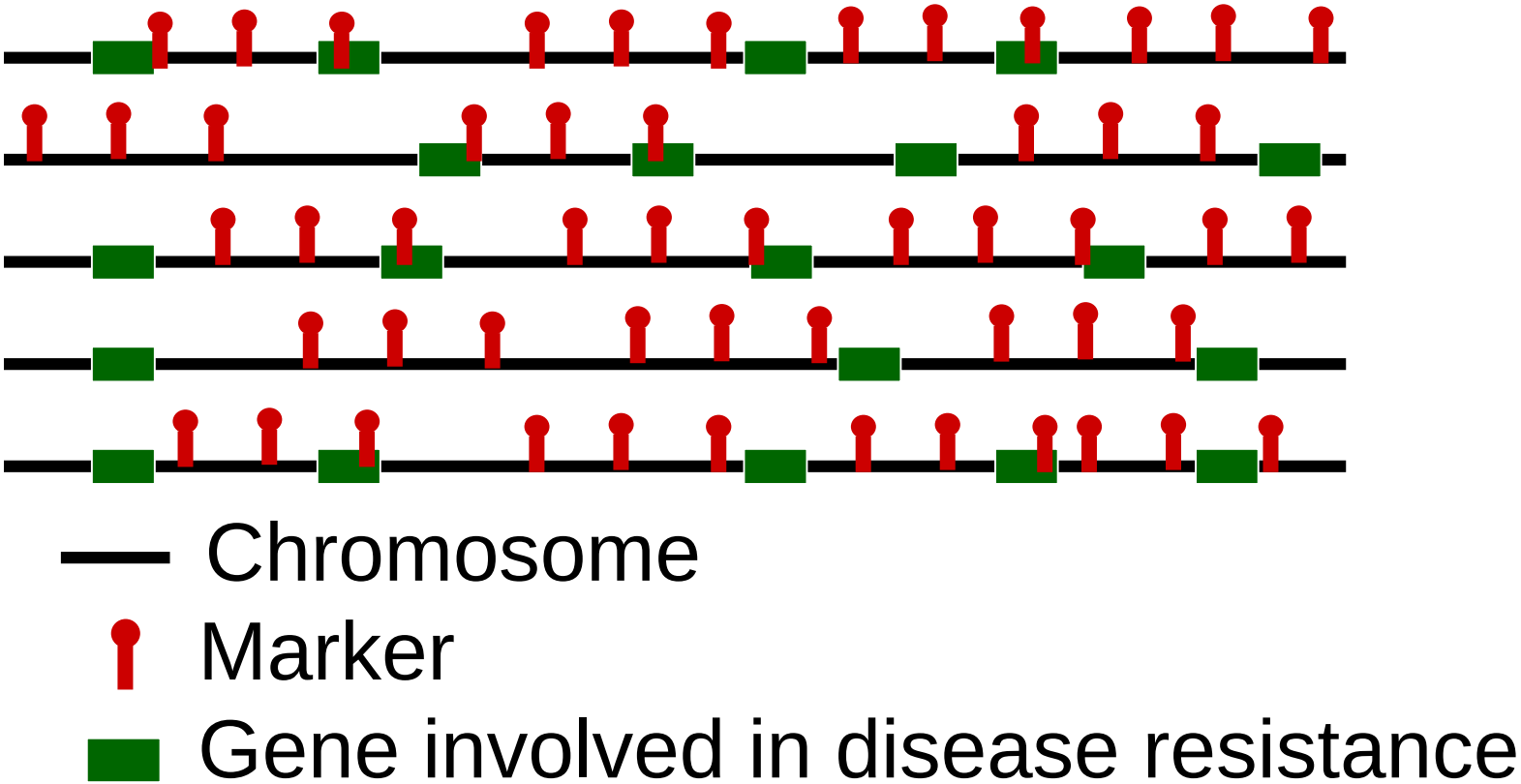


DNA marker

Gene involved in blight or PRR resistance

How genomic selection works

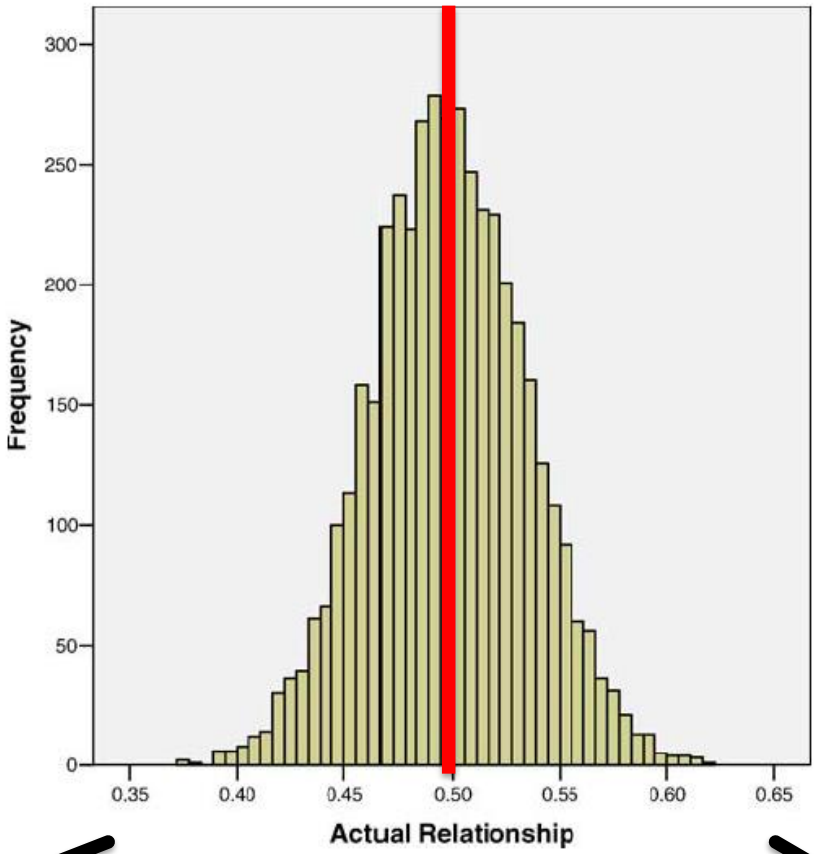
Disease resistance predicted from the summed effects of DNA markers near disease resistance genes



How genomic selection works

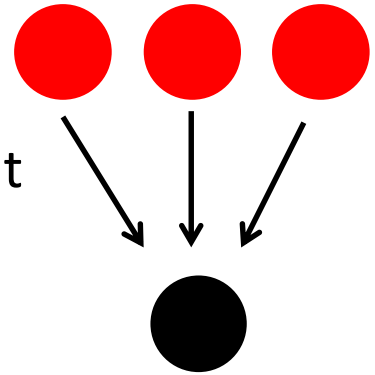
Full sibs expected to share 50% of genome

N of pairs of individuals

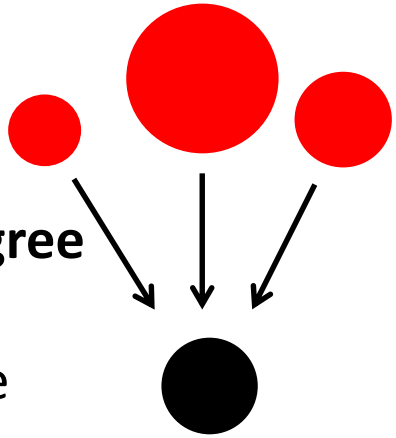


DNA markers trace variation around expected pedigree-relationships

A better weighted average



Pedigrees weight sibs equally



Genomics + pedigree weights sibs in proportion to true relatedness

How are DNA markers are generated

Genotyping-by-sequencing

Genomic DNA

…TAACG**AACC**TTGGATCGTCATTCGCATACTACTACGAAAATTGCATCATA**AACC**CGC…

Restriction digestion

...TAACG**AA** ▼ **CC**TTGGATCGTCATTCGCATACTACTACGAAAATTGCATCATA**AA** ▼ **CC**CGC...

DNA Sequencing

CCTTGGATCGTCATTCGCATACTACTACGAAAATT — Template strand

GGAACCT*AGCA* → — Complementary strand

Alignment to reference genome and SNP detection

SNP ↓ SNP ↓

CC**A**TCGAGCGTC**C**TT — Individual A

CC**T**TGGAGCGTC**A**TT — Individual B

.....TAACG**AACC**TTGGATCGTCATTCGCATACTACTACGAAAATTGCATC..... — Reference genome

Development/validation of genomic prediction models for disease resistance

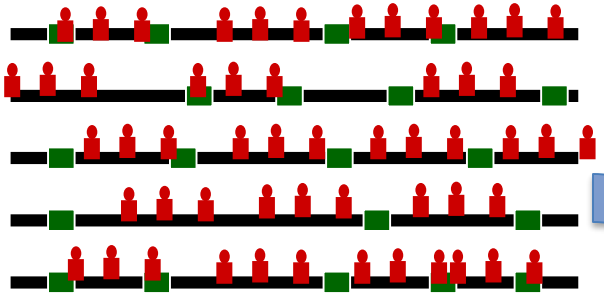
9/10th of training population

Canker size/root rot severity

$= \mu + X\beta + \begin{bmatrix} -0.1 \\ +0.5 \\ +0.9 \end{bmatrix}$

Experimental design

Estimated marker effects



Genome-wide markers

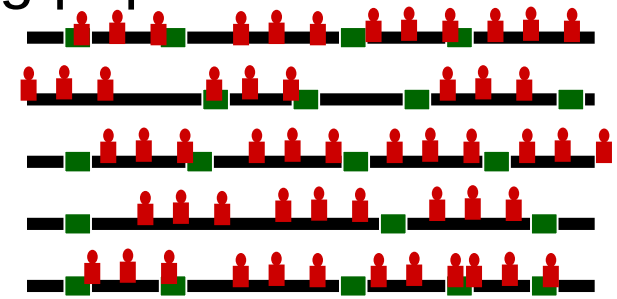
Repeat 10 x

Accuracy = correlation

1/10th of training population

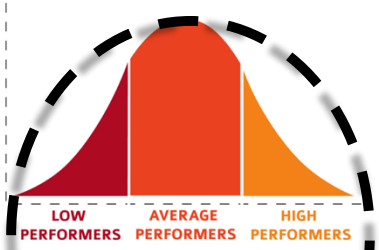
$\sum_{i=1}^{N\ markers} \begin{bmatrix} -0.1 \\ +0.5 \\ +0.9 \end{bmatrix} \times$

Marker effects



Marker genotypes

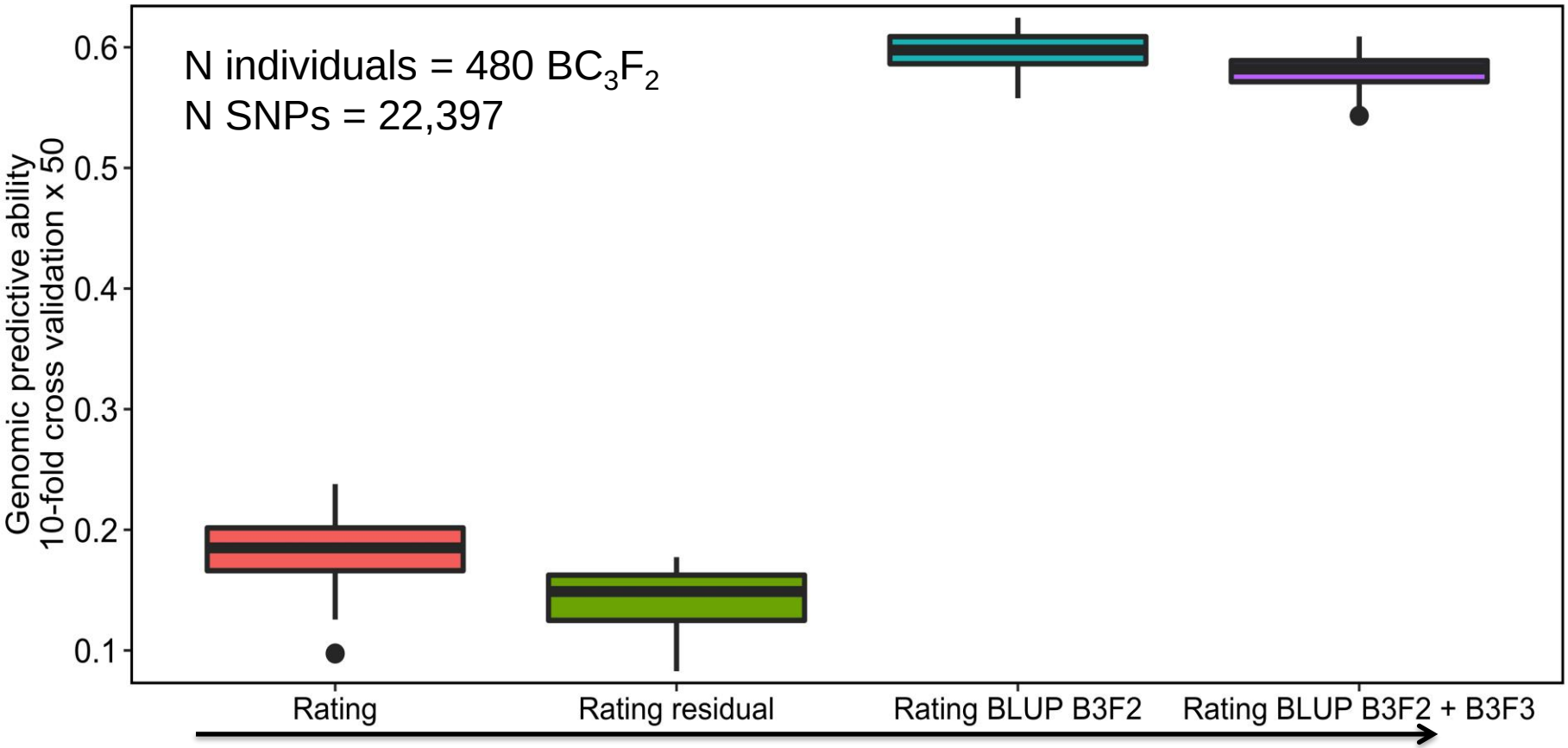
=



Predicted pathogen resistance

Proof-of-concept

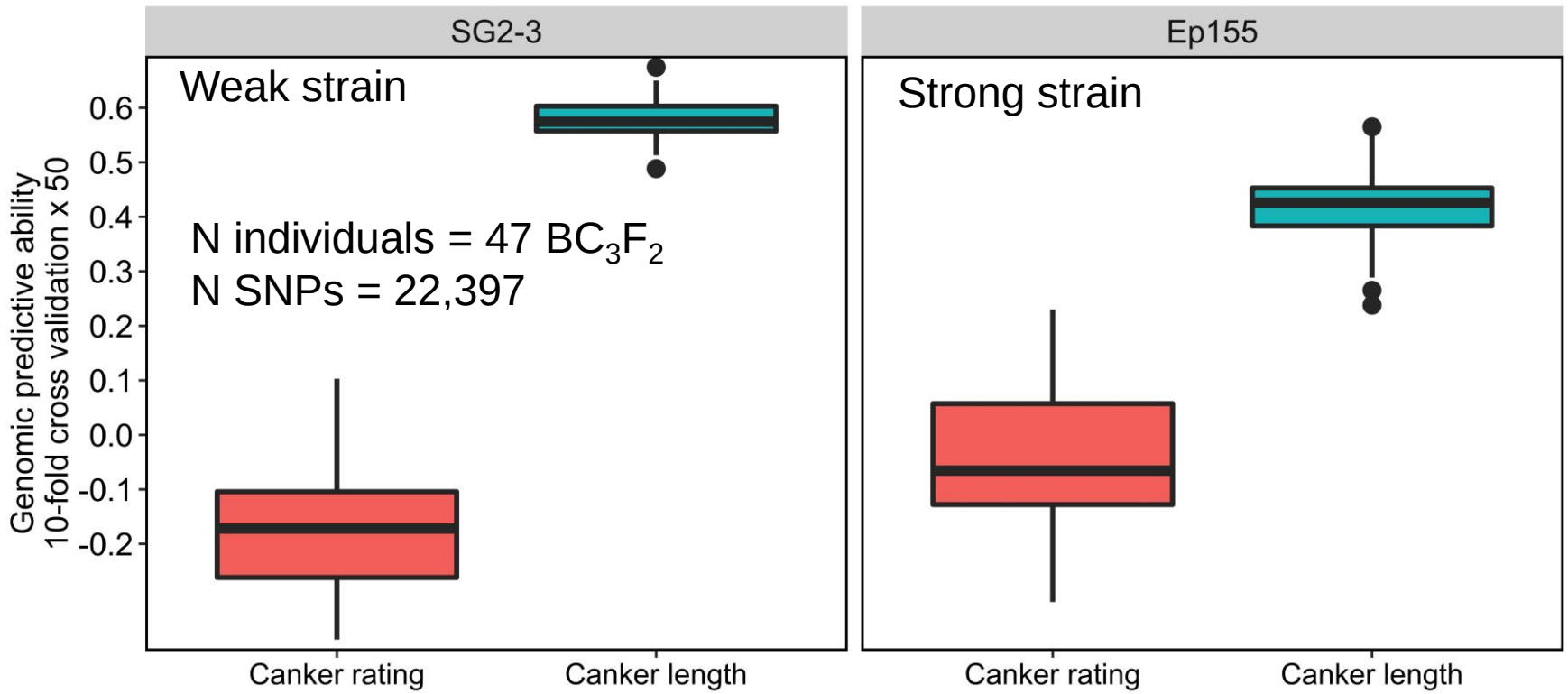
Genomic prediction of canker severity ratings of BC_3F_2 trees



Degree of accounting for phenotypic Information from relatives and environmental effects

Proof-of-concept

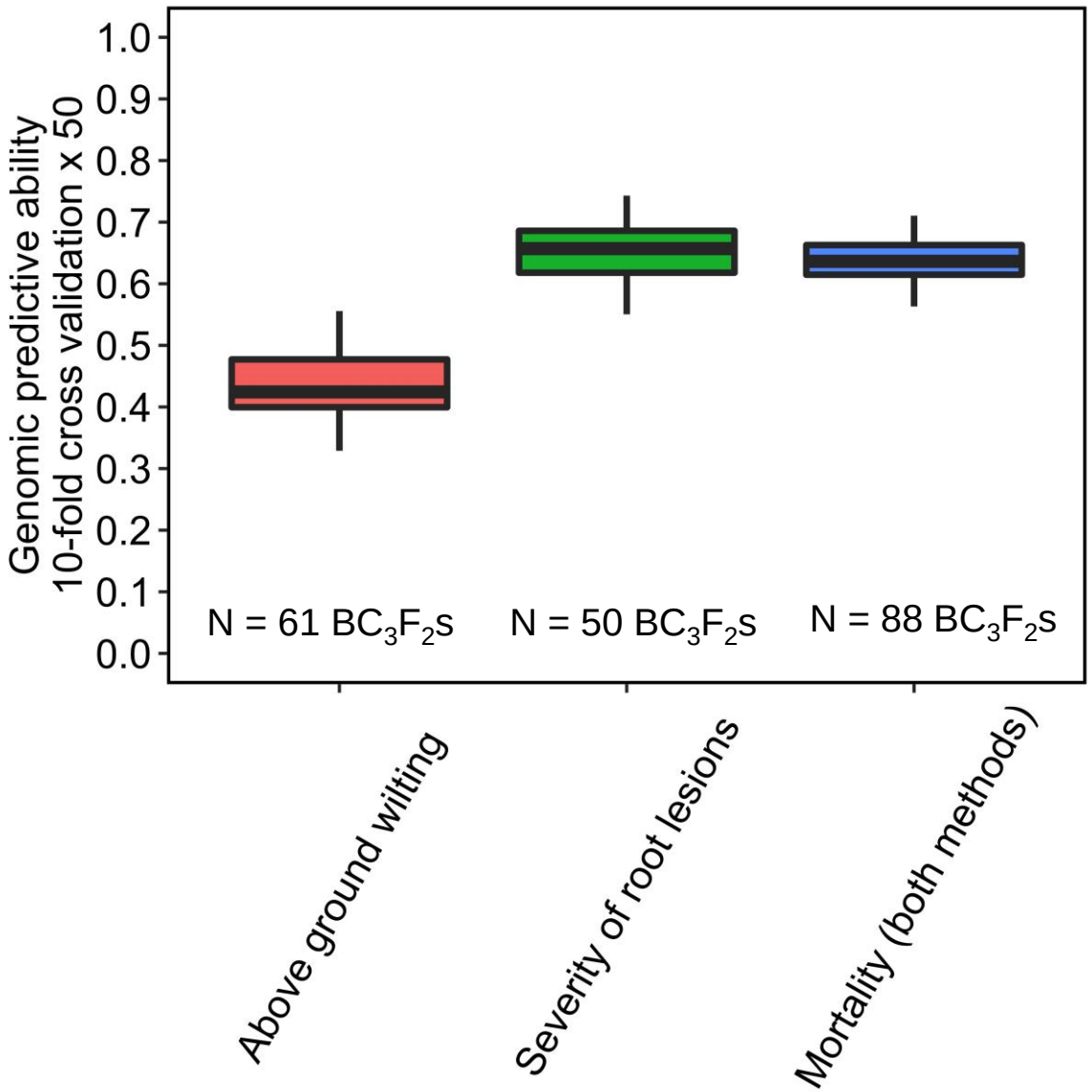
Genomic prediction of blight resistance of BC_3F_3 progeny



Response variable: BLUPs estimated from canker rating and canker lengths of 11 – 30 open pollinated progeny of each BC3-F2 mother

Proof-of-concept

Genomic prediction of Phytophthora root rot resistance among BC_3F_3 progeny



Conclusions

- Genomic predictive abilities differ among disease severity traits
- Blight: Canker length more predictable than subjective canker severity rating
- Phytophthora: mortality and severity of root lesions more predictable than above ground wilting
- The genomic predictive abilities were encouragingly high despite the small training populations used to develop the prediction models

Ongoing genotyping for genomic selection in Meadowview seed orchards

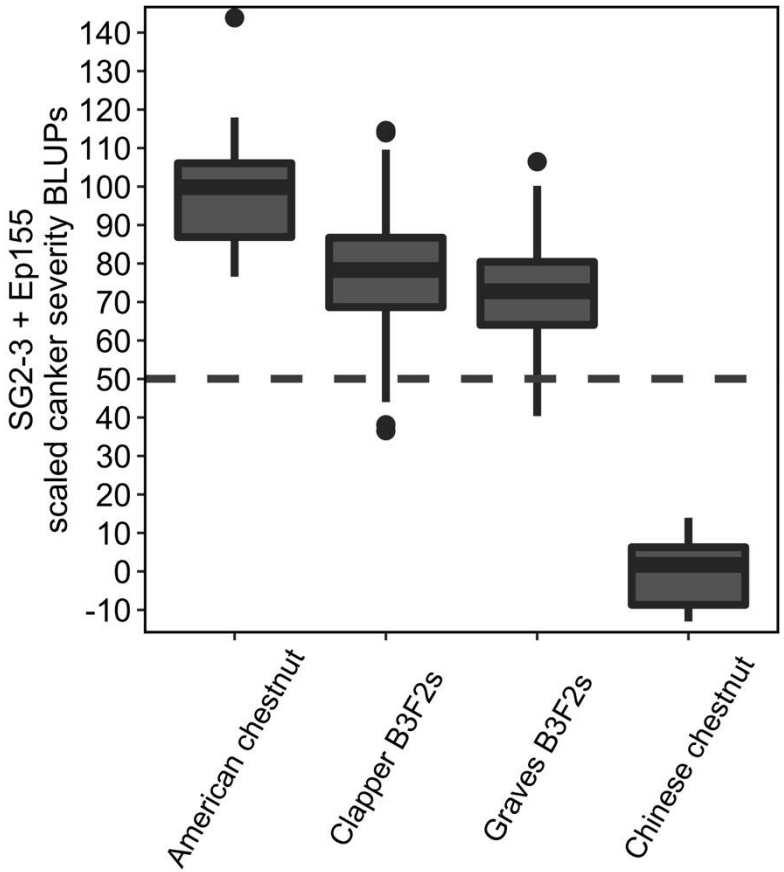
	Clapper	Graves
N BC_3F_2 mothers progeny tested for blight resistance (2011 - 2019)	273	294
N BC_3F_2 mothers progeny tested for root rot resistance (2012 – 2017)	102	217
N BC_3F_2 to predict resistance from genotype alone	1223	865

Jason Holliday

Progeny testing will continue until genomic predictive abilities increase to 0.6 to 0.8

How blight resistant are BC_3F_3 progeny expected to be after selection is complete in BC_3F_2 seed orchards?

Scale
100 = American chestnut mean
0 = Chinese chestnut mean



Dashed line
prediction of average canker severity of B3F3s after selection is complete in B3-F2 seed orchards

American chestnut BC_3F_2 trees with improved blight resistance

BC_3F_2 tree

American chestnut

Implementation of genomic selection in chapter seed orchards

Small stem assays may be used to expedite progeny testing in chapters