“"So many genomes, so little time: the future of plant breeding"”

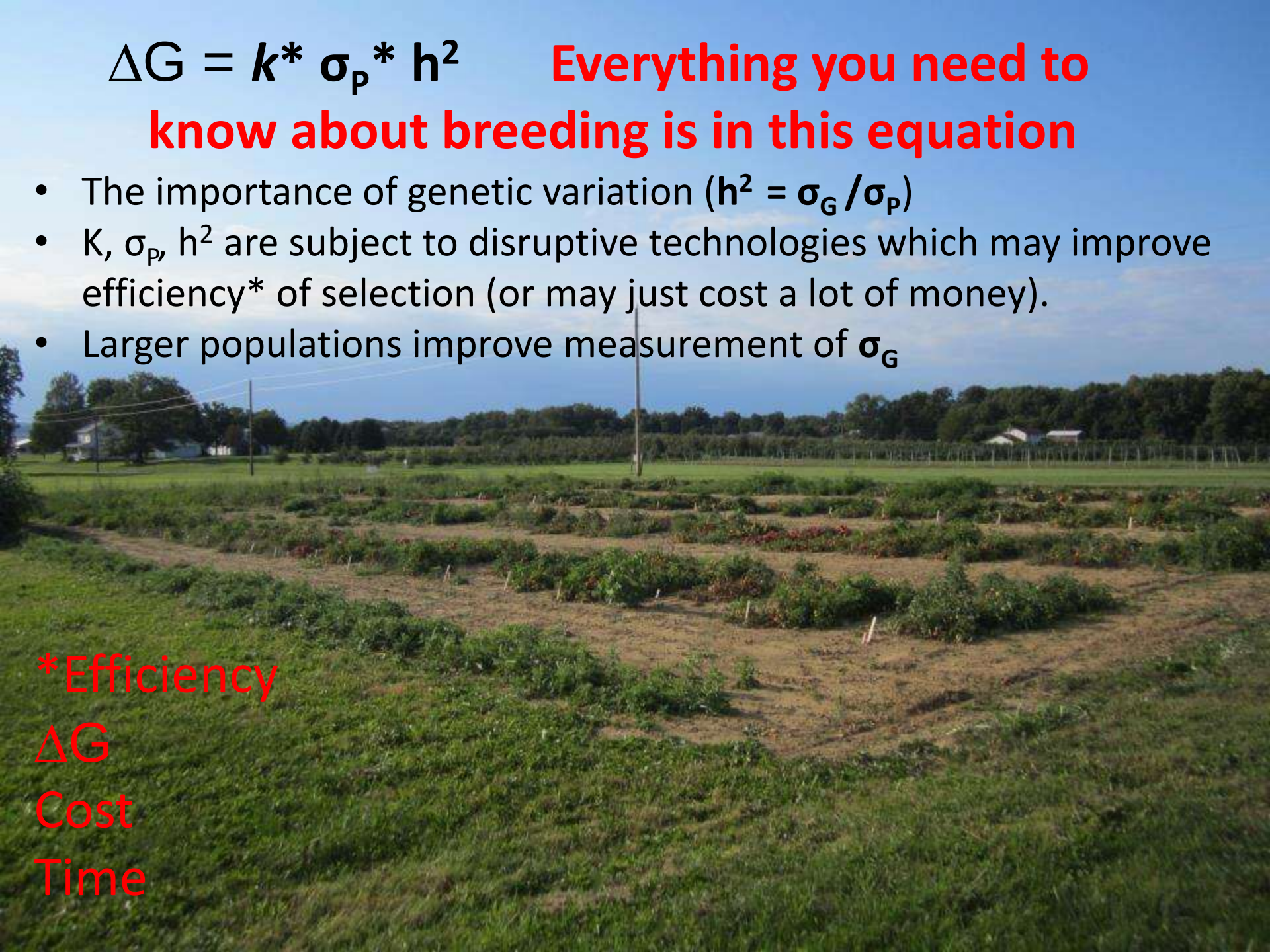
THE OHIO STATE UNIVERSITY
COLLEGE OF FOOD, AGRICULTURAL, AND ENVIRONMENTAL SCIENCES

David Francis
(francis.77”at”osu.edu)

The perspective of a public plant breeder: an opinion on the direction of our discipline and the role of technology.

$\Delta G = k^* \sigma_P^* h^2$ **Everything you need to know about breeding is in this equation**

- The importance of genetic variation ($h^2 = \sigma_G / \sigma_P$)
- K, σ_P, h^2 are subject to disruptive technologies which may improve efficiency* of selection (or may just cost a lot of money).
- Larger populations improve measurement of σ_G

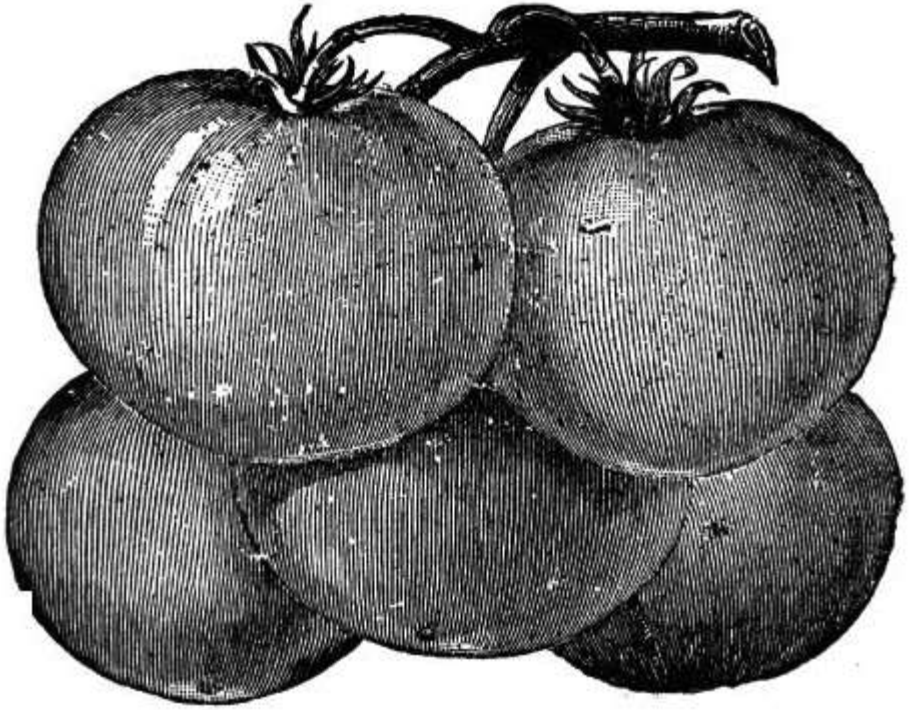


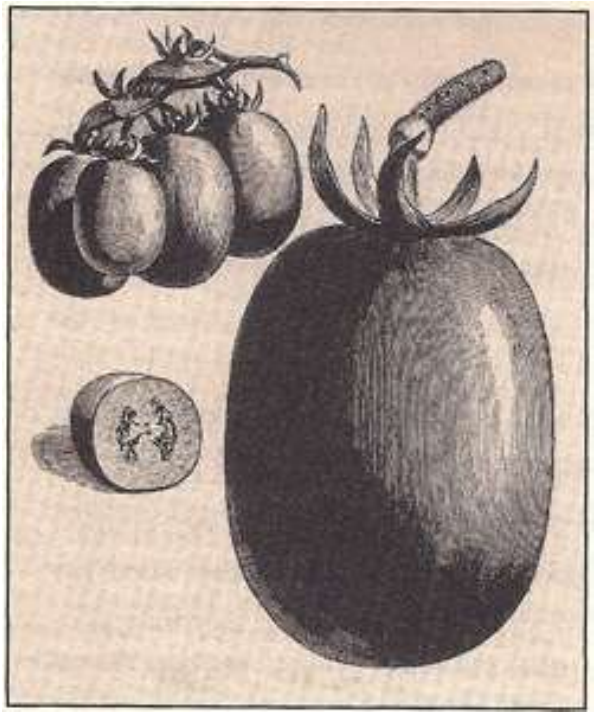
*Efficiency
ΔG
Cost
Time

"Those that fail to learn from history, are doomed to repeat it."
Winston Churchill

"We learn from history that we learn nothing from history."
George Bernard Shaw

Plant breeding has always been more effective when coupled to new technology, whether that technology is production, harvesting, or breeding (e.g. development of mechanically harvested tomato)





S. pimpinellifolium, S. galapagense (plant form)
S. pennellii, S. peruvianum, S. pimpinellifolium (resistance)
as source of σ_G

Most of our disease resistance has come from wild species σ_G

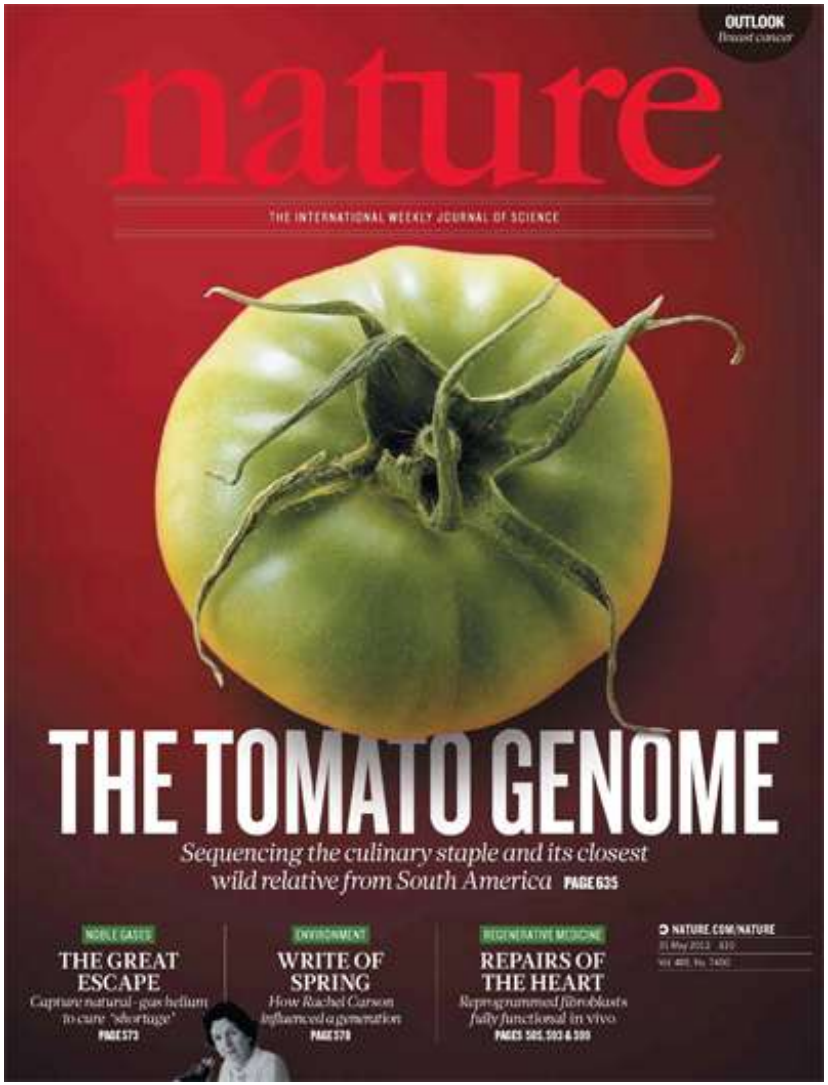
Many of the differences between market classes are due to genes from wild species σ_G

Take home messages:

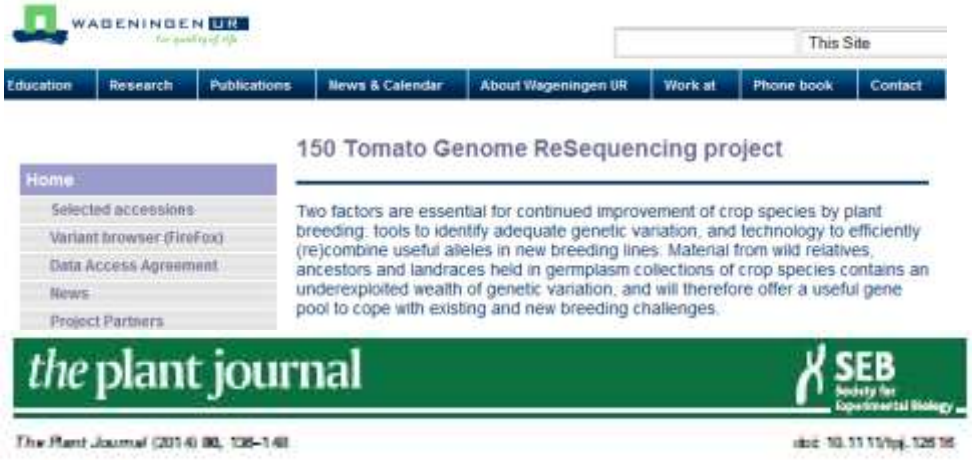
- NGS sequence data is providing a resource for allele identification, but…
  - Lack Reference (elite material)
  - Lack structure-function information
- Fastest way to evaluate new alleles is breeding
- CRISPR/CAS9 is the newest mutation breeding tool (loss of function will be more common)
- GS models show promise for prediction of performance
- Large populations and biological assessment Knowledge of traits and trait relationships

Since October 2014 We have ~500 tomato genomes in public databases: how can we use this information?

Tomato Genome Consortium - 2012
(Reference sequence)



Resequencing projects 2014



RESOURCE

Exploring genetic variation in the tomato (*Solanum* section *Lycopersicon*) clade by whole-genome sequencing

アクセス
日本語要約にアクセスするためには、*Nature Genetics* の購読が必要です（右参照）。

nature.com > Journal home > Table of Contents

Article

Nature Genetics **46**, 1220–1226 (1 November 2014) | doi:10.1038/ng.3117

Genomic analyses provide insights into the history of tomato breeding

```
mcbl-user-13@MCBL-host-R19: ~/Tomato_Sequences
File  Edit  View  Terminal  Help
mcbl-user-13@MCBL-host-R19:~/Tomato_Sequences$ ls
Fruit_Specific_B_cyclase.fa  T100584_Slycopersicum.fa
mcbl-user-13@MCBL-host-R19:~/Tomato_Sequences$
```

```
LA0716      ATGGAAgCTCTTCTCAAGCCTTTTCCATCT
LA1364      ATGGAAACTCTTCTCAAGCCTTTTCCATCT
CGN15532    ATGGgAACTCTTCTCAAGCCTTTTCCATCT
LA2157      ATGGAAACTCTTCTCAAGCCTTTTCCATCT
CGN15530    ATGGAAACTCTTCTCAAGCCTTTTCCATCT
T_1248      ATGGAAACTCTTCTCAAGCCTTTTCCATCT
LA1365      ATGGAAACTCTTCTCAAGCCTTTTCCATCT
LA1983      ATGGAAACTCTTCTCAAGCCTTTTCCATCT
H1706       ATGGAAACTCTTCTCAAGCCTTTTCCATCT
T100584     ATGGAAACTCTTCTCAAGCCTTTTCCATCT
NO20212     ATGGAAACTCTTCTCAAGCCTTTTCCATCT
EA00465     ATGGAAACTCTTCTCAAGCCTTTTCCATCT
EA00325     ATGGAAACTCTTCTCAAGCCTTTTCCATCT
EA00488     ATGGAAACTCTTCTCAAGCCTTTTCCATCT
EA00371
LYC_1365
LYC_1969
LYC_3897
LYC_3476
TR00003
CGN15464
LYC_3340
EA01155
EA01049
LYC_3153
LYC_3155
PI_272654
EA00990     ATGGAAACTCTTCTCAAGCCTT
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CGN20815    ATGGAAACTCTTCTCAAGCCTT
PI_303721   ATGGAAACTCTTCTCAAGCCTT
EA00027     ATGGAAACTCTTCTCAAGCCTT
V710092     ATGGAAACTCTTCTCAAGCCTT
PC711092    ATGGAAACTCTTCTCAAGCCTT
PI_93302    ATGGAAACTCTTCTCAAGCCTT
SG_16       ATGGAAACTCTTCTCAAGCCTT
```

MUSCLE

Input form | Web services | Help & Documentation

Tools > Multiple Sequence Alignment > MUSCLE

Multiple Sequence Alignment

MUSCLE stands for **MU**ltiple **S**equence **C**omparison by **L**og- **E**xpectation.

	LA0716	LA1777	PI134418	LYC4	LA1718	CGN15792	CGN15791	LA407	LA1278
LA0716	0	0.017245	0.023125	0.018303	0.022038	0.016202	0.018851	0.020434	0.028443
LA1777	0.017245	0	0.0						
PI134418	0.023125	0.018324							
LYC4	0.018303	0.0104	0.0						
LA1718	0.022038	0.013031	0.0						
CGN15792	0.016202	0.014622	0.0						
CGN15791	0.018851	0.013036	0.0						
LA407	0.020434	0.013559	0.0						
LA1278	0.028443	0.031151	0.0						

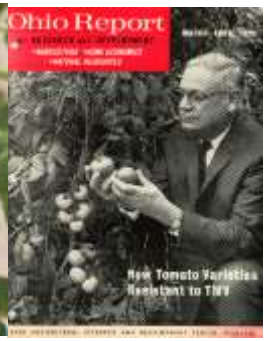
Francis ▸ Dropbox ▸ Francis Lab 2014 ▸ Carotenoid_Pathway_Genes ▸

e in library ▾ Share with ▾ Burn New folder

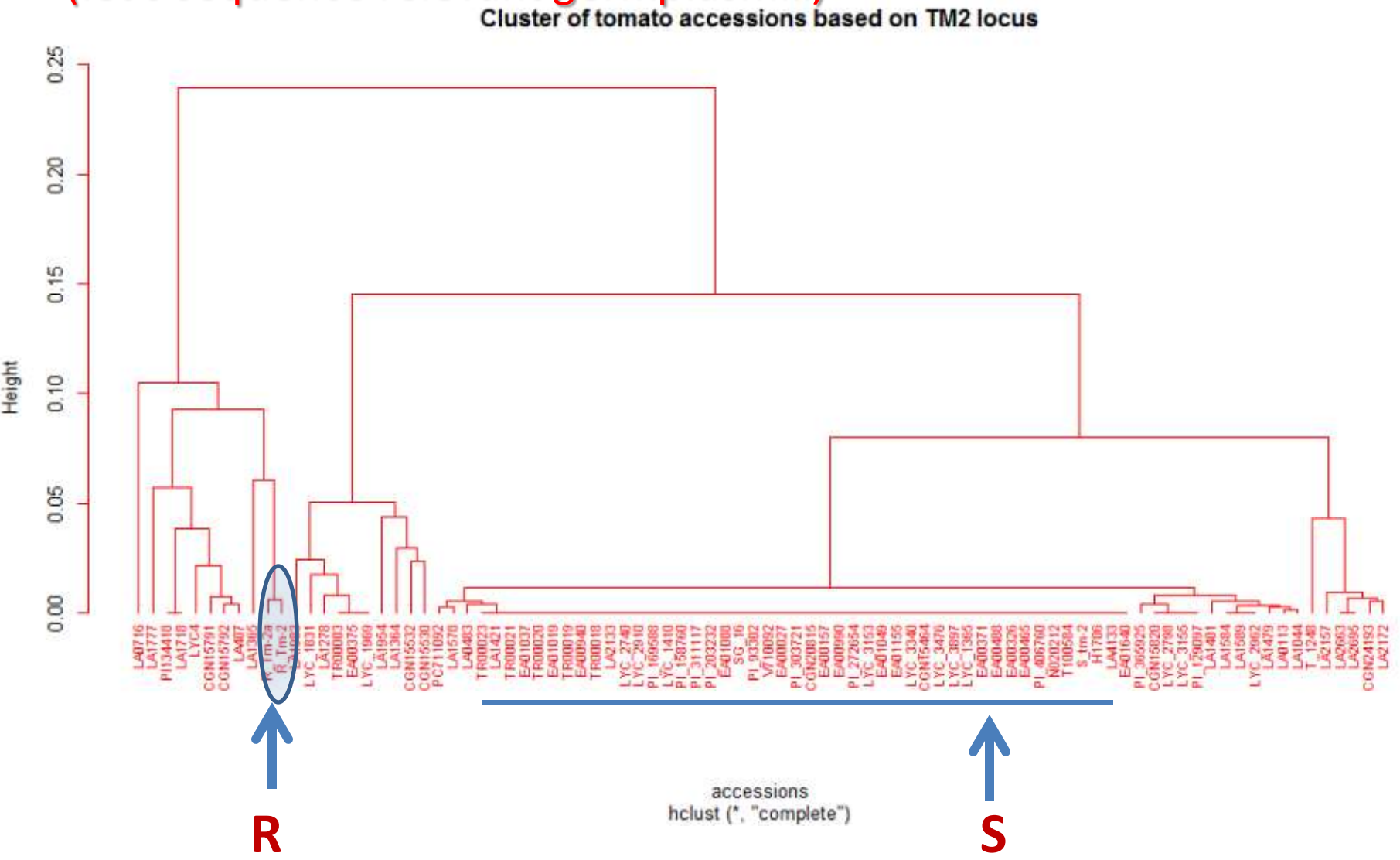
Name	Date modified	Type
Beta_Cyclase	11/6/2014 4:43 PM	File folder
CRITISO	8/4/2014 8:19 AM	File folder
LUT2		
Ohase1		
Ohase2		
PDS		
PSY1		
PSY2		
ZDS		
ZE		

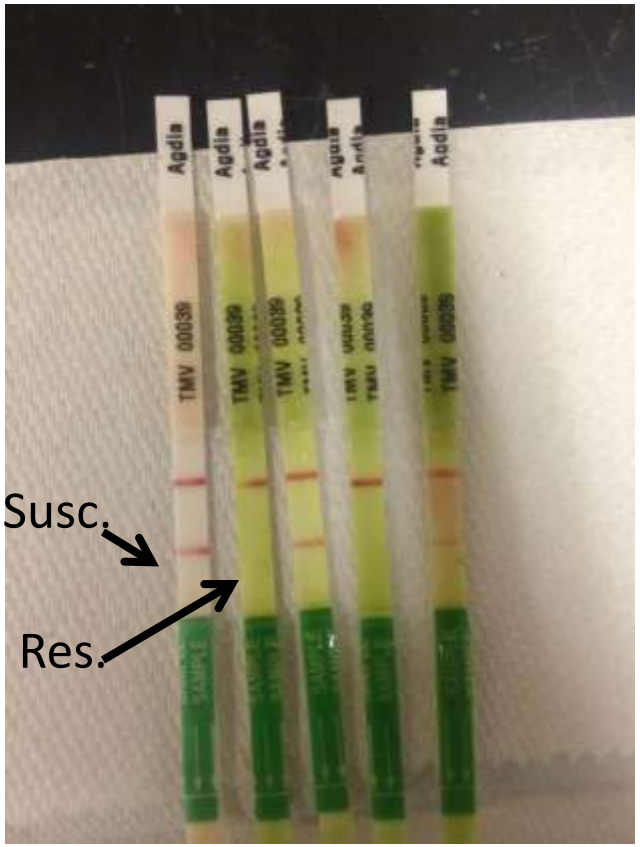
Name	Date modified
Five_Prime_2000bp	8/8/2014 1:12 PM
Gene	8/8/2014 1:12 PM
Protein	8/8/2014 1:12 PM
Three_Prime_500bp	8/8/2014 1:12 PM
AccessionID_PCA_Beta	6/4/2014 3:54 PM
B_Clustering	6/4/2014 5:08 PM

Cluster of tm-2 alleles from of 85 unique genomes in “150 genome” project



Cluster of tm-2 alleles from of 85 unique genomes in “150 genome” project + 2 resistance alleles Tm-2 and Tm-2^a (let’s sequence relevant germplasm…)





- Evaluation of accessions for Tm2 DNA Sequence, virus symptoms, and antibody reactivity.
- Resistant phenotypes found on most nodes of accession tree Susceptible phenotypes found on most nodes of accession tree.
- Only predictability when we all ready know the allele.
- We lack sufficient structure-function information to predict new resistance alleles.

Scientific Correspondence

Efficient Gene Editing in Tomato in the First Generation Using the Clustered Regularly Interspaced Short Palindromic Repeats/CRISPR-Associated9 System[1]

Christopher Brooks, Vladimir Nekrasov*, Zachary B. Lippman*, and Joyce Van Eck*

Cold Spring Harbor Laboratory, Cold Spring Harbor, New York 11724 (C.B., Z.B.L.); Sainsbury Laboratory, Norwich Research Park, Norwich NR4 7UH, United Kingdom (V.N.); and Boyce Thompson Institute for Plant Science, Ithaca, New York 14853 (J.V.E.)

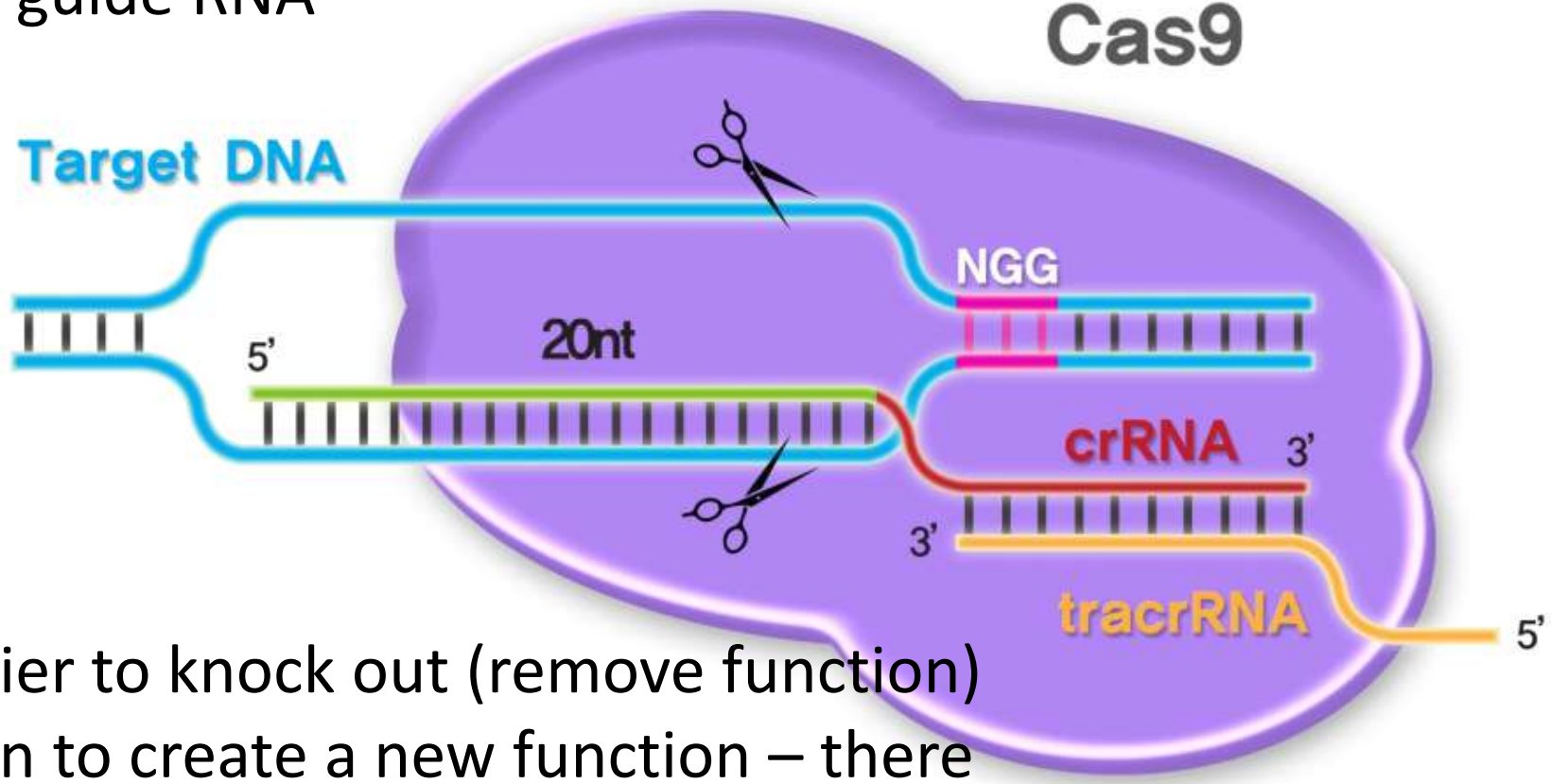
Creation of new genetic variation

"Gene Editing" technologies

1) Zinc finger nucleases
2) Transcription activator-like nucleases (TALENs)
3) Clustered regularly interspaced short palindromic repeats (CRISPR)/CRISPR-associated 9(Cas9) endonuclease

1 and 2 are based on protein-DNA interactions, 3 is an RNA-guided DNA endonuclease system

To alter a target gene, supply Cas9 and the guide RNA



Easier to knock out (remove function) than to create a new function – there are exceptions to this rule

*Image from: Horvath P, Barrangou R (2010). "CRISPR/Cas, the immune system of bacteria and archaea". Science **327** (5962): 167–170.*

Andolfo et al. BMC Plant Biology 2014, 14:120
http://www.biomedcentral.com/1471-2229/14/120

How do we identify targets?

BMC Plant Biology

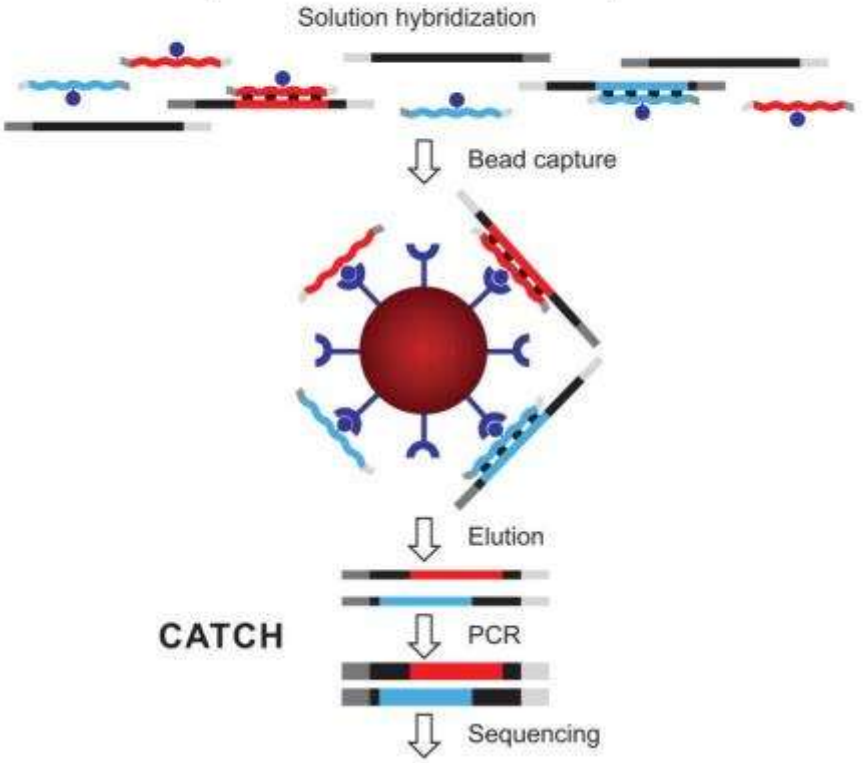
RESEARCH ARTICLE Open Access

Defining the full tomato NB-LRR resistance gene repertoire using genomic and cDNA RenSeq

Giuseppe Andolfo[1,2], Florian Jupe[1*], Kamil Witek[1], Graham J Etherington[1], Maria R Ercolano[2] and Jonathan D G Jones[1*]

Image from:

Gnirke A, Melnikov A, Maguire J, et al. Solution Hybrid Selection with Ultra-long Oligonucleotides for Massively Parallel Targeted Sequencing. *Nature biotechnology*. 2009;27(2):182-189



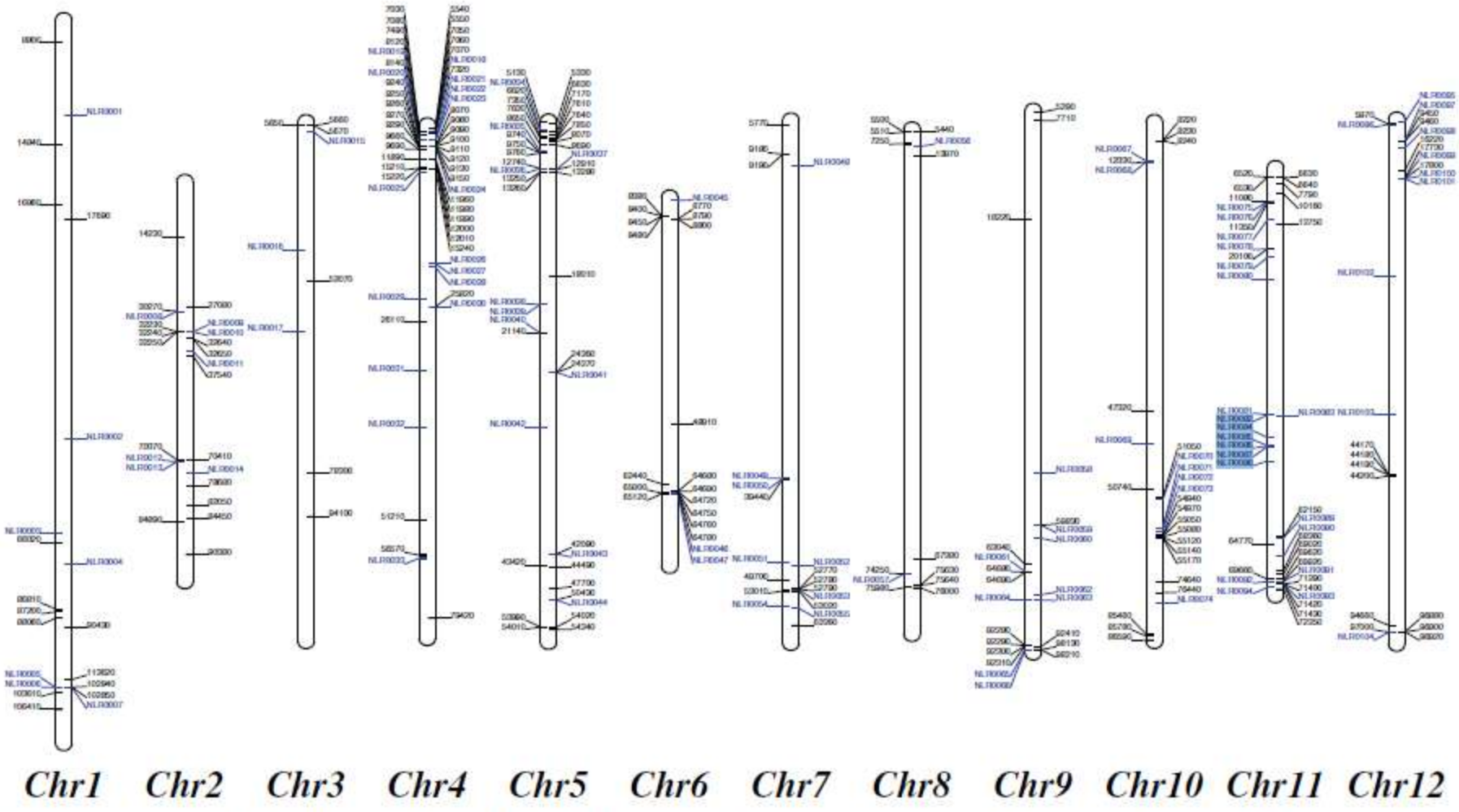
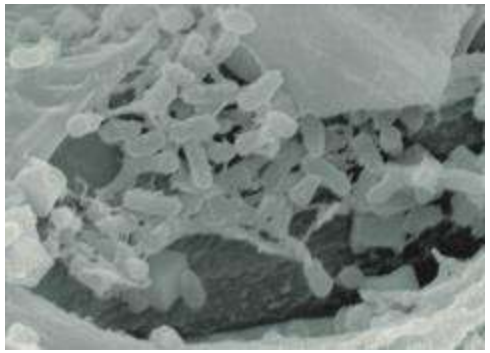


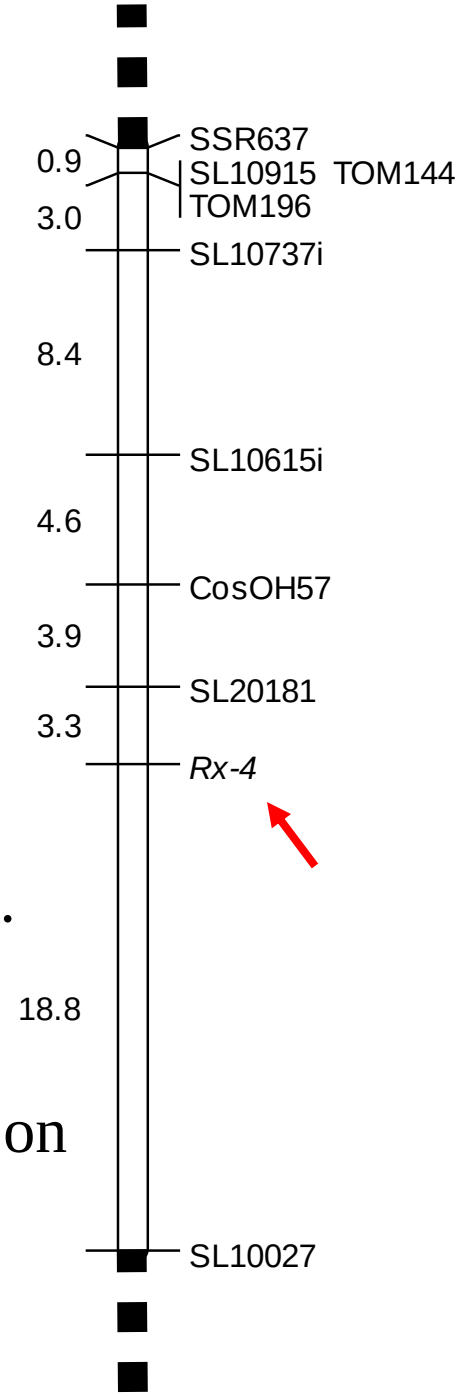
Figure 3 Chromosomal distribution of Heinz 1706 NB-LRR genes. The previously annotated NB-LRR genes [7] are shown in black and those discovered in this study are blue. Genes depicted to the left of the chromosome are on the forward strand and those on the right are on the reverse strand.

Example:
T3 resistance from PI128216 IBC population

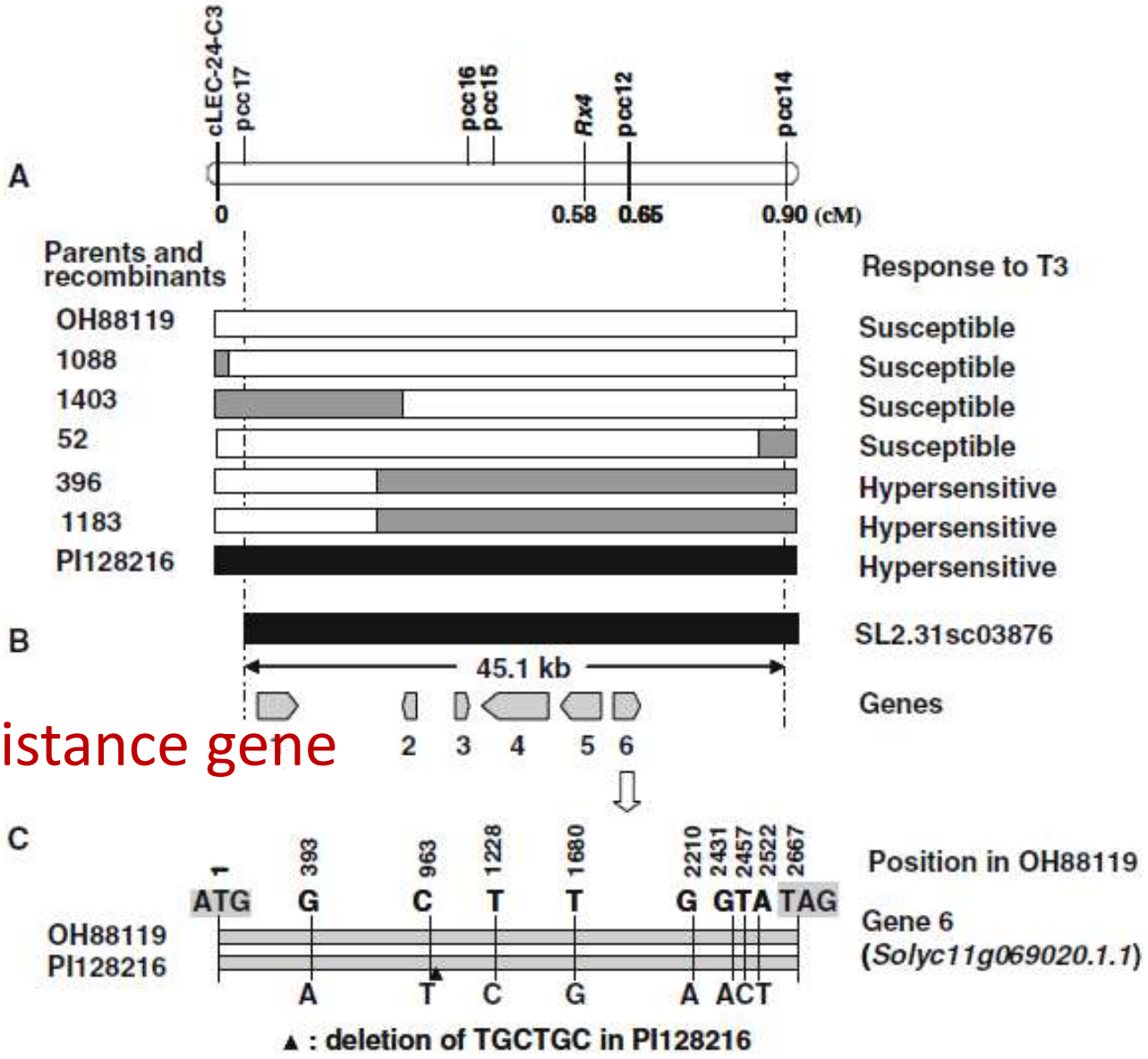


Robbins et al., 2009. Phytopathology

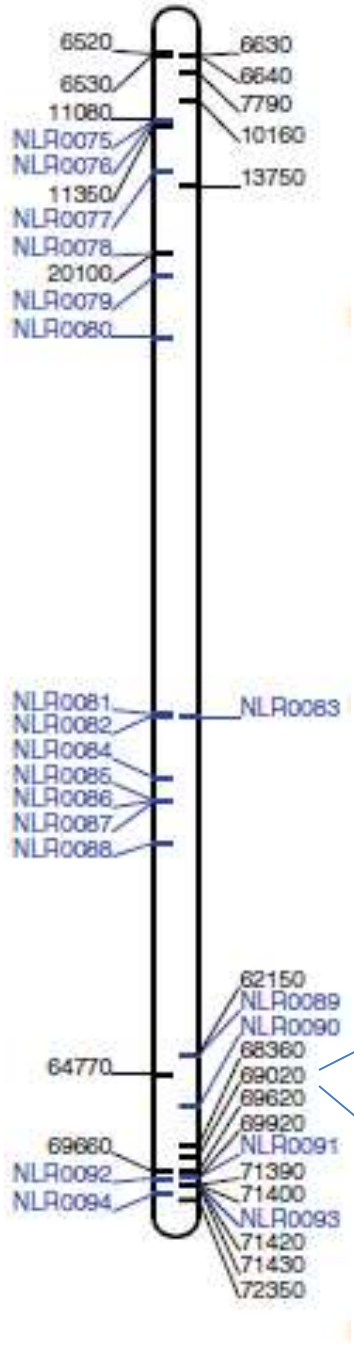
4 markers in 30 cM on chromosome 11

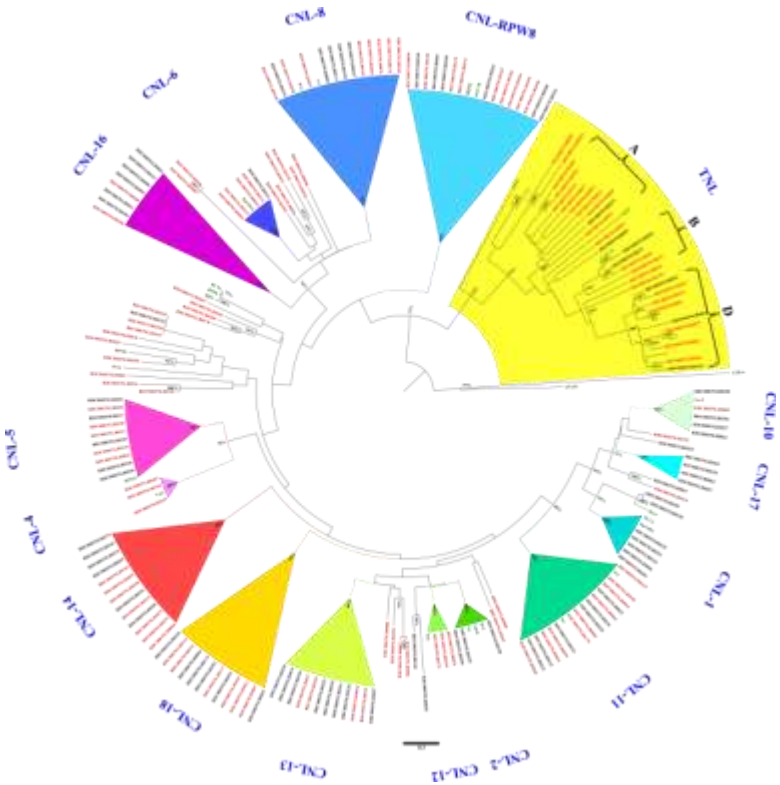


Potential targets based on candidate gene identification



CC-NBS-LRR resistance gene





CC-NBS-LRR resistance gene

Solyc11g069020 = XV3/Rx4

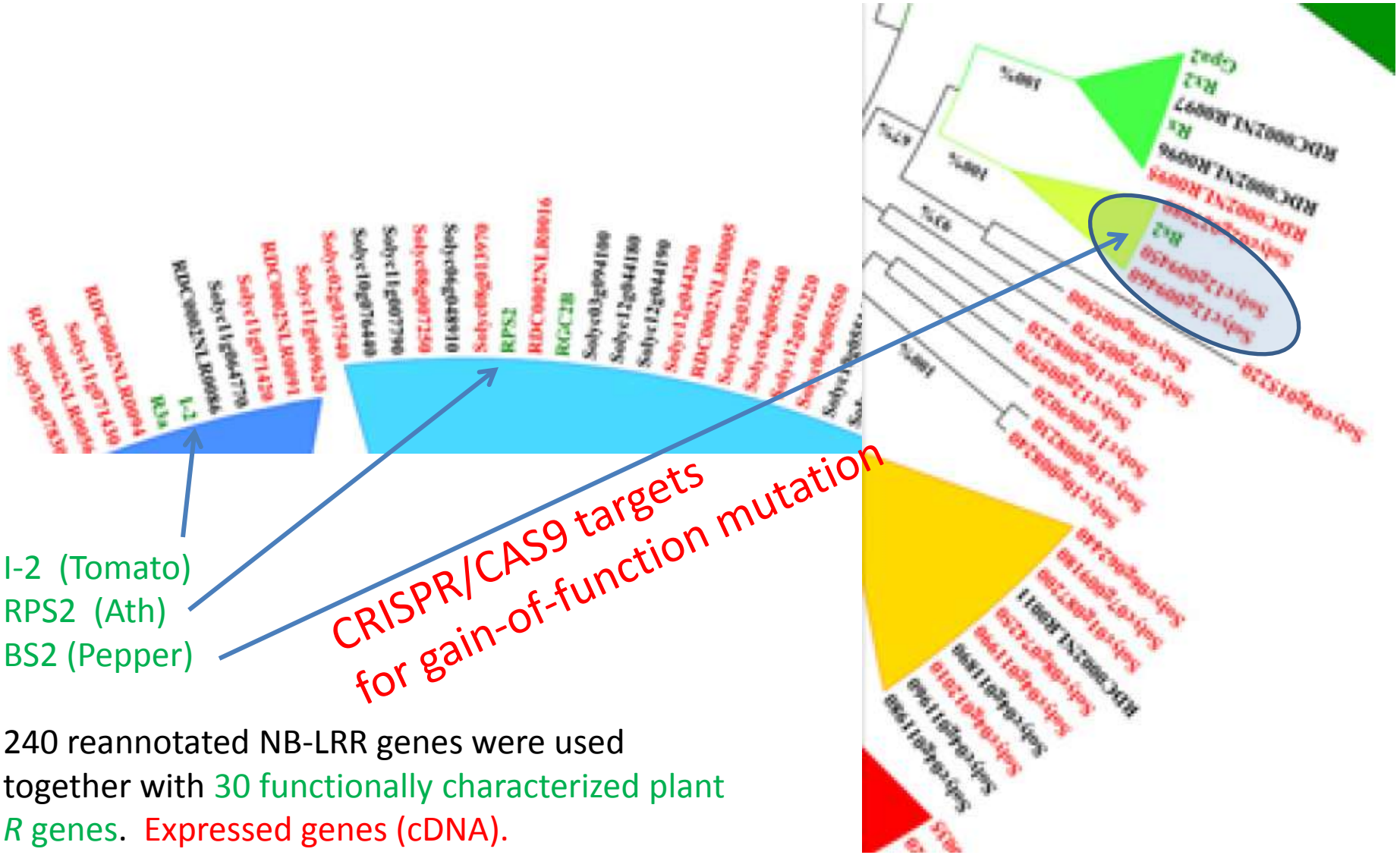
```
Solyc11g069020.1.1      AGCTGGAAGCTGTTGCAAAAGAAGATTTTTGGATTAGATGATCCAAGCTGCTGCTGCTGC
OH88119                 AGCTGGAAGCTGTTGCAAAAGAAGATTTTTGGATTAGATGATCCAAGCTGCTGCTGCTGC
PI128216                AGTTGGAAGCTGTTGCAAAAGAAGATTTTTGGATTAGATGATCCAA------GCTGCTGC
Hawaii7981              AGTTGGAAGCTGTTGCAAAAGAAGATTTTTGGATTAGATGATCCAA------GCTGCTGC
                        ** ****************************************      ********

Solyc11g069020.1.1      GATGACGAAATGGAAAGGATTGGAATGGAAATTTCAAAAAAATGCAAAGGATTACCACTA
OH88119                 GATGACGAAATGGAAAGGATTGGAATGGAAATTTCAAAAAAATGCAAAGGATTACCACTA
PI128216                GATGACGAAATGGAAAGGATTGGAATGGAAATTTCAAAAAAATGCAAAGGATTACCACTA
Hawaii7981              GATGACGAAATGGAAAGGATTGGAATGGAAATTTCAAAAAAATGCAAAGGATTACCACTA
                        ************************************************************

Solyc11g069020.1.1      GCAATTGTTATGGTAGCTGGGATACTTTCTAAAGAAAGCGCGACAGCAAGTAAATGGAGT
OH88119                 GCAATTGTTATGGTAGCTGGGATACTTTCTAAAGAAAGCGCGACAGCAAGTAAATGGAGT
PI128216                GCAATTGTTATGGTAGCTGGGATACTTTCTAAAGAAAGCGCGACAGCAAGTAAATGGAGT
Hawaii7981              GCAATTGTTATGGTAGCTGGGATACTTTCTAAAGAAAGCGCGACAGCAAGTAAATGGAGT
                        ************************************************************
```

CNL-8

CNL-RPW8



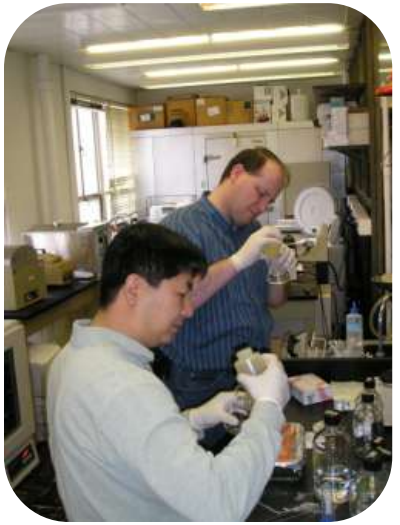
240 reannotated NB-LRR genes were used together with 30 functionally characterized plant *R* genes. Expressed genes (cDNA).

Yield Analysis and Prediction

OHIO STATE

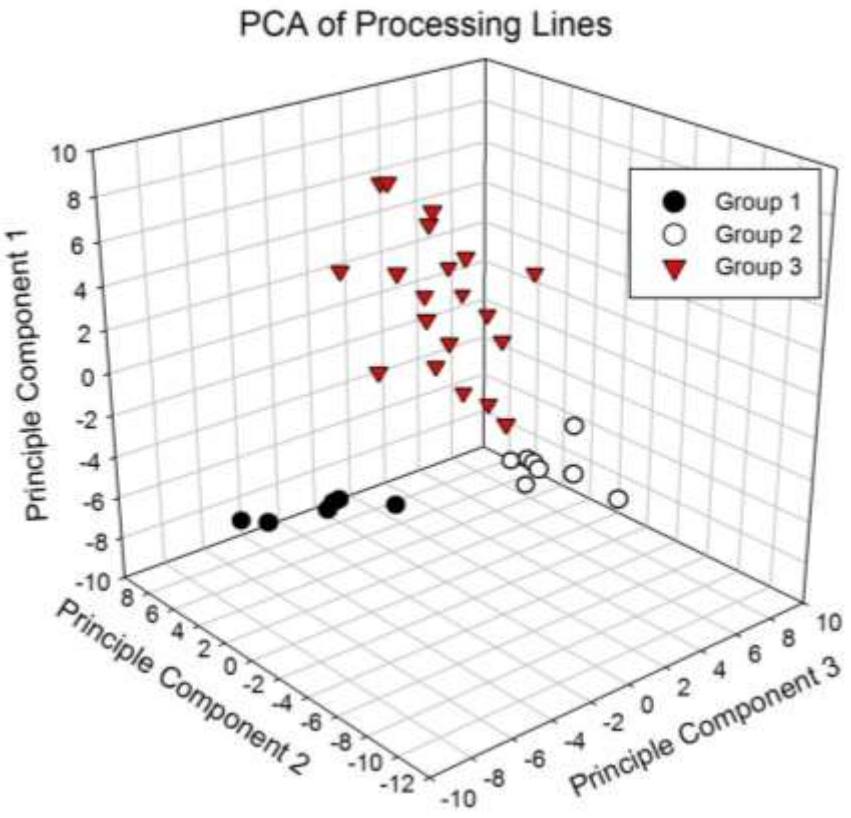
Why is David excited about GS and prediction?

This is Matt Robbins



Long-term Goal: Learn how to make a better hybrid

- Evaluate a partial diallele with 96 hybrids and parents (2 years, 2 locations, 2 reps/location RBC)
- Some evidence for hybrid vigor (hybrids preform ~5-10% better than parents)
- No evidence for heterotic groups

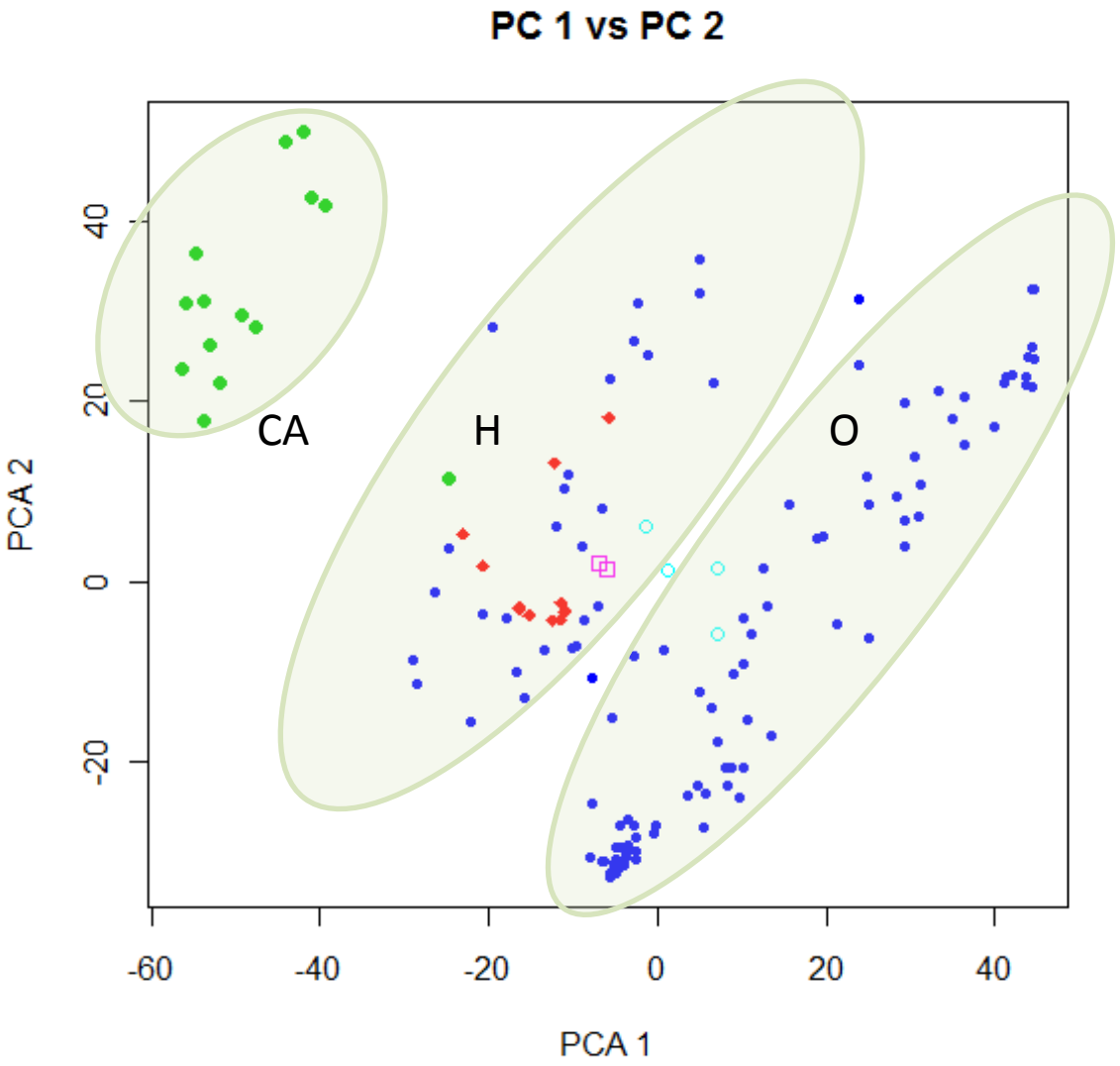


			Ton/acre	Group
	A		49.8	O
B	A		49.2	CA
B	A		48.5	O x H
B	A	C	46.4	O x CA
B	A	C	45.1	H
B D	A	C	44.5	H x CA
B D		C	43.4	inbred O
D		C	41.5	inbred H
D			39.0	inbred CA

Best prediction of hybrid performance was parent performance (good parents make good hybrids)

Diversity in tomato populations (processing)

California
Ohio
Undeterimined
Ridgetown College, Ontario
Oregon



Clustering based on 7,700 SNPs

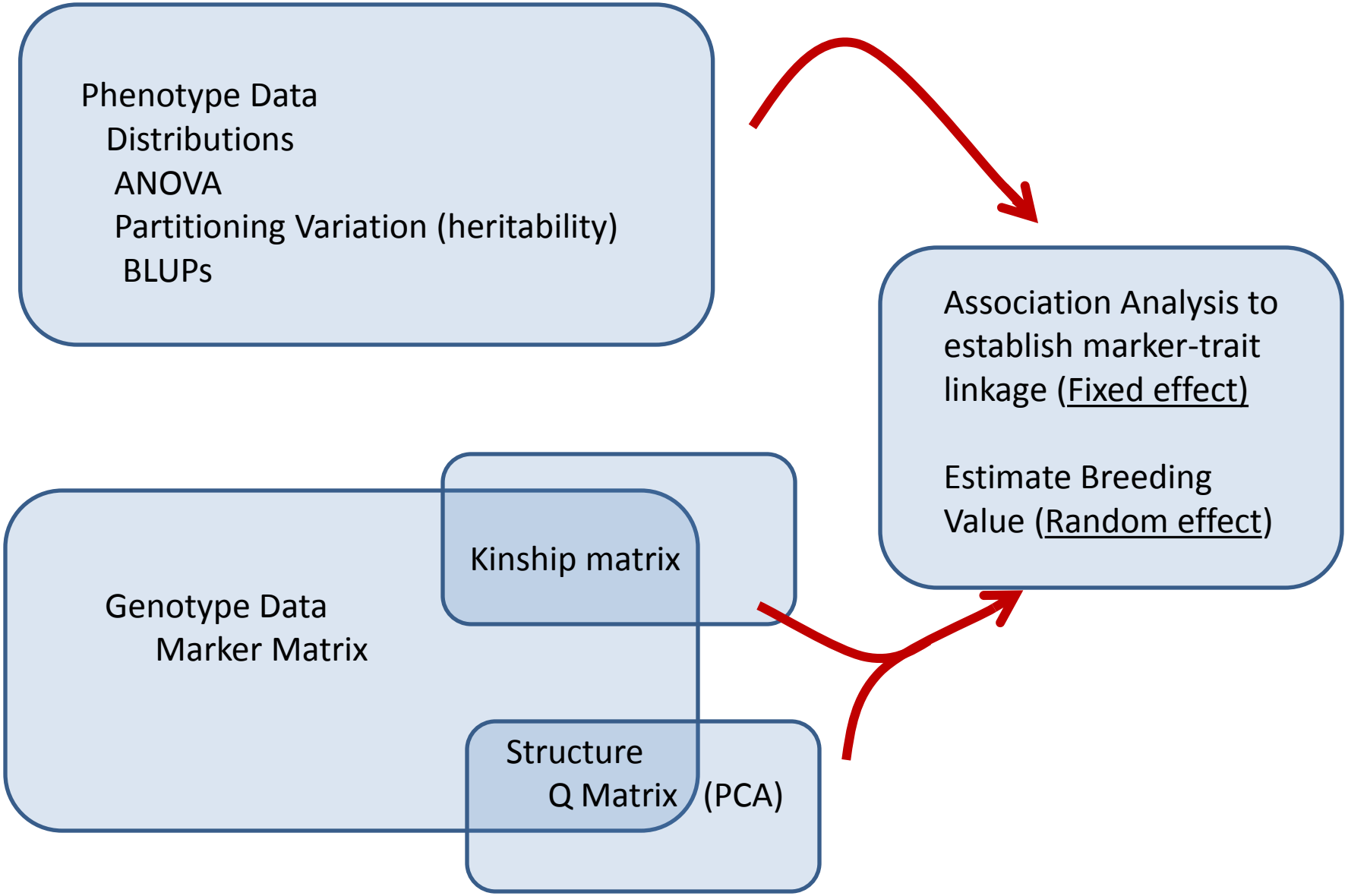
Genome Wide Selection (*Meuwissen T.H., Hayes B.J., Goddard M.E. (2001) Prediction of total genetic value using genome-wide dense marker maps. Genetics, 157, 1819–1829.)*

- Detection of sequence variation is no longer limiting
- Promise of predictive models

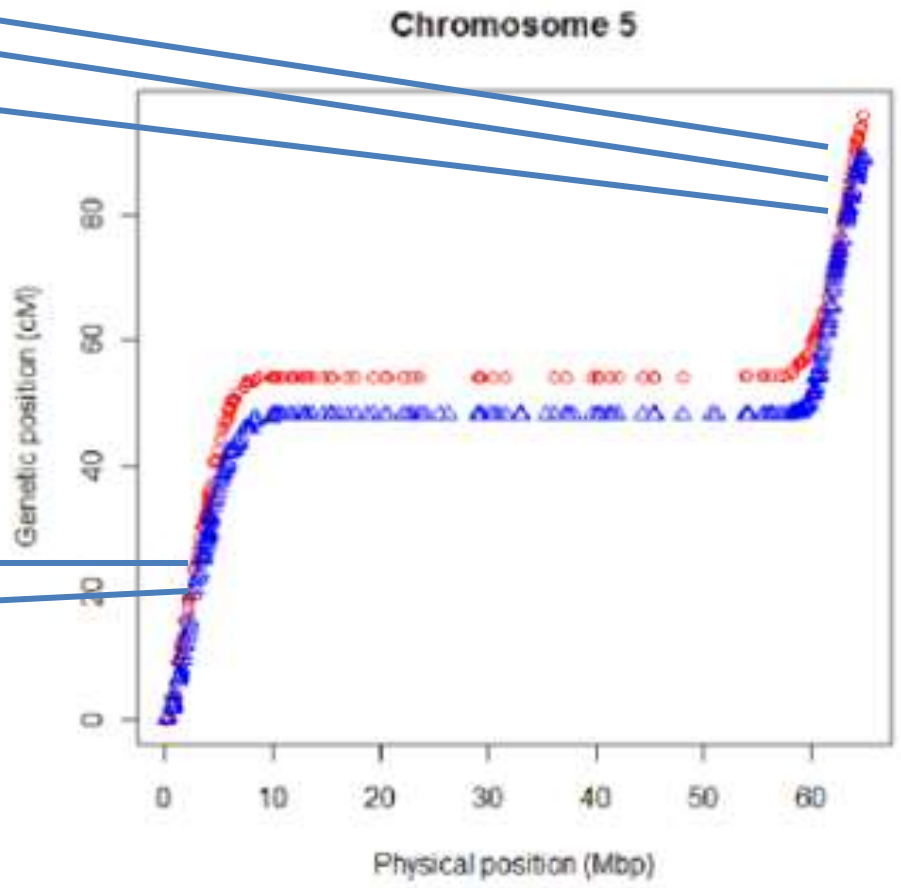
$$\boldsymbol{\gamma} = \boldsymbol{\mu} + \ddot{\mathbf{X}}\,\boldsymbol{\beta} + \in$$

$\boldsymbol{\gamma}$ is the vector of phenotypic values for n individuals
$\ddot{\mathbf{X}}$ is the n x K marker matrix for K markers
$\boldsymbol{\beta}$ is the estimated breeding value associated with each marker

Goal: Predict the performance of an individual based on genotype

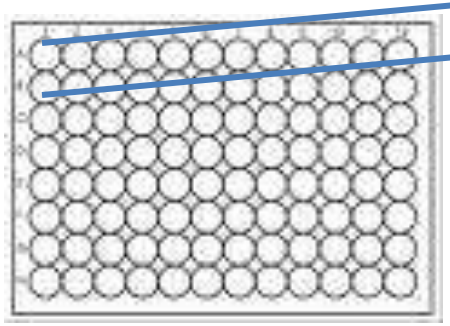

Phenotype Data
Distributions
ANOVA
Partitioning Variation (heritability)
BLUPs
Association Analysis to establish marker-trait linkage (Fixed effect)
Estimate Breeding Value (Random effect)
Kinship matrix
Genotype Data
Marker Matrix
Structure
Q Matrix (PCA)

	A	B
1		V1
2	M1	-0.00038
3	M2	-0.00013
4	M3	-0.00277
5	M4	-0.00375
6	M5	-0.00363
7	M6	0.005726
8	M7	-0.00401
9	M8	0.010731
10	M9	0.008691
11	M10	-0.0041
12	M11	-0.00046
13	M12	3.10E-06
14	M13	0.001184
15	M14	0.004107
16	M15	-0.00118
17	M16	0.000306
18	M17	-0.00126
19	M18	-0.00386
20	M19	0.0038
21	M20	-0.00296
22	M21	-0.00472
23	M22	-0.00279
24	M23	0.002641



Genomic Selection (GS) is exciting because it promises the ability to predict performance based on sequence variation (C/T).

How prediction models work:



X1[1:5, 1:8]

	M1	M2	M3	M4	M5	M6	M7	M8
1	1	0	0	1	-1	0	0	1
2	0	0	0	-1	1	0	1	1
3	1	0	0	1	-1	0	1	1
4	1	1	1	0	0	0	0	1
5	0	-1	-1	0	0	0	0	1

DNA extracted and allele specific assays conducted to determine genotypes.

The result is a matrix of marker data coded based on allele dose.

Selections made based on “model” (developed from previous experience with performance and sequence information).

X1[1:5, 1:8]

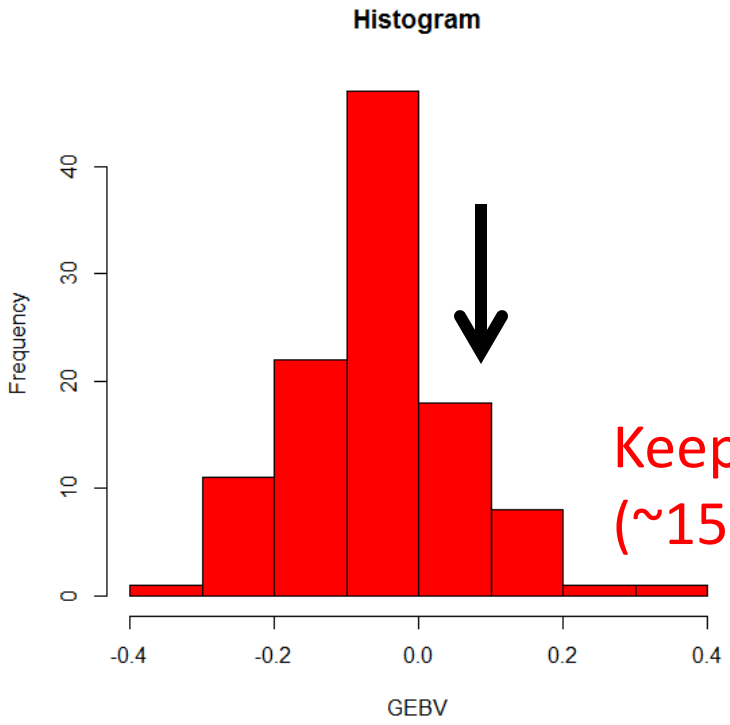
	M1	M2	M3	M4	M5	M6	M7	M8
1	1	0	0	1	−1	0	0	1
2	0	0	0	−1	1	0	1	1
3	1	0	0	1	−1	0	1	1
4	1	1	1	0	0	0	0	1
5	0	−1	−1	0	0	0	0	1

X

	A	B
1		V1
2	M1	-0.00038
3	M2	-0.00013
4	M3	-0.00277
5	M4	-0.00375
6	M5	-0.00363
7	M6	0.005726
8	M7	-0.00401
9	M8	0.010731
10	M9	0.008691
11	M10	-0.0041
12	M11	-0.00046
13	M12	3.10E-06
14	M13	0.001184
15	M14	0.004107
16	M15	-0.00118
17	M16	0.000306
18	M17	-0.00126
19	M18	-0.00386
20	M19	0.0038
21	M20	-0.00296
22	M21	-0.00472
23	M22	-0.00279
24	M23	0.002641

[96 x 384] x [384 1] = [96 1]

[G x M] x [M] = Prediction for 96 Genotypes



Keep those at K = 1
(~15% of the population)

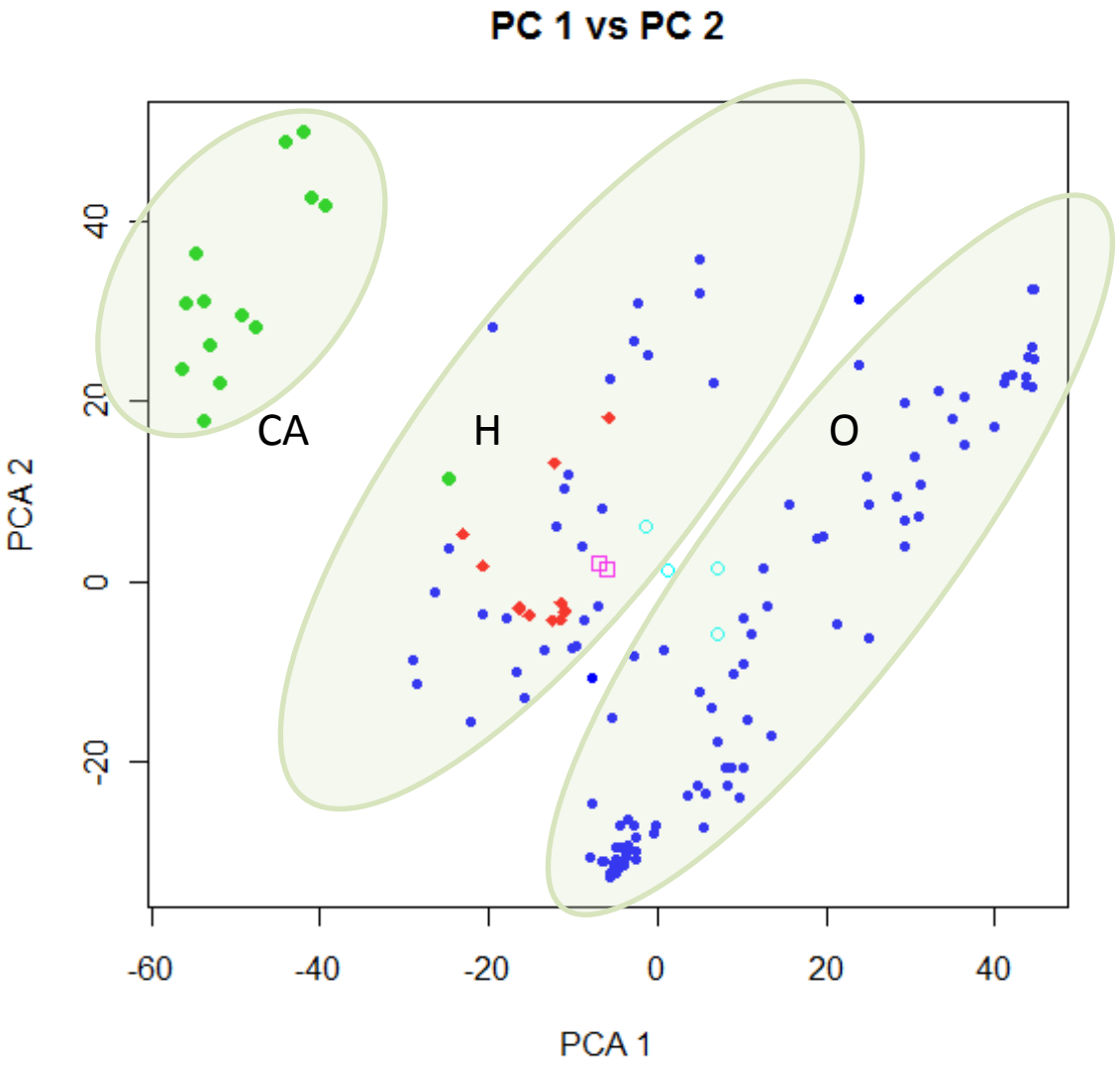
	A	B
1		x
2	14	-0.36451
3	17	-0.2875
4	104	-0.28532
5	15	-0.27402
6	76	-0.27182
7	96	-0.27018
8	8	-0.26794
9	9	-0.25418
10	49	-0.24986
11	92	-0.20341
12	23	-0.20324
13	11	-0.20033
14	34	-0.19169
15	66	-0.18804
16	39	-0.18763
17	65	-0.17746
18	16	-0.16764
19	28	-0.16176
20	89	-0.16098
21	100	-0.14011
22	4	-0.13922
23	69	-0.138
24	63	-0.13526
25	35	-0.13342
26	48	-0.12348

SolCAP Collection
140 inbred lines evaluated in CA and OH (2 year, 2 locations RBC design)

288 Nested RIL progeny
(OH2641 x OH987034; OH7814 x OH987034; OH2641 x OH981136)
(O x H; O x H, O x CA)
Augmented Experimental design (2 year, 2 locations)

Populations (SolCAP) and (OxH; OxH, OxCA)

California
Ohio
Undeterimined
Ridgetown College, Ontario
Oregon

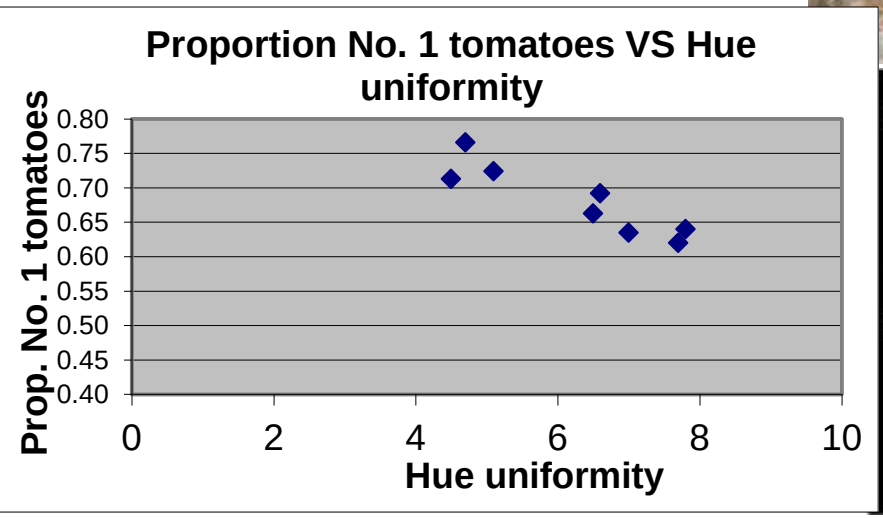


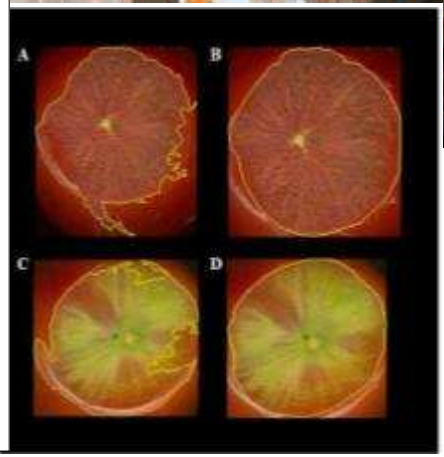
Clustering based on 7,700 SNPs

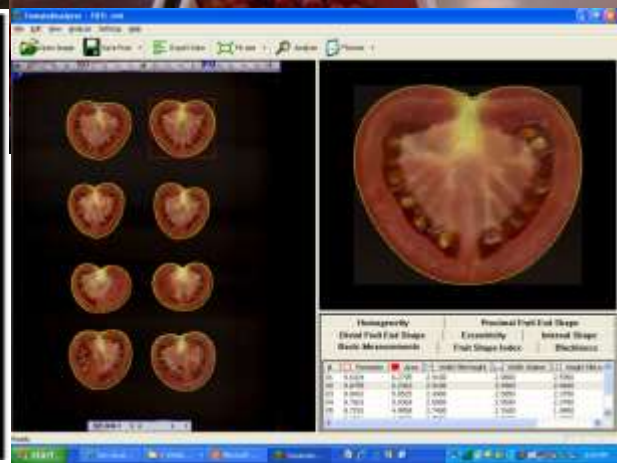
Traits: Total traits measured: 52
Yield, digital phenotyping and chemical meas.

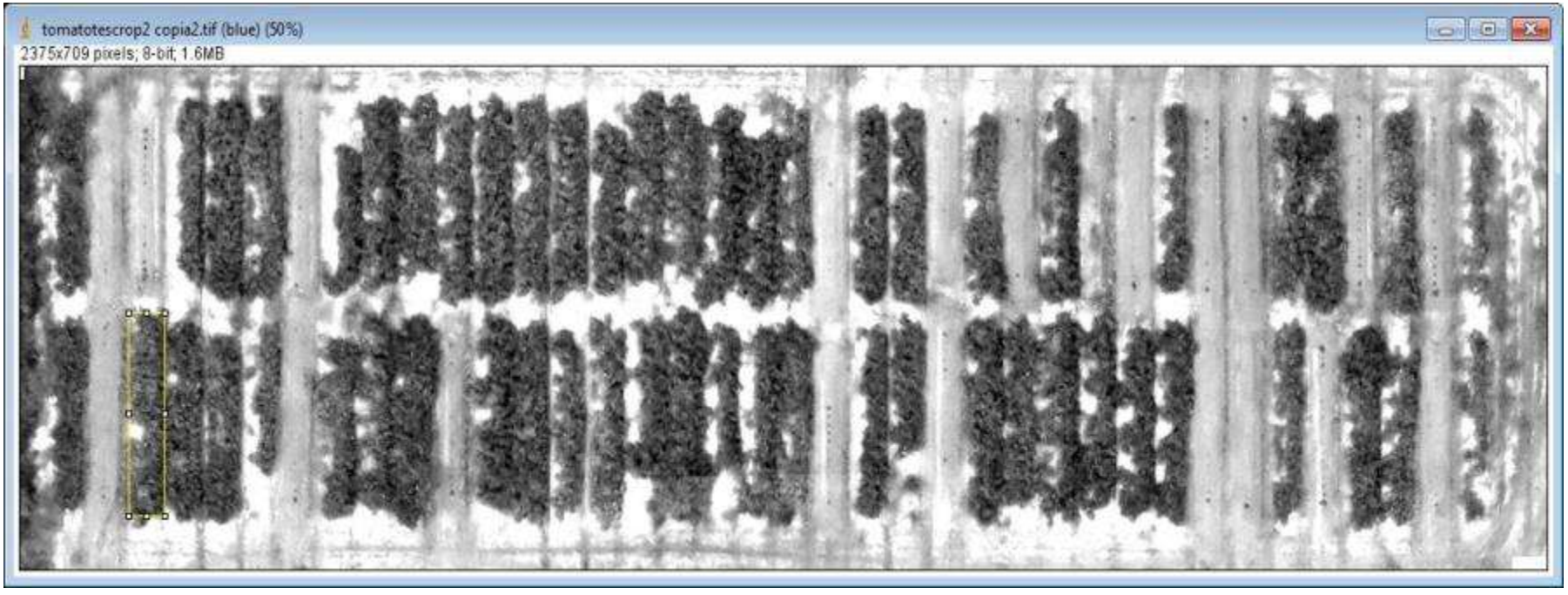
Reduced to 22 most informative
(h^2, PCA and other methods)

- Yield (total and marketable)
- Color and Color uniformity
- BRIX
- pH
- Vitamin C
- Fruit Size and Shape





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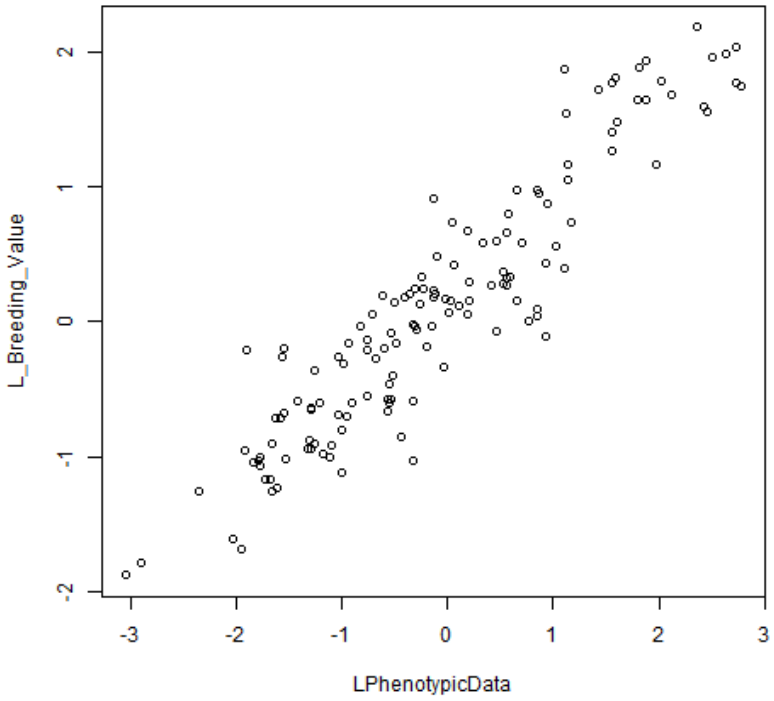
2375x709 pixels; 8-bit; 1.6MB

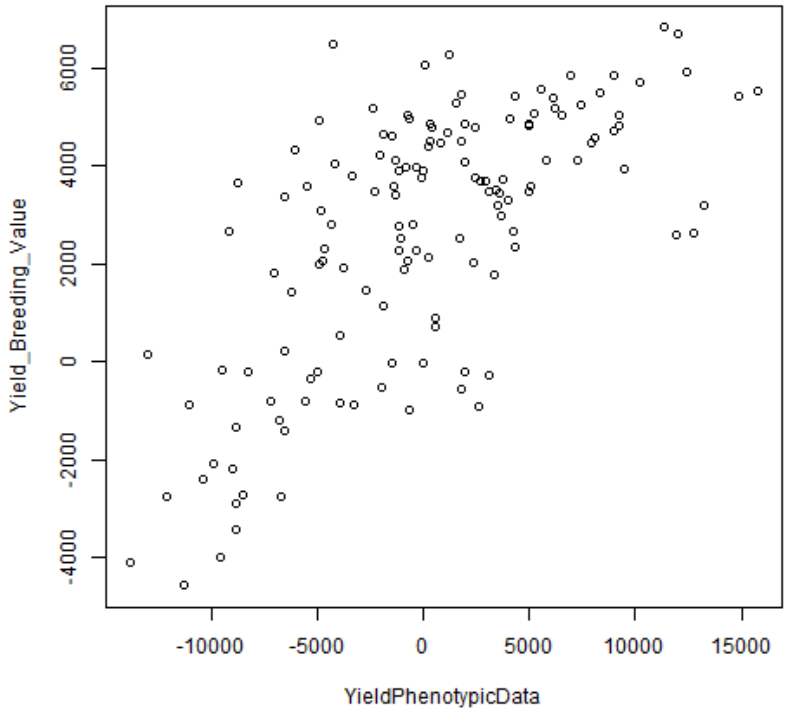
Predicting inbred-line performance from inbred line data
Data from SolCAP data (140 varieties, 7,700 markers)

Trait	P_value	R^2
Color_Unifromity	3.99E-69	0.895
L	3.98E-61	0.863
hue	8.97E-52	0.812
Fruit Size	1.15E-30	0.618
Yield	6.11E-20	0.454
Brix	1.77E-66	0.885

← **Fruit Size**

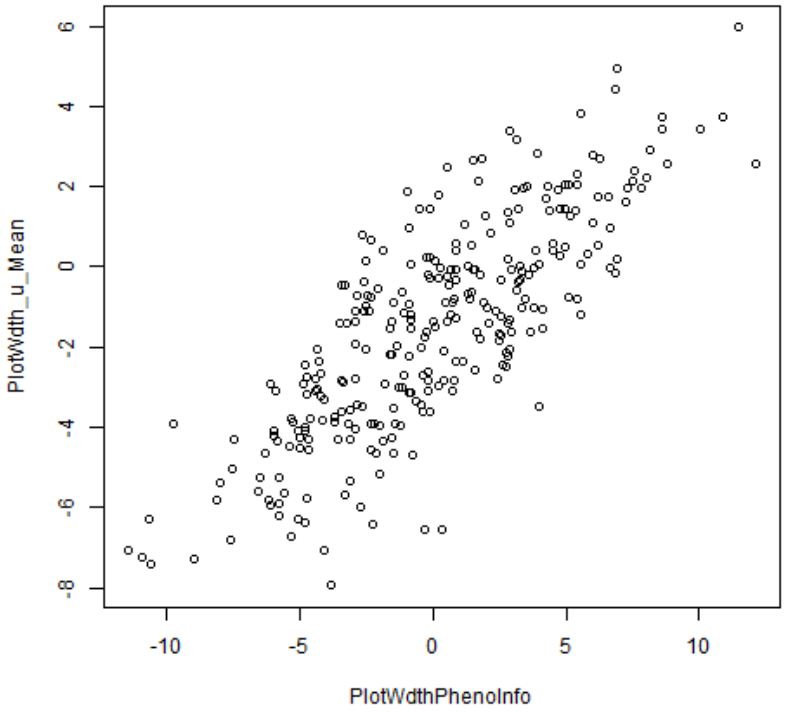
← **Yield**

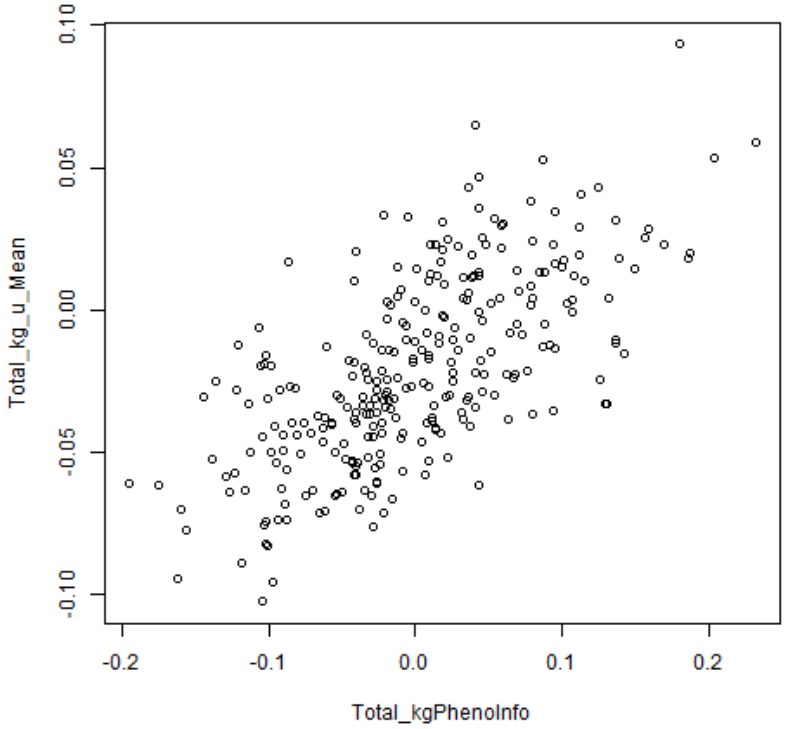




Predicting inbred-line performance from inbred line data
Results from nested RIL (280 x 384 markers)

Trait	P_value	R^2	
PlotWdth	1.75E-64	0.639	
Total_kg	1.29E-38	0.449	← Yield
Total_Frt	6.27E-33	0.396	
Ripe_kg	1.48E-16	0.212	
Ripe_Frt	1.64E-35	0.421	
Frt Size	7.02E-68	0.658	← Fruit Size





Predict hybrid performance from inbred data

Training Populations (Genotype and Phenotype)

- SolCAP (inbreds)
- Nested RIL (inbreds)

Hybrids

- Predict genotype from inbred data
- Predict performance using GW model(s) developed for inbreds
- Compare prediction with actual performance

	M1	M2	M3	M4	M5
Inbred 1	1	1	0	0	0
Inbred2	1	0	1	1	0
Inbred3	0	1	0	1	1
F1 1x2	1	0.5	0.5	0.5	0
F1 1x3	0.5	1	0	0.5	0.5
F1 2x3	0.5	0.5	0.5	1	0.5

Hybrid genotype matrix
(estimated from inbred genotypes)

[384 1] x [96 384] = [96 1]

M x [G x M]

Model:
Vector of Marker Estimated Breeding Value (Contribution of each marker to trait)

	A	B
1		V1
2	M1	-0.00038
3	M2	-0.00013
4	M3	-0.00277
5	M4	-0.00375
6	M5	-0.00363
7	M6	0.005726
8	M7	-0.00401
9	M8	0.010731
10	M9	0.008691
11	M10	-0.0041
12	M11	-0.00046
13	M12	3.10E-06
14	M13	0.001184
15	M14	0.004107
16	M15	-0.00118
17	M16	0.000306
18	M17	-0.00126
19	M18	-0.00386
20	M19	0.0038
21	M20	-0.00296
22	M21	-0.00472
23	M22	-0.00279
24	M23	0.002641

	M1	M2	M3	M4	M5
Inbred 1	1	1	0	0	0
Inbred2	1	0	1	1	0
Inbred3	0	1	0	1	1
F1 1x2	1	0.5	0.5	0.5	0
F1 1x3	0.5	1	0	0.5	0.5
F1 2x3	0.5	0.5	0.5	1	0.5

[384 1] x [96 384] = [96 1]

M x [G x M] = Prediction for 96 Hybrids

Model:
Vector of Marker Estimated Breeding Value (Contribution of each marker to trait)

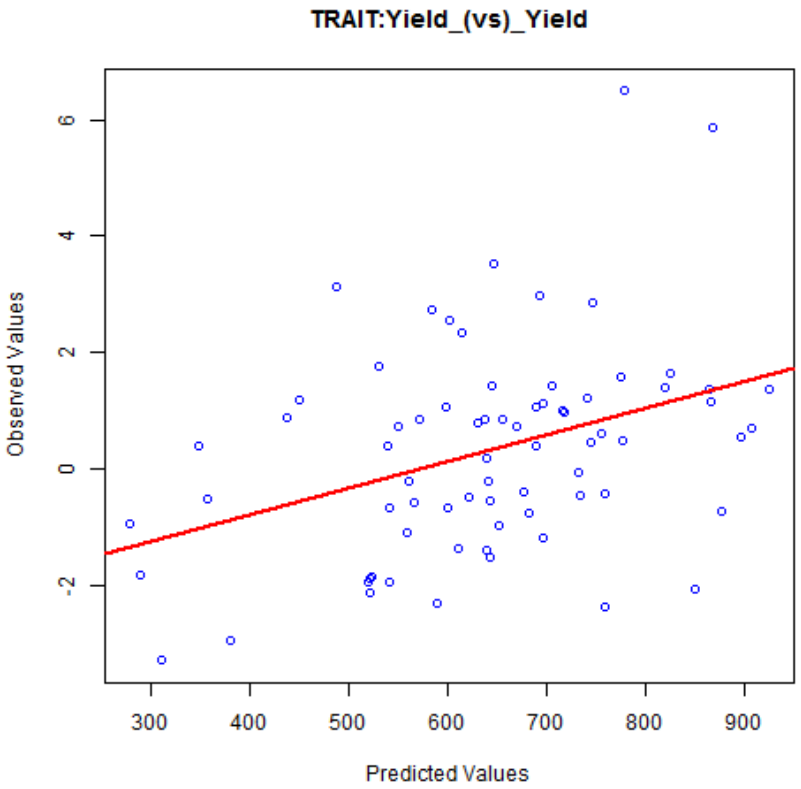
Hybrid genotype matrix
(estimated from inbred genotypes)

How does predicted performance relate to actual performance?

Predicting Hybrid Performance from inbred-line data

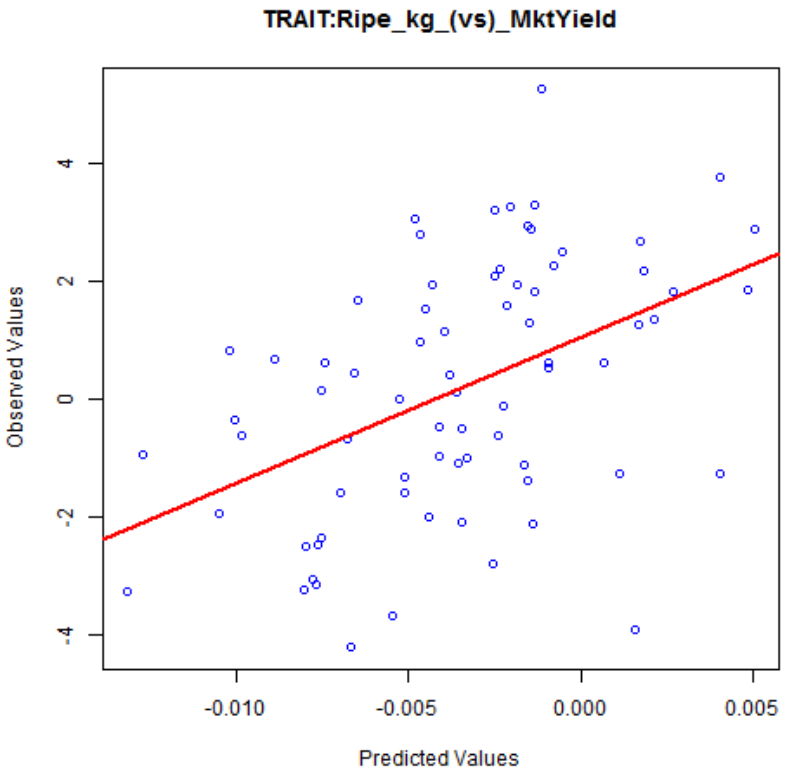
Model from SolCAP (n =140 K = 7,700)

from RIL (n = 280 K = 384)



Yield_(vs)_Yield P = 0.001182

R^2 = 0.126445

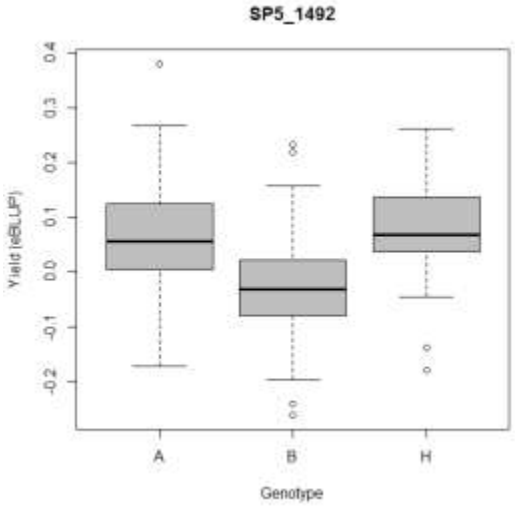


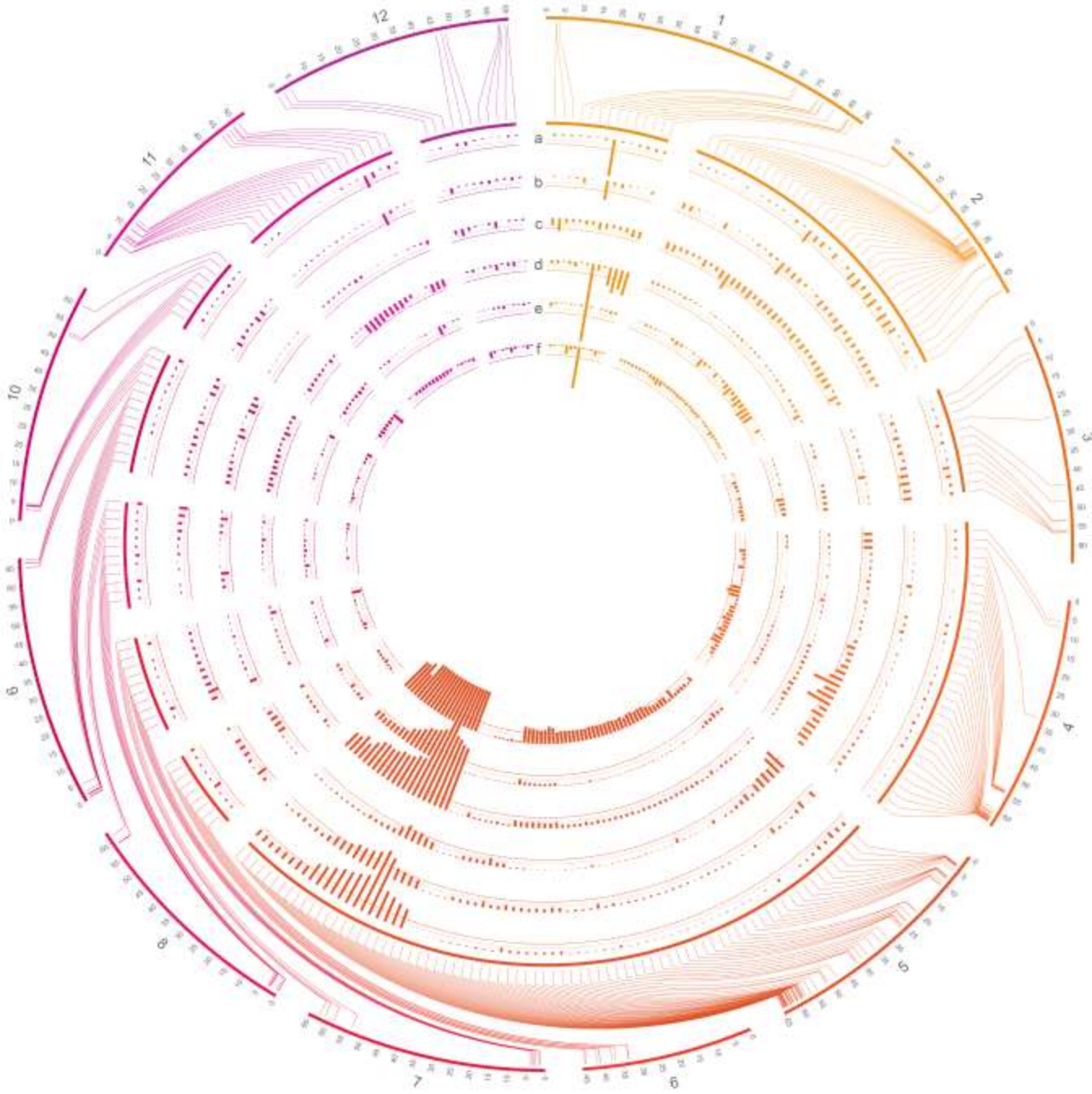
Ripe_kg_(vs)_MktYield P = 4.42E-05

R^2 = 0.19958

Association analysis

a = Yield as BLUP
b = Yield normalized
c = fruit weight
d = fruit number
e = vine size

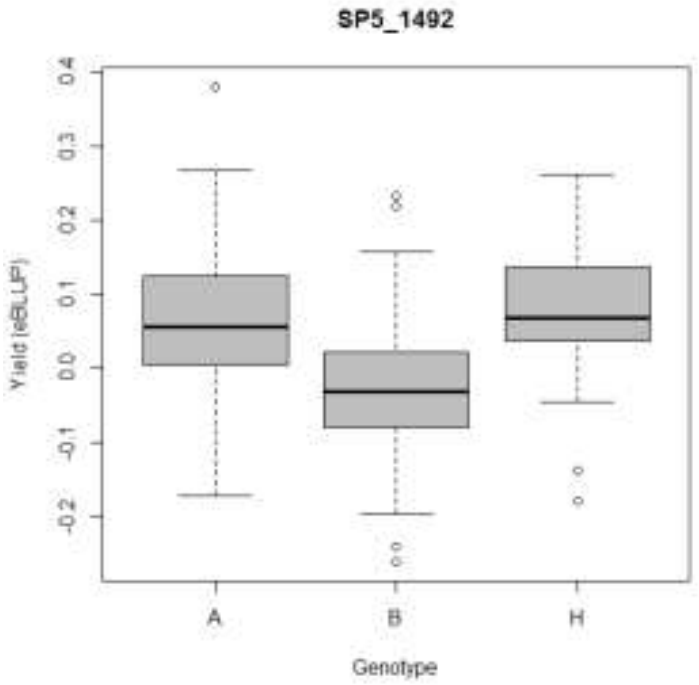




Currently: Testing to see if additive models can be improved by incorporating non-additive effects

	A	B
1		V1
2	M1	-0.00038
3	M2	-0.00013
4	M3	-0.00277
5	M4	-0.00375
6	M5	-0.00363
7	M6	0.005726
8	M7	-0.00401
9	M8	0.010731
10	M9	0.008691
11	M10	-0.0041
12	M11	-0.00046
13	M12	3.10E-06
14	M13	0.001184
15	M14	0.004107
16	M15	-0.00118
17	M16	0.000306
18	M17	-0.00126
19	M18	-0.00386
20	M19	0.0038
21	M20	-0.00296
22	M21	-0.00472
23	M22	-0.00279
24	M23	0.002641

+

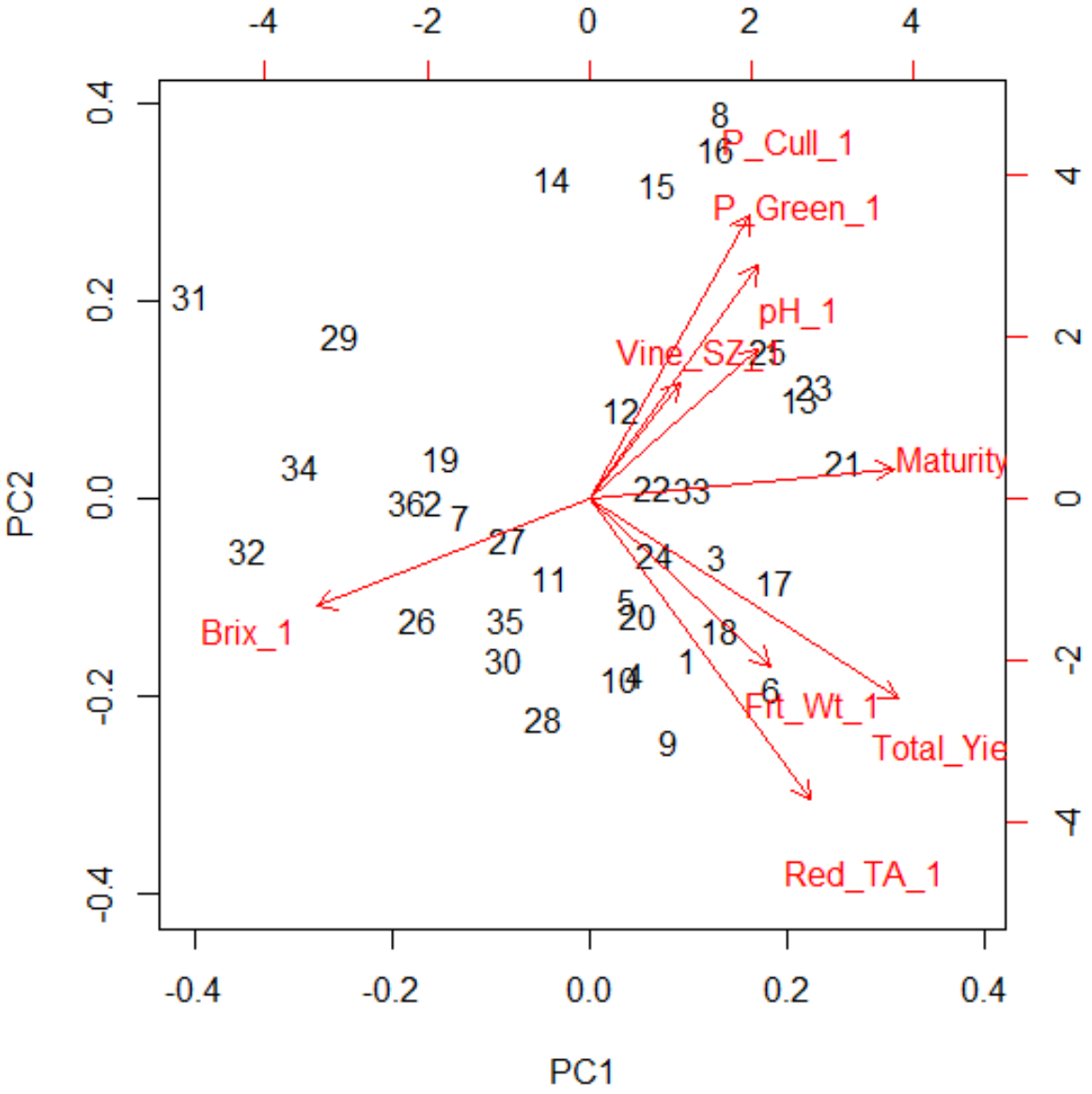


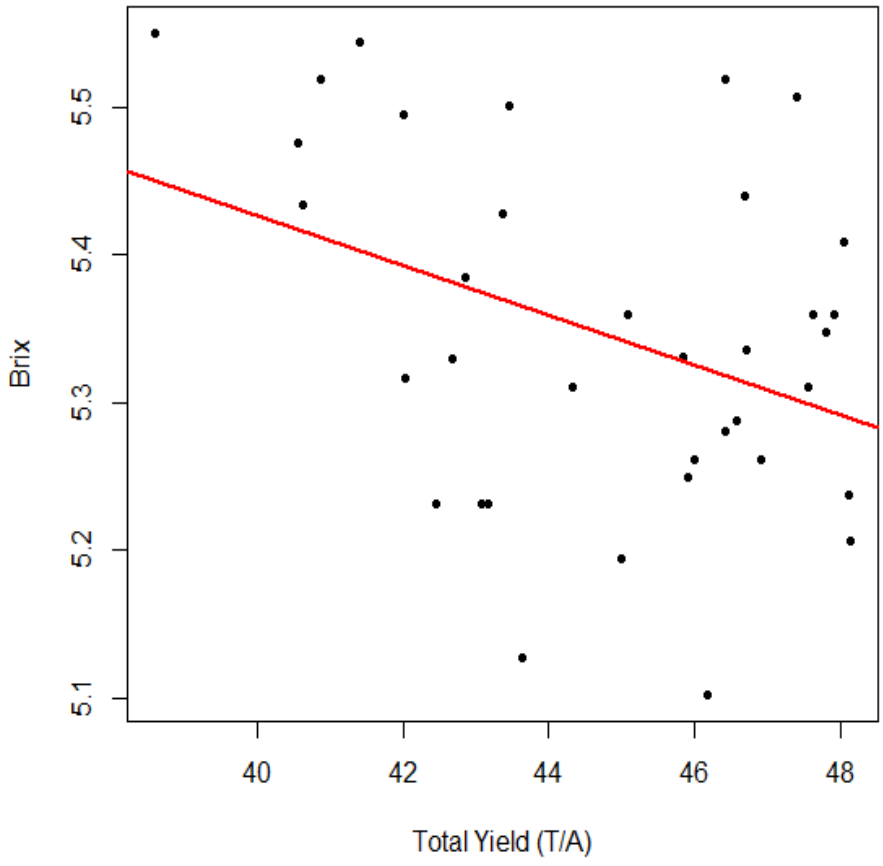
= **better prediction?**

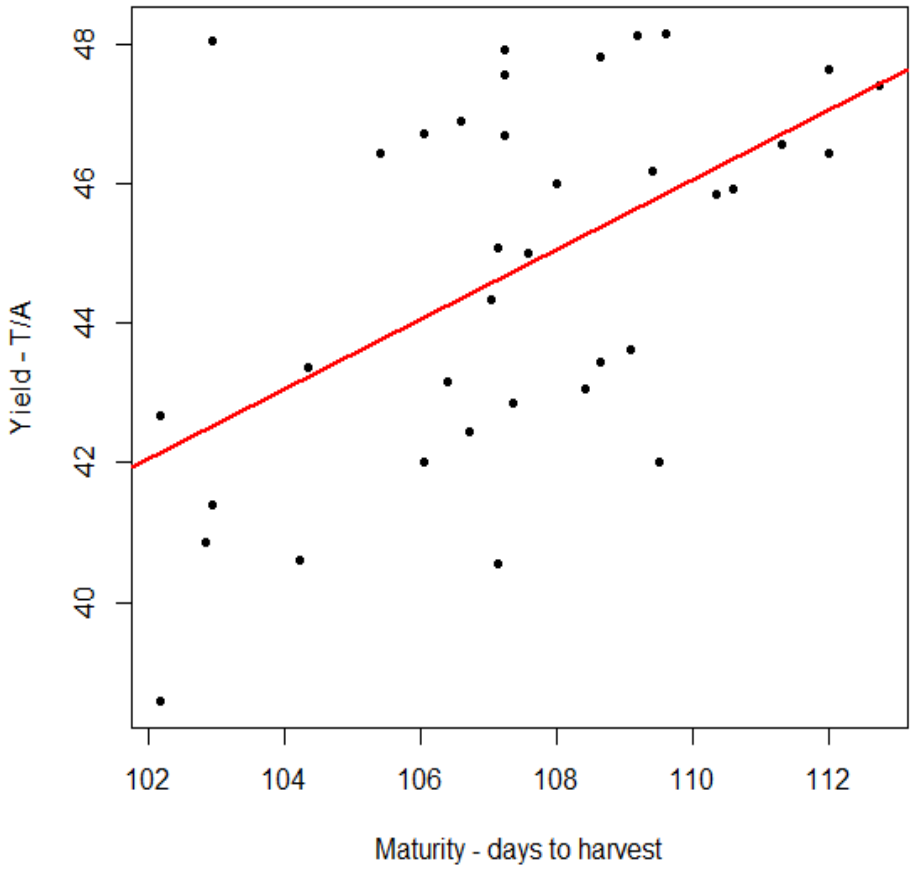
Ability to predict performance based on genetics is an exciting development, but "beyond mountains there are mountains“.

- What are we selecting for $(\gamma)\ \gamma = \mu + \ddot{X}\ \beta + \in$?
- Yield, Brix, Color, Viscosity, Resistance (n = 5-17)
- GWS for multiple traits requires that we have robust Multi Trait Indices (MTI) for selection

Trait weights







Trait	Weight
Yield	+2
Color	-1
Brix	0
etc…	

Traits: What can historical data tell us about trait models?

California PTAB

- 20 years
- 585 varieties
- 8.8 million of loads

Farm Advisor Variety Trials

- 10 years
- 173 varieties

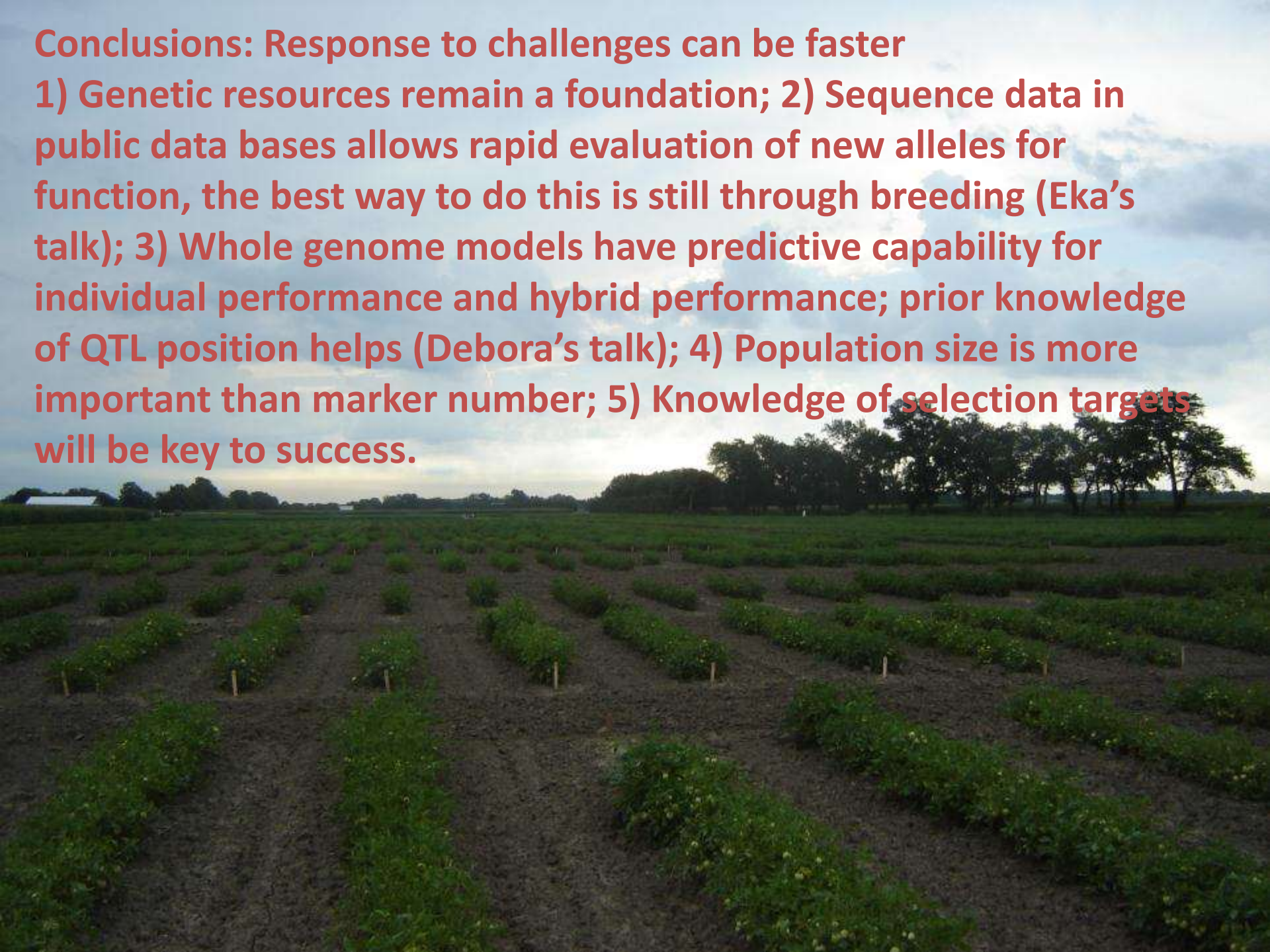
Traits Measured

- Yield
- Brix
- pH
- Color
- Defects
- Number of loads produced

- **Can we predict performance in market with traits value?**

Model	P-value	Percent accuracy	Stand. dev.
MTI_2 [v]	0.001	35	9
yield	0.03	29	9
Yield xBrix	0.534	23	12
random	-	14	7

[v] = Multi-Trait Index weighting Yield, BRIX, Color and limited use. Evaluated based on ability to predict market success (% load and longevity) in varieties from PTAB and UCCE year data set.



Conclusions: Response to challenges can be faster

1) Genetic resources remain a foundation; 2) Sequence data in public data bases allows rapid evaluation of new alleles for function, the best way to do this is still through breeding (Eka's talk); 3) Whole genome models have predictive capability for individual performance and hybrid performance; prior knowledge of QTL position helps (Debora's talk); 4) Population size is more important than marker number; 5) Knowledge of selection targets will be key to success.

Thank you for your time.

Questions?

Some up coming meetings

5th International Symposium on Tomato Diseases

IHSM CSIC

Málaga, Spain June 13-16, 2016

ISHS

15-18 August, Raleigh NC

National Association of Plant Breeders

NAPB

Improving Plants to Improve Lives

The 13th Solanaceae Conference

SolGenomics: From Advances to Applications

September 12 – 16, 2016 • Davis California USA

Shameless advertisement:

THE OHIO STATE UNIVERSITY OARDC

Plant Breeding Summer Workshops

Session 1: Field Design and Analysis

May 23-27 2016

- Introduction to R Statistical Software
- Linear models of phenotype, heritability, & gain under selection
- Randomized Complete Block Designs
- Augmented and lattice designs for trials with many entries
- Best Linear Unbiased Predictors (BLUPs)
- Partitioning Variation and estimating heritability
- Genotype by environment interactions
- Selection indices
- Field Tour

Session 2: Marker Assisted Selection

June 6-10 2016

- Introduction to R for marker-trait analysis
- Molecular marker platforms and scoring
- Basic marker-trait models
- Populations for breeding and mapping
- Linkage analysis and Linkage disequilibrium (LD)
- Genetic Variation in Populations
- Selecting for Recombination
- Background Genome Selection
- Population sizes required for selection
- Field Tour

Session 3: Genome Wide Analysis

June 27-July 1 2016

- Introduction to R packages rrBLUP, GAPIT, BLR
- Random effects models
- The structure of breeding populations
- Association Mapping
- Genome wide selection (GWS)
- Incorporating genomic selection in a breeding program
- Selection for multiple traits

All 3 = HCS 8825

Individual workshops as HCS 8806 (Methods)

Reminder: Support germplasm center(s)

http://tgrc.ucdavis.edu/Donate/

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Acknowledgments

Collaborators, OSU

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Sung-Chur Sim
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John Hamilton
Dan Zarka
Kelly Zarka

Collaborators, UFL

Sam Hutton
Jay Scott

Collaborators, CAU

Wencai Yang
Hui Wang

Collaborators, INRA

Mathilde Causse

Collaborators, UIB

Hipolito Medrano
Pep Cifre
Josefina Bota
Miquel Angel Conesa

Collaborators, Industry

Cindy Lawley, Illumina
Martin Ganal, Trait Genetics
Hirzel Canning
Red Gold Canning

National Cancer Institute at the National Institutes of Health

SEEDS

OPBC

USDA NIFA United States Department of Agriculture National Institute of Food and Agriculture