

# The Intersection of Genomics and Wheat Breeding for Developing Superior Cultivars and Hybrids.

P. Stephen Baenziger, Katherine Frels, Vikas Belamkar, Ibrahim El-Basyoni, Nicholas Garst, Amir Ibrahim, Yusheng Zhao, and Jochen Reif



# P. Stephen Baenziger

- Great honor to be asked to present this lecture.
- I am an applied plant breeder who uses science to create new cultivars.
- I have released 44 wheat, 7 barley, and 13 triticale cultivars.



“If I have seen further it  
is by standing on the  
shoulders of Giants”

Sir Isaac Newton, 1675 (in a letter to Robert  
Hooke)



# Topics:

- Plant Breeding and its use of genetics and genomics are the context of this talk.
- Building the foundation for a better future for plant breeding through genetics and genomics.
- Evolving plant breeding and the interaction with genomics and phenomics—the latter will not be discussed in this presentation.

## *Objective:*

- *To provide insight on how genomics are used by plant breeders.*

# Why Do Plant Breeders Change their Strategy?

- **Novelty:** We can do something that we could not do before.
- **Efficiency:** Doing something to do more efficiently in how we use our resources. Doing more with resources that plant breeding has. *Plant breeding is expensive.*

# What is Necessary: USDA-University of Nebraska



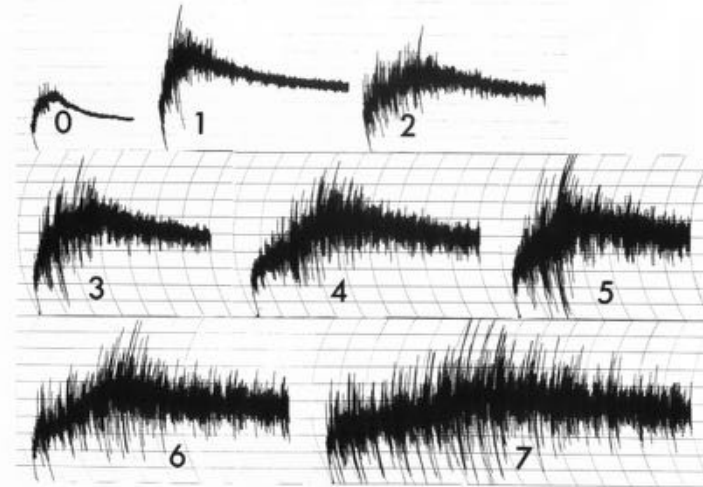
Survive the Winter



Perform well in the Field



Have stem rust resistance

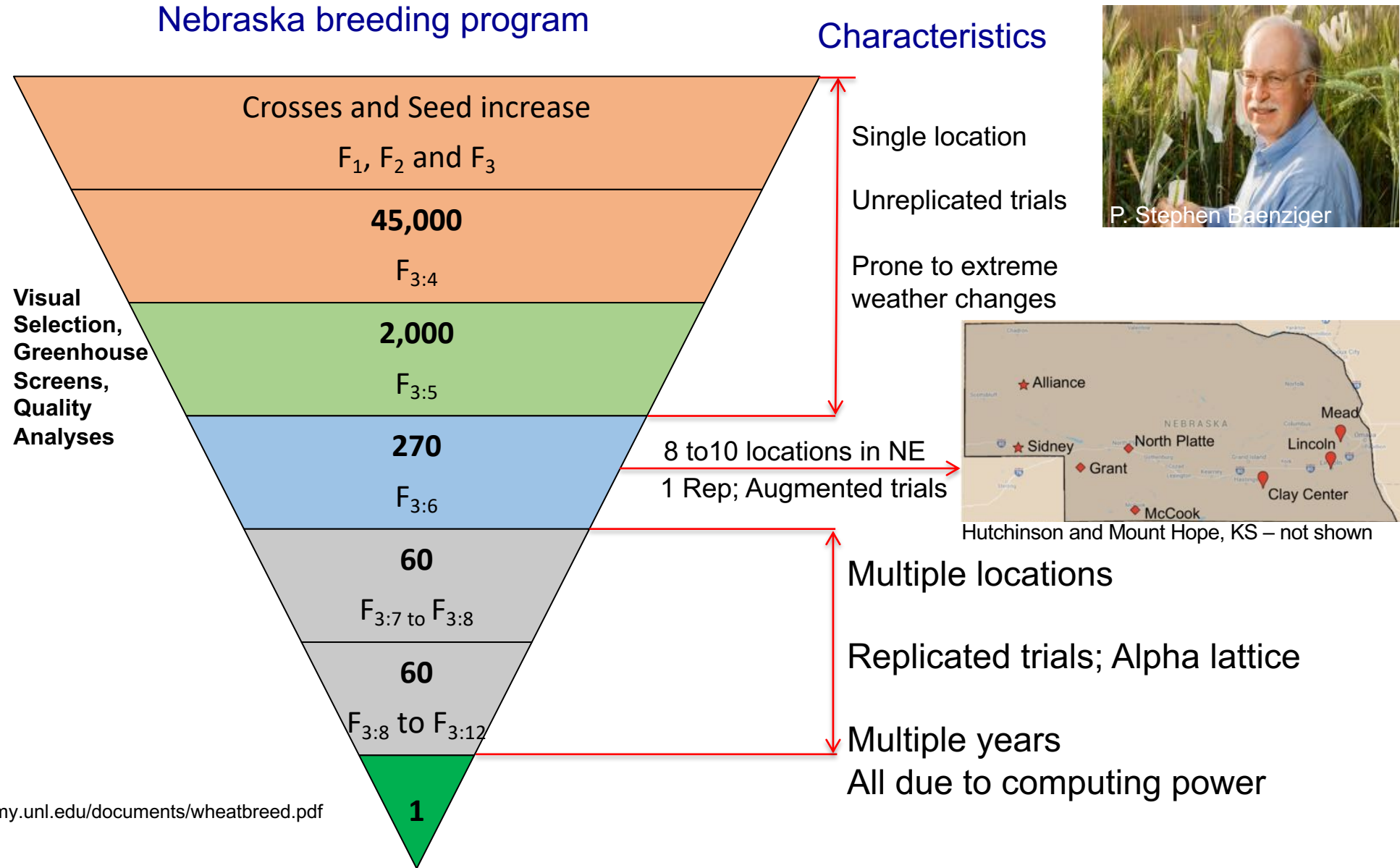


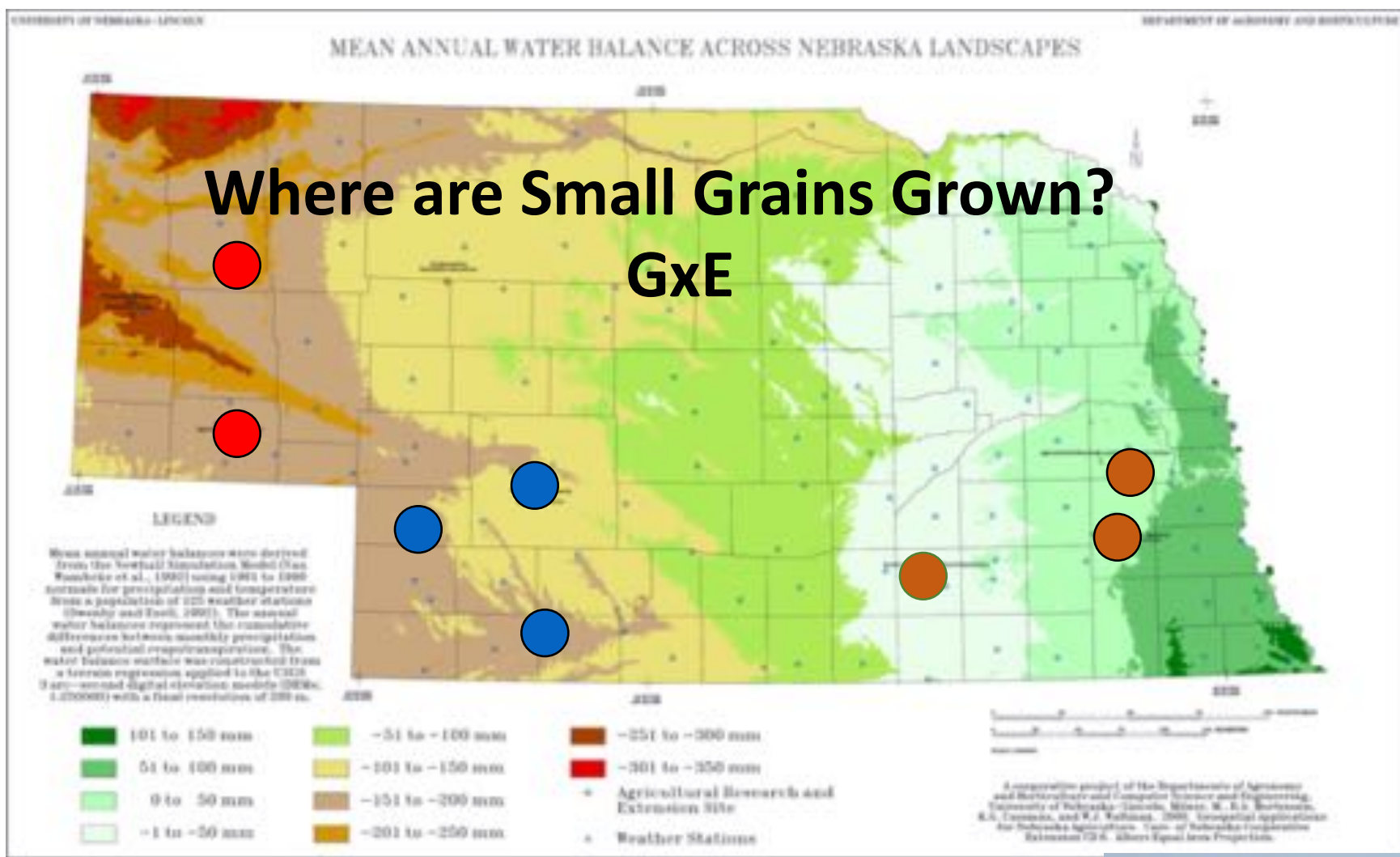
Make a good loaf of bread





# Nearly 100,000 lines are screened over 12 years to find a cultivar for release ( for the past ~70 years)



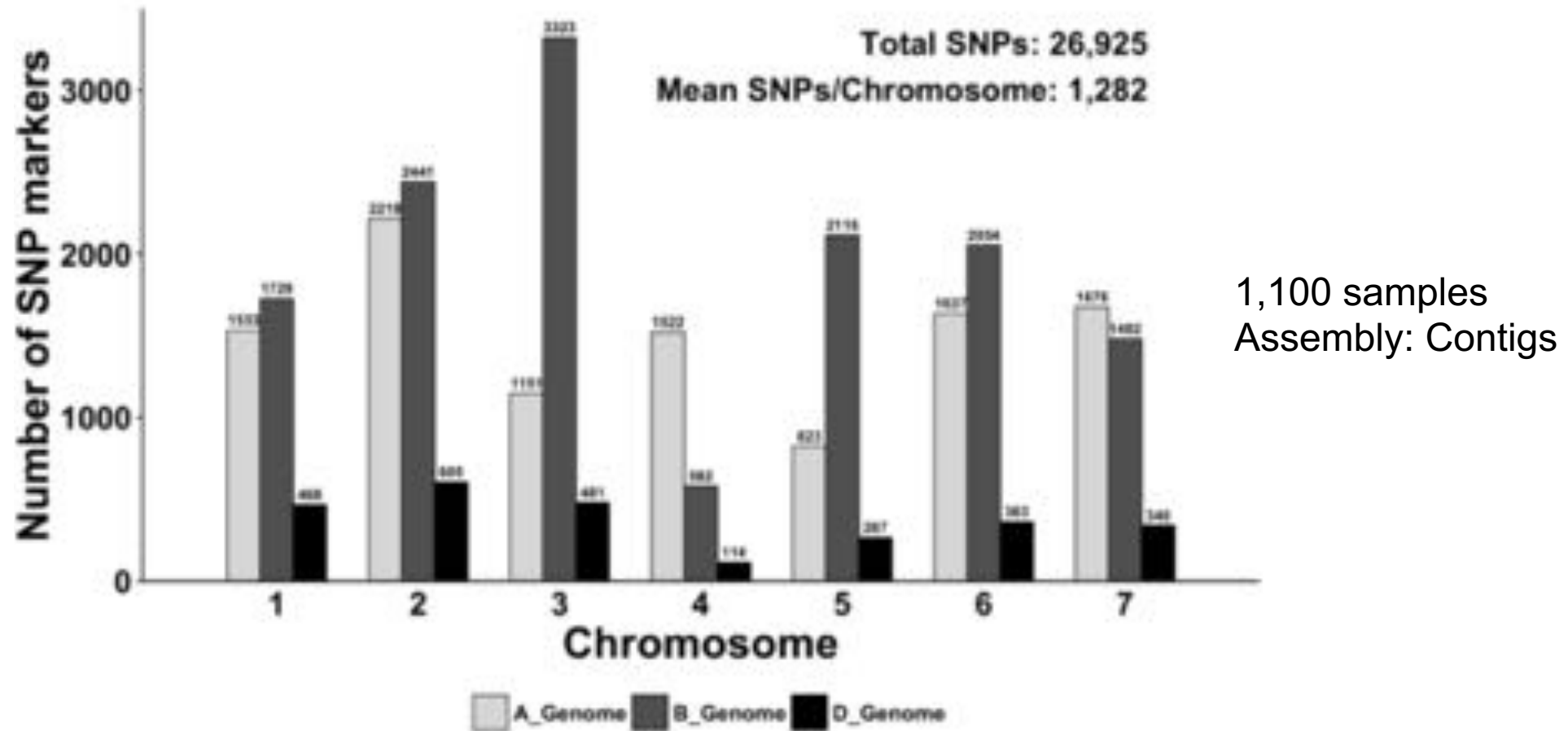




# Integrating Genetics/Genomics into Breeding

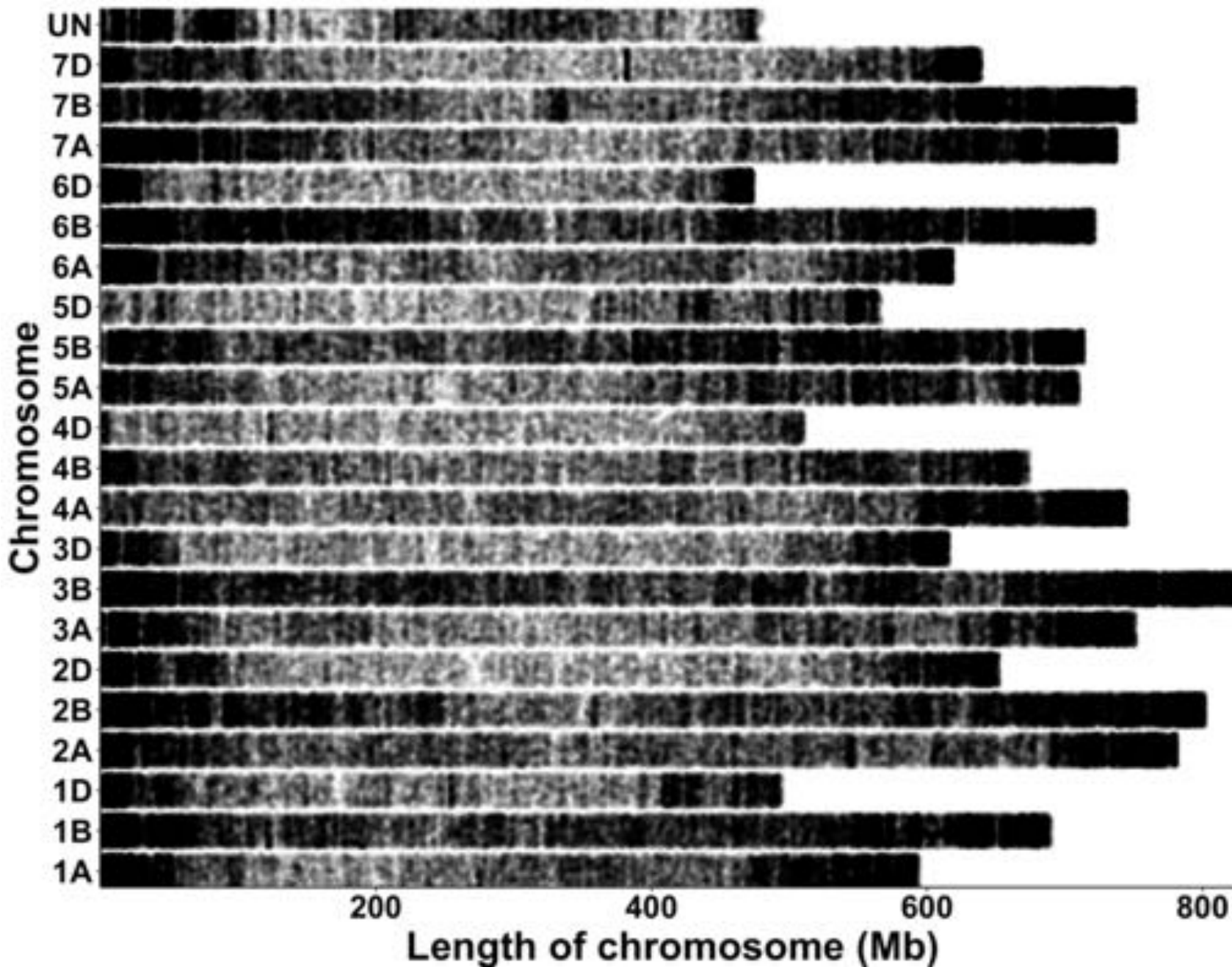
- Our marker platform.
- GWAS for known markers.
- Genomic selection.

# GBS can provide large number of SNPs



Genomic selection (GS)  
Until 2015 – 25 to 50K SNPs

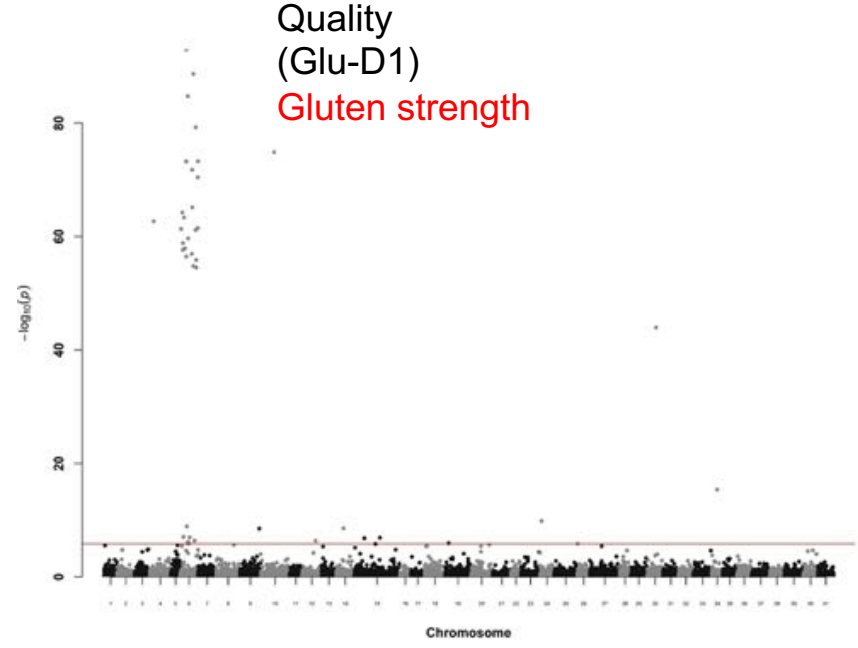
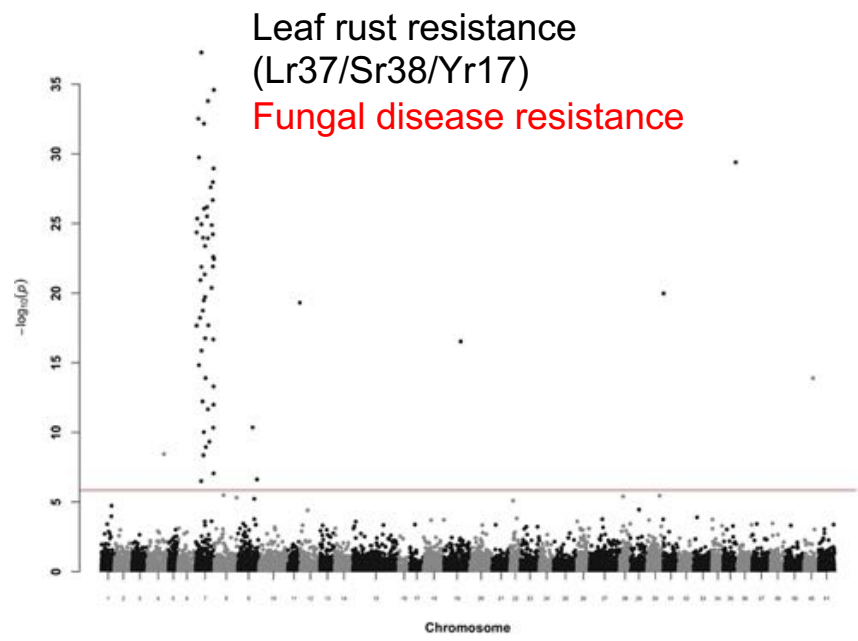
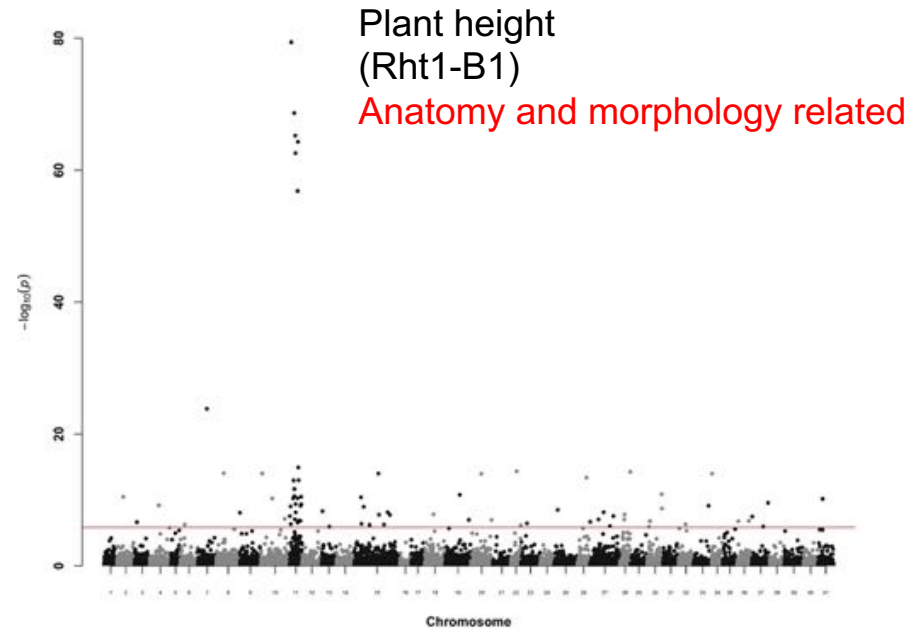
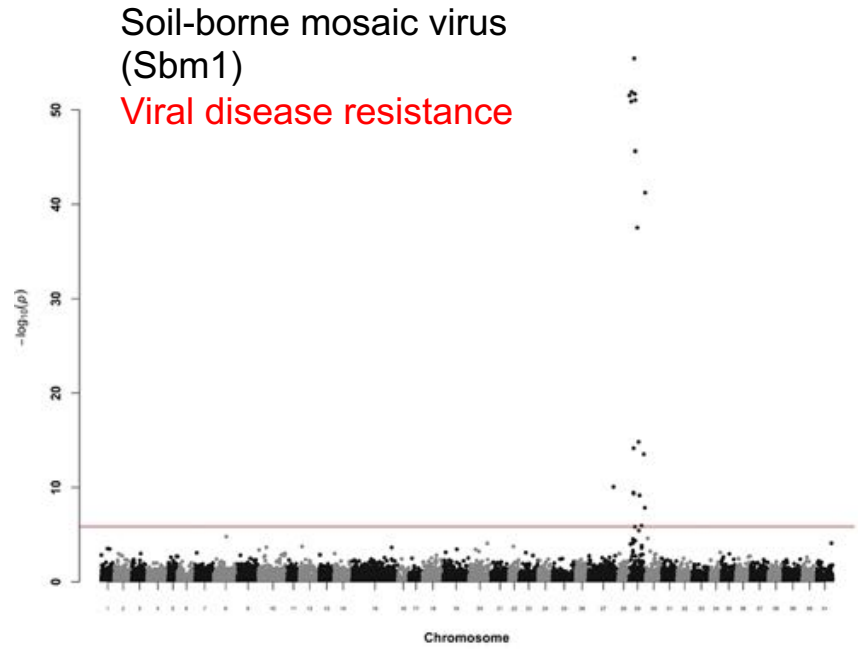
Note the lack of SNPs in the D genome

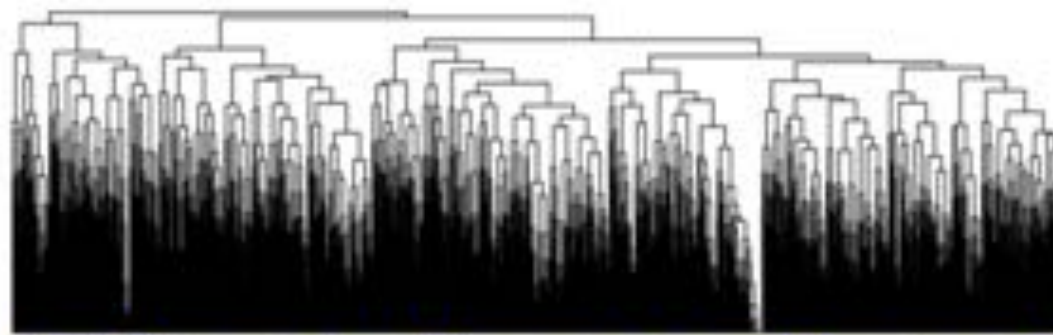
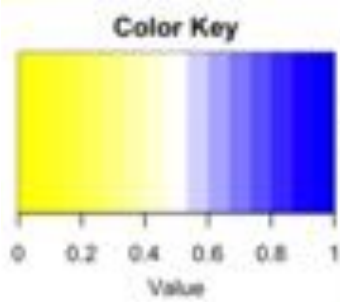


~7,000 samples  
Pseudomolecule  
high-quality genome  
assembly IWGSC  
RefSeq v1.0

2016: >95k SNPs  
2017: >100K SNPs  
2021: > 350,000  
SNPs; 113,000  
filtered SNPs

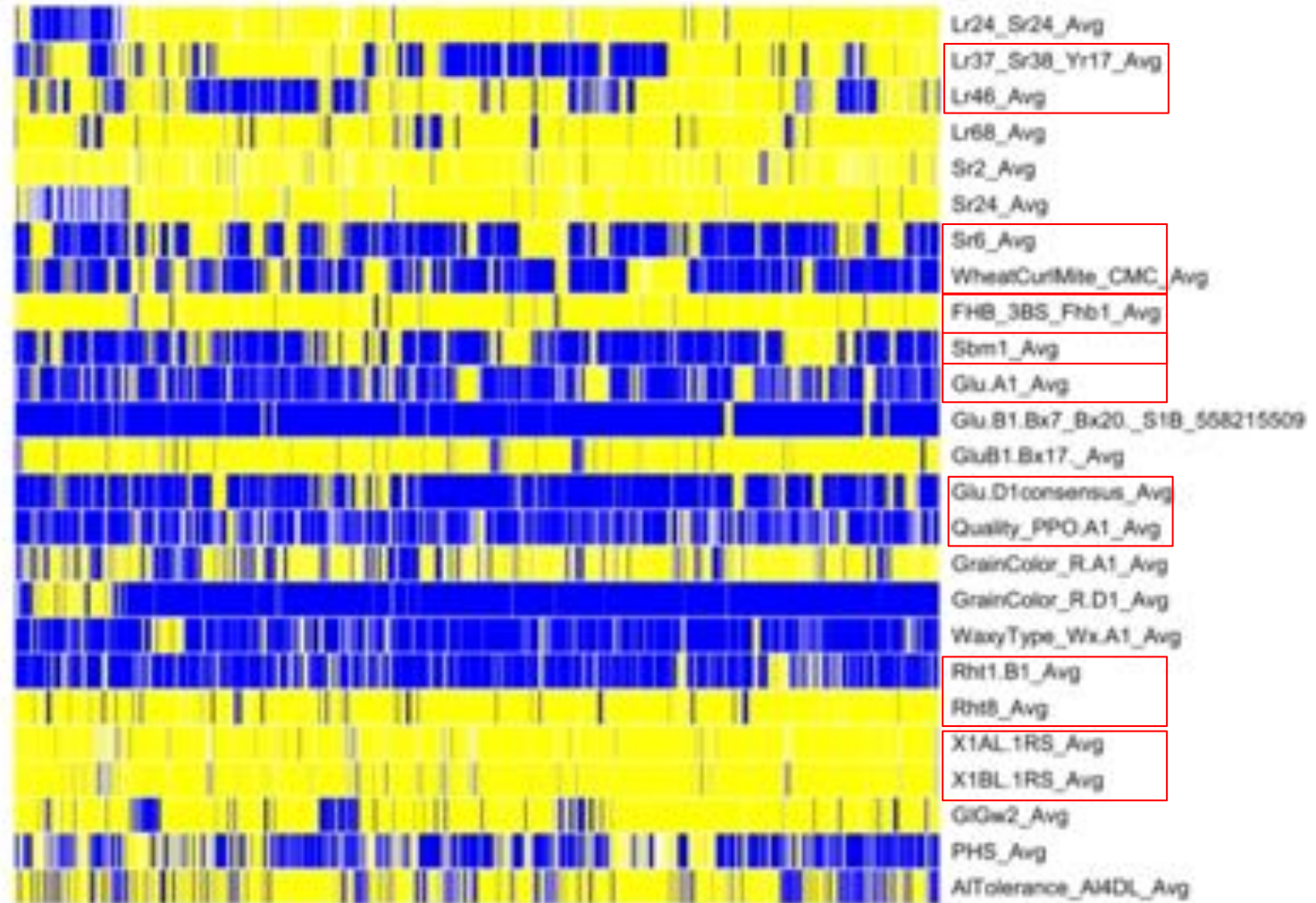
Converted our single gene markers to GWAS so that we can identify numerous QTL using GBS.





## Estimating Diversity

F<sub>3:5</sub> – 2017  
~1,380 lines





# Comparing Marker Assisted Selection to Genomic Selection

- Ron Phillips once described:
  - A genetic marker is like playing a musical note
  - Understanding the genome is like playing a symphony



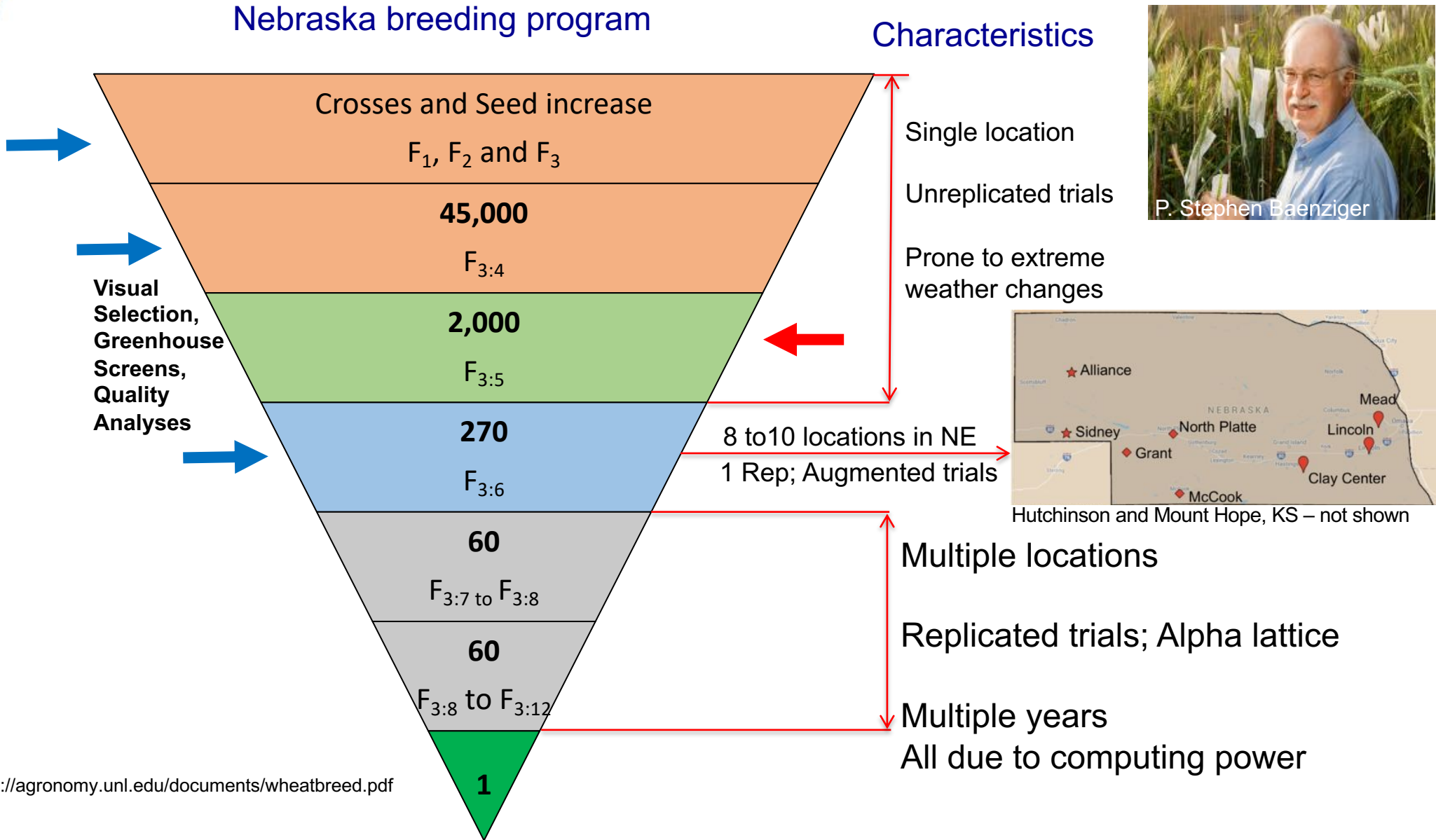
En.Wikipedia.org



nytimes.com



# Which step(s) are the most vulnerable: single location genotype trials.



<http://agronomy.unl.edu/documents/wheatbreed.pdf>



# Problem: Unreplicated Lines

- You are vulnerable at the grow-out/selection site.
- There is a difference between a selection nursery (magnifies differences) and evaluation/testing sites (represents where the cultivar should or should not be grown).
- **It is one and done.** *What happens when you have an unusual year?*
- You cannot estimate GxE.
- **Can you replicate over markers instead of replicating lines? (Use marker assisted or genomic selection)**



# What is an Unusual Year?

- 1990: Excessive rains and flooding in eastern NE.
- 1991: Heat temperature spike in late January, followed by a cold snap which killed lines with low vernalization requirement.
- 2000: Flowering dates were 2 weeks earlier than normal (photoperiod sensitive wheats remained later)
- 2011: Hail at Mead and at Sidney
- 2012: Flowering dates were 3-5 weeks earlier than normal
- 2015: Preliminary Observation Trial: Hail damage near maturity on 50% of the trial, also heavy rains and FHB.
- 2019: Heavy floods in eastern Nebraska during the early spring.
- 2020 Preliminary Observation Trial: Heavy rains after planting (crusting and washing, reduced heritability) on 60% of the trial.
- **Drought and heat stress are normal.**





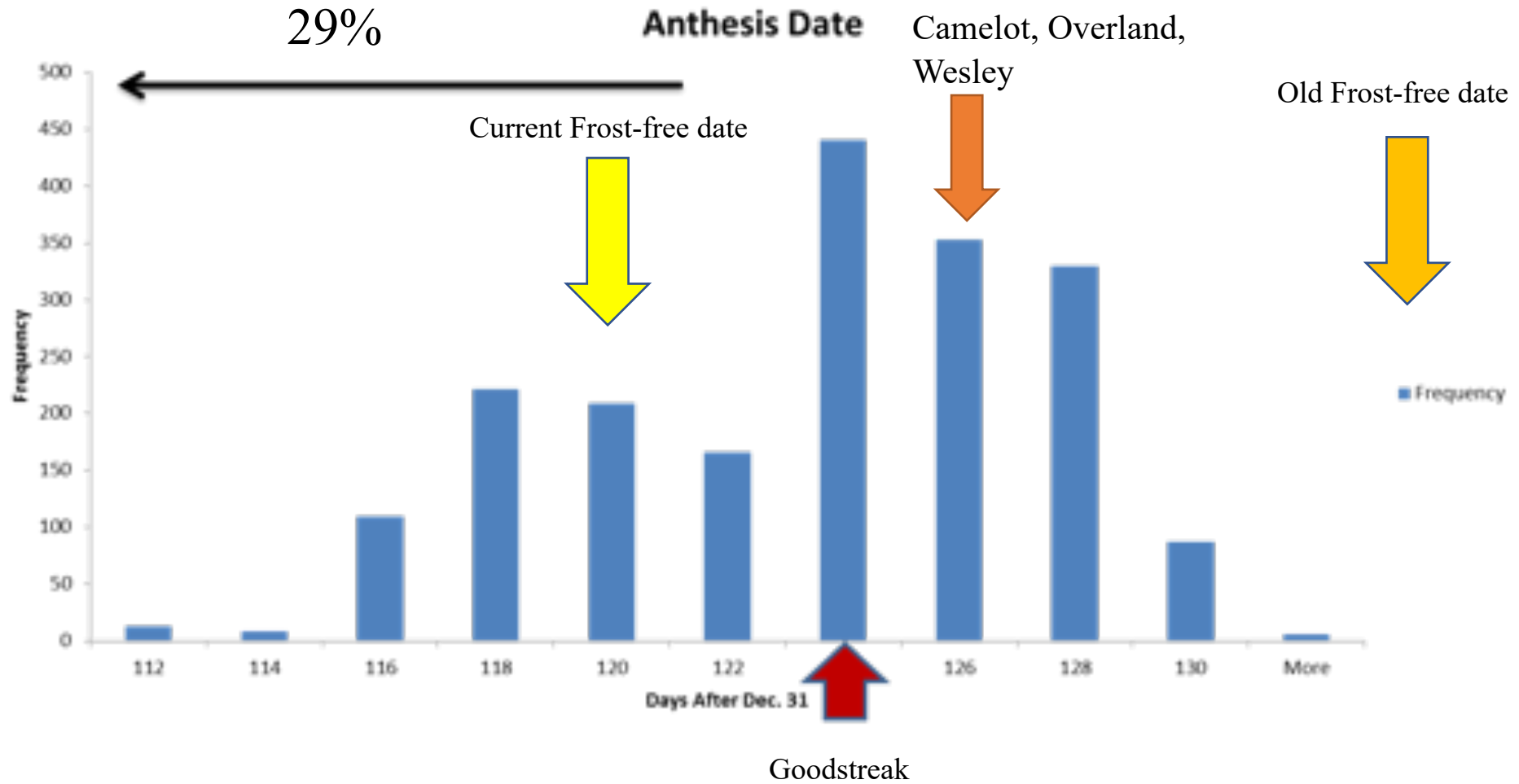
# The Importance of Vernalization:







# Anthesis Date 2012



# Hail storm damaged ~900 plots (~50%) in the 2016 F<sub>3:5</sub> nursery

## Ranks based on GEBV vs. BLUP

PLOT	GEBV	BLUP
16397	110	1672
16840	243	1717
16898	276	1732
16433	1440	35
16262	344	1725
16905	381	1740
16689	375	1716
16593	1489	154
16263	551	1858
16280	506	1809

Predictions made on 2016 F<sub>3:5</sub> lines for grain yield using F<sub>3:6</sub> 2012-2015 as training population



Before hail storm



After hail storm

## GS recovered lines from the 2016 F<sub>3:5</sub> nursery that were damaged due a hail event

	F <sub>3:5</sub> (2016)	F <sub>3:6</sub> (2017)	F <sub>3:7</sub> (2018)	F <sub>3:8</sub> (2019)
Total	1719	254	53	21
Less hail damaged lines	812	189 (74.4 %)	35 (66 %)	17 (81%)
Severe hail damaged lines	907	65 (25.6 %)	18 (34 %)	4 (19%)

**Ranks of 4 lines advanced to 2019: 3, 5, 8 and 15 in 2018.**  
**Two are still being tested in 2021.**

GS recovered lines have yielded well in subsequent years



# How Can We Select For Average & Variable Years?

- Can we prevent losing a year due to poor data?
- For Variable Years: Can we use historical marker data and GEBVs to average through an unusual year?
- For Variable Years: Can we learn something unique/beneficial from the data (remember there has never been an average year).

**“Do not let the perfect be the enemy of the good.”** Based on Voltaire from an Italian proverb.

Can genomic selection help make better or more efficient selections?

**GEBV**  
(Preceding years)

		2.1	1
75 <sup>th</sup> percentile (Q3)			
		3	2.2
Mean			
			4
	Mean		75 <sup>th</sup> percentile (Q3)

**Priority groups to rank lines**

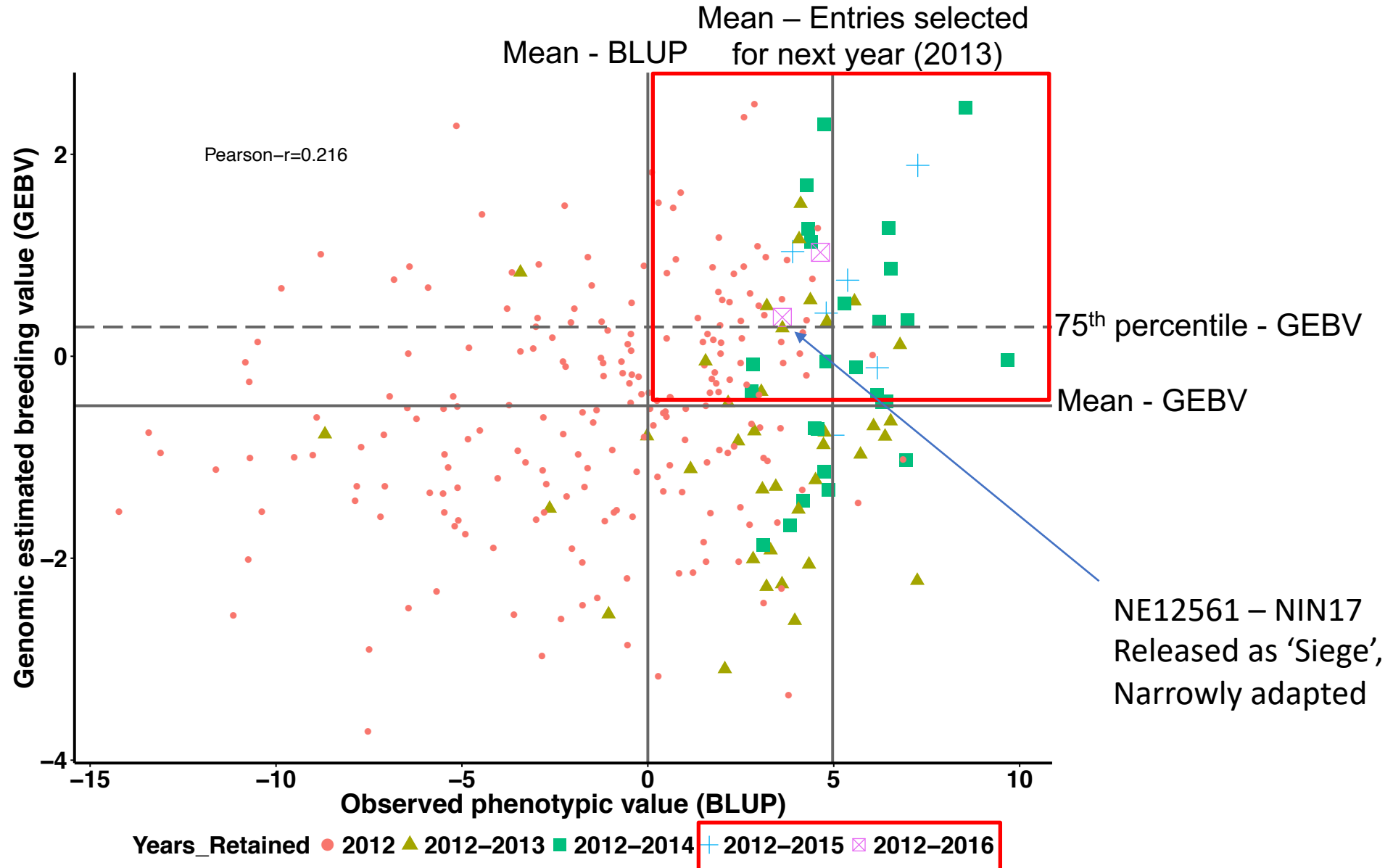
**Implemented beginning in 2016**

Note can use some of or all of current year data (direct or correlated).

**BLUP**  
(Current year)



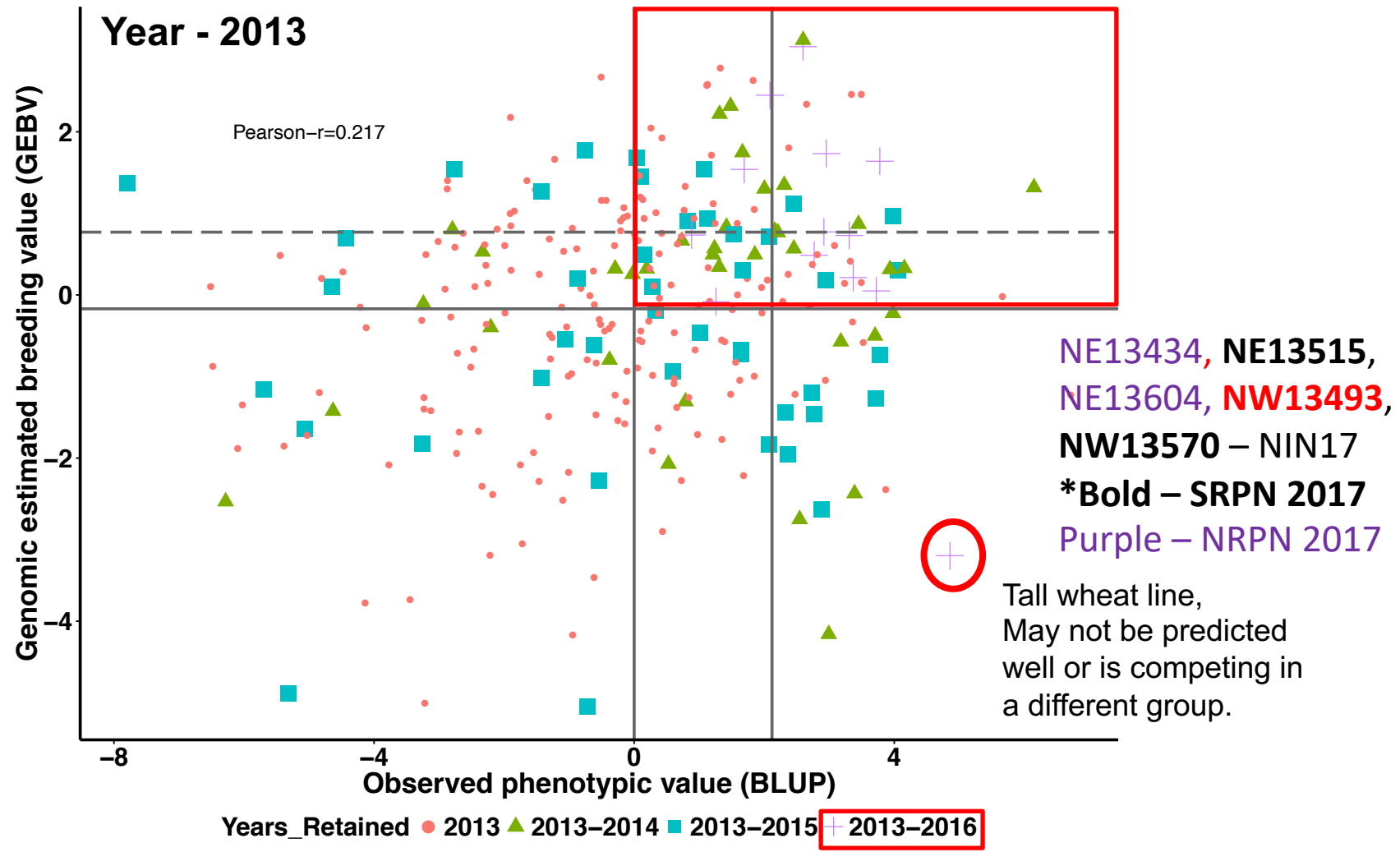
# Predictions made on 2012 (F<sub>3:6</sub>) lines for grain yield using 2013, 2014 and 2015 as training population





# Understanding Plant Breeding

- Almost no selection experiment replicates the selection protocol.
- The outcomes of selection are replicated for comparison.
- To understand selection protocols you have to consider similarities: are patterns being repeated.

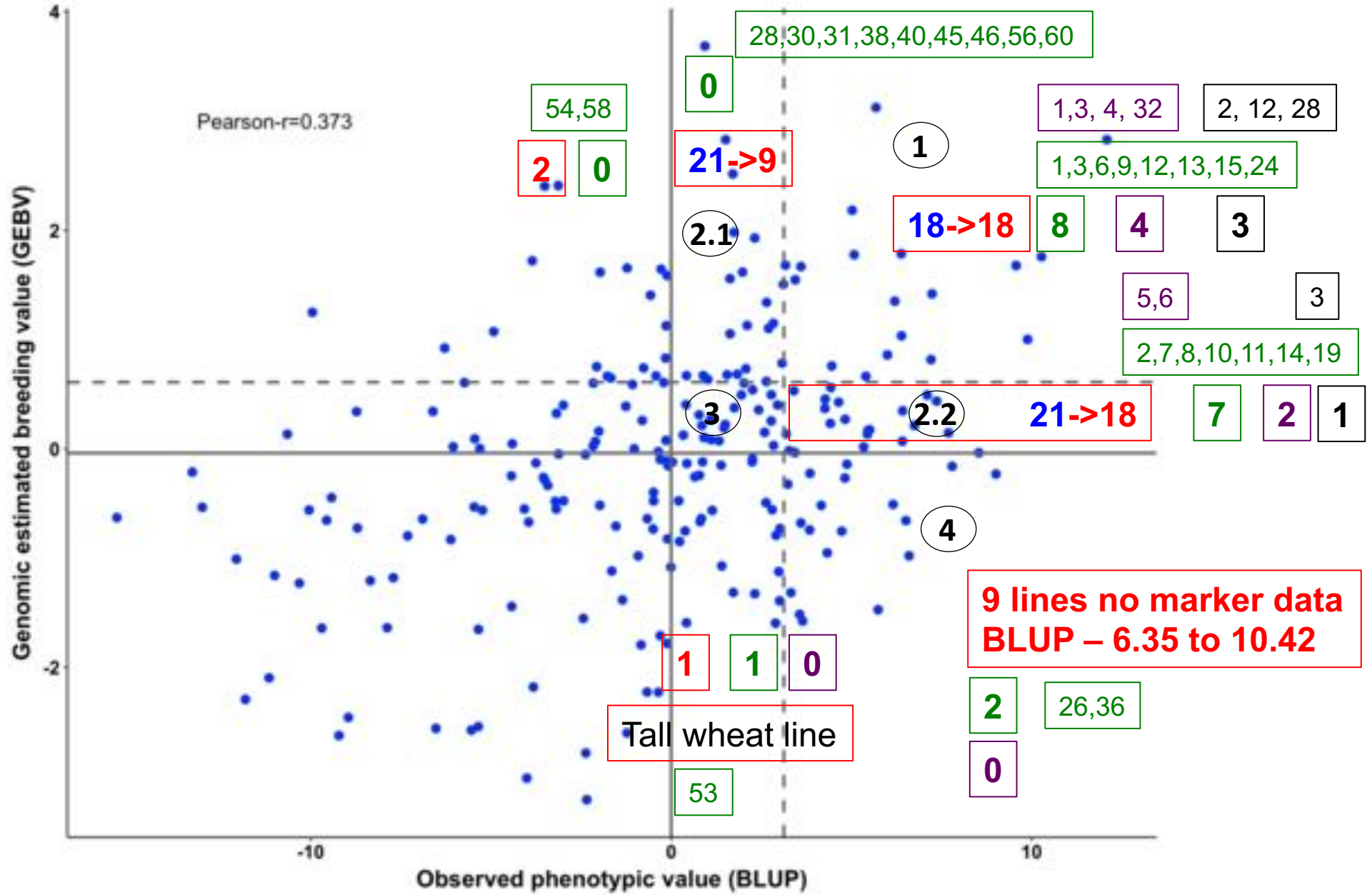


Lines with **both** above average “GEBV and BLUP values” are retained for more years as compared to lines with either above average GEBV or BLUP alone

Note the prediction abilities are lower ~0.20

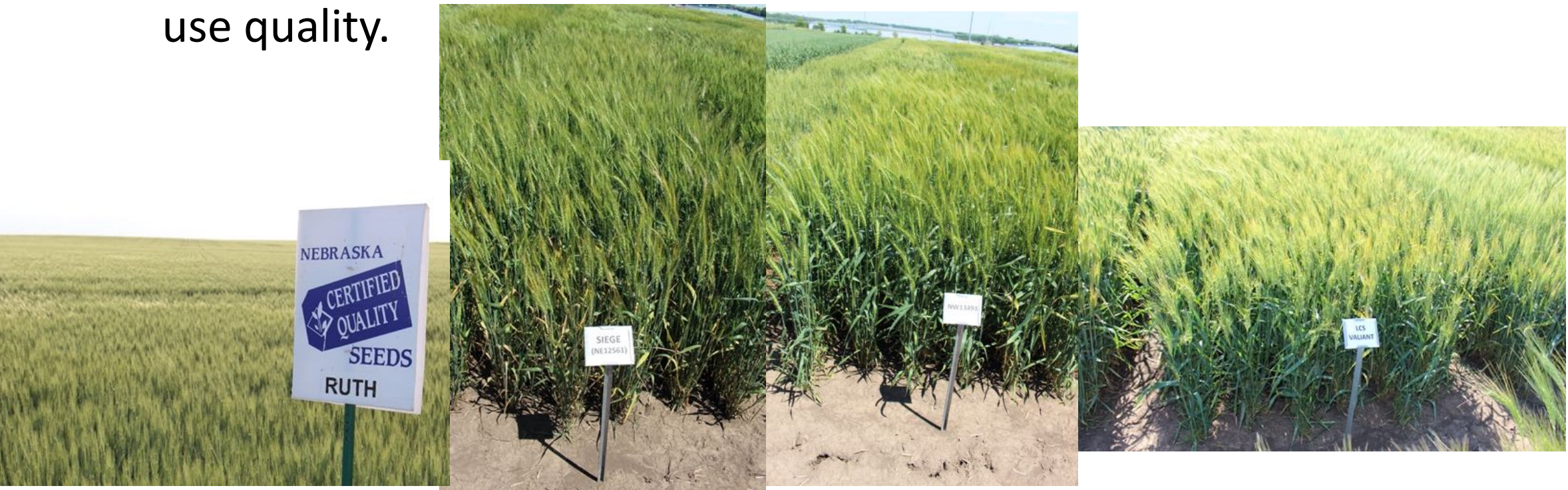
Improve accuracy of selection decisions

GEV & Phenotype      Phenotype      Phenotype      Phenotype  
**F<sub>3:6</sub>(2016) lines** -> **F<sub>3:7</sub>(2017)** -> **F<sub>3:8</sub>(2018)** -> F<sub>3:9</sub>(2019) -> F<sub>3:10</sub>(2020)



# Does it Work?

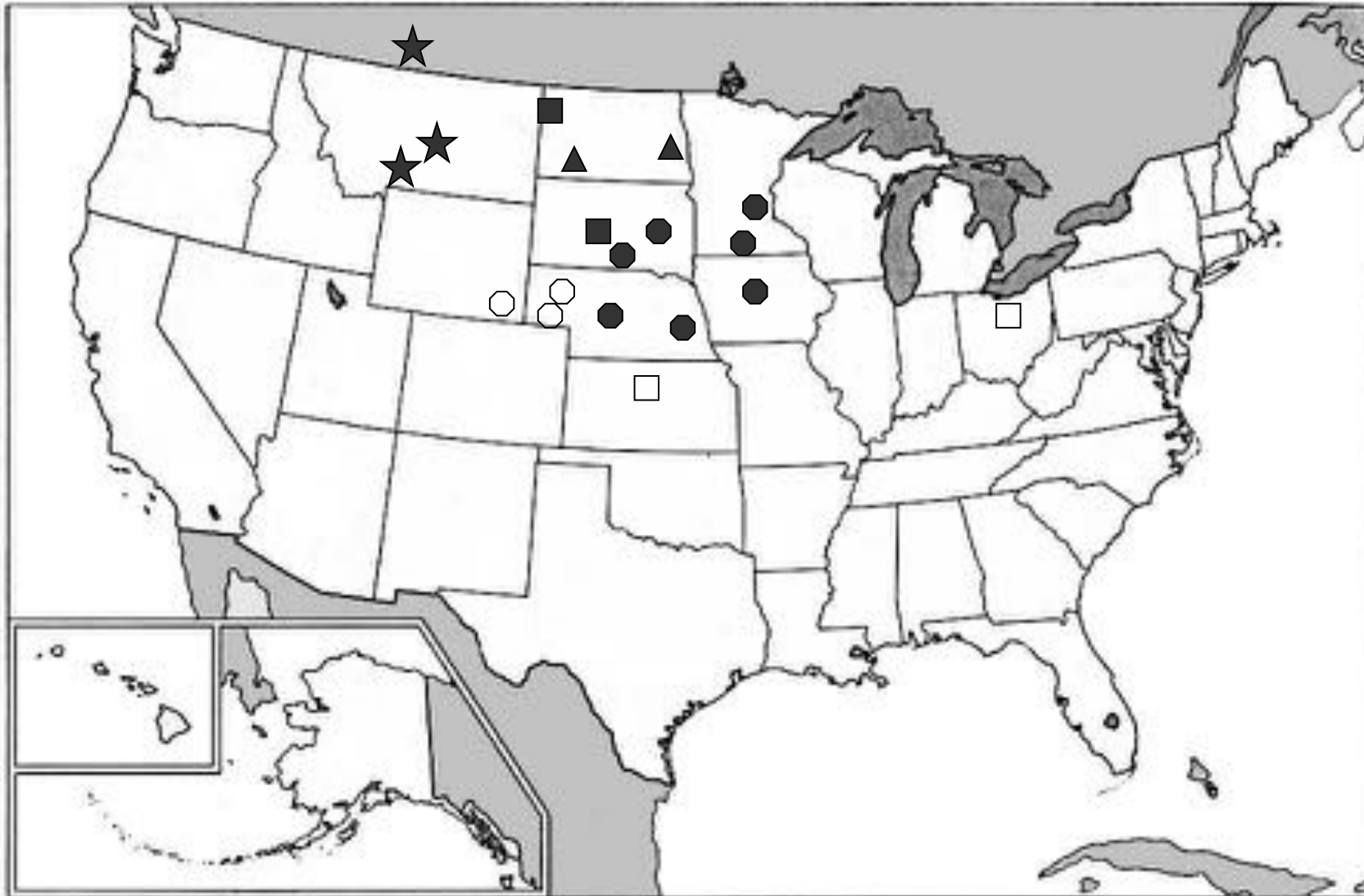
- NE10589 (Husker Genetics Brand Ruth) was released in 2015
- NE10478-1 (LCS Valiant, 2020) and NE12561 (Siege, 2020) were released
- NW13493 was licensed to Bay State Milling for its grain yield and end-use quality.





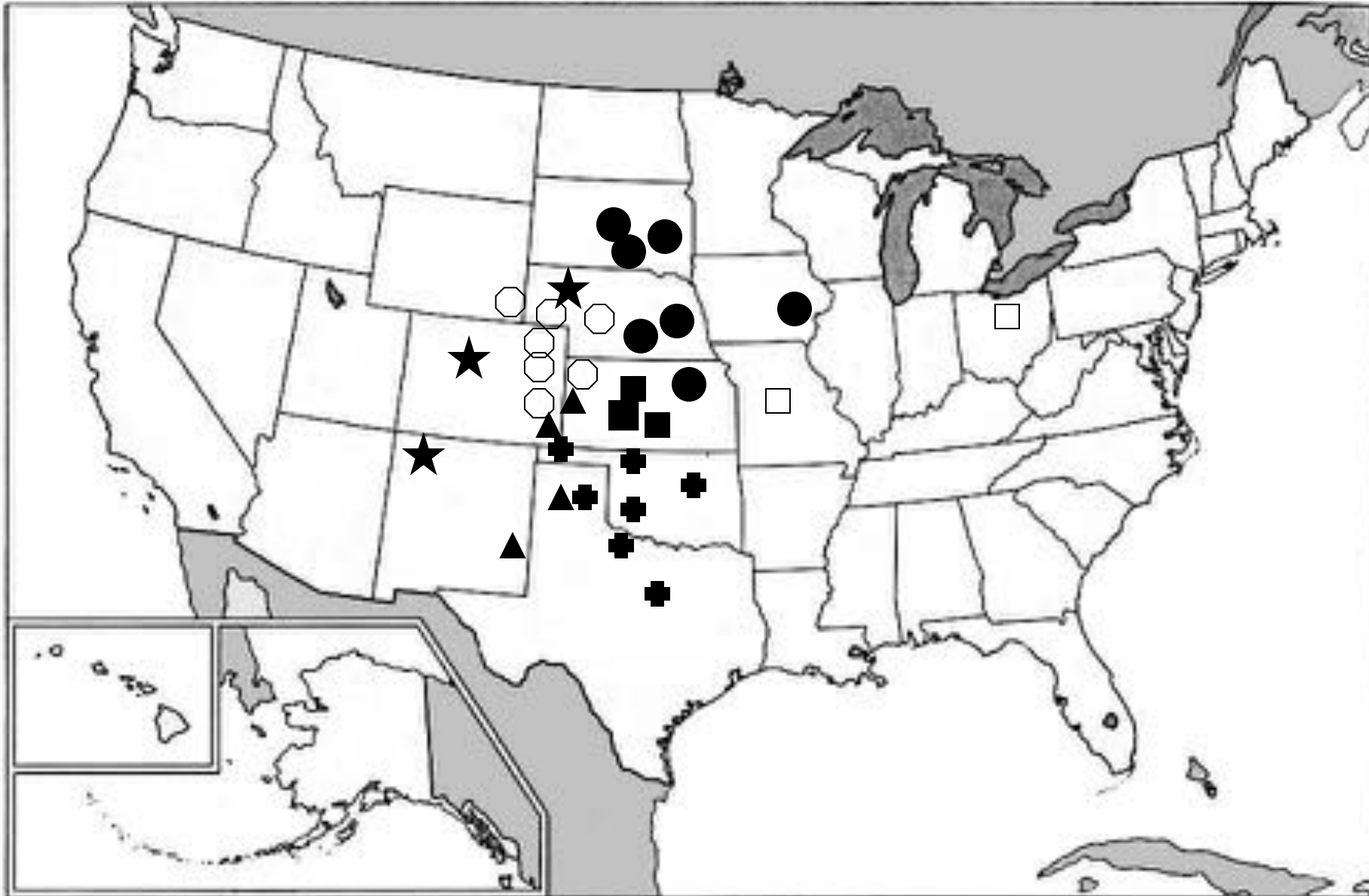
# NRPN: location of replicated yield trials and regional production zones.

- North central plains
- Northwest plains
- ▲ Northern plains
- ◊ Northern high plains
- ★ Northwest plains
- unassigned



# SRPN: location of replicated yield trials and regional production zones.

- North central plains
- Central plains
- ⬡ Northern high plains
- ▲ Southern high plains
- ⊕ Southern plains
- ★ Intermountain
- unassigned

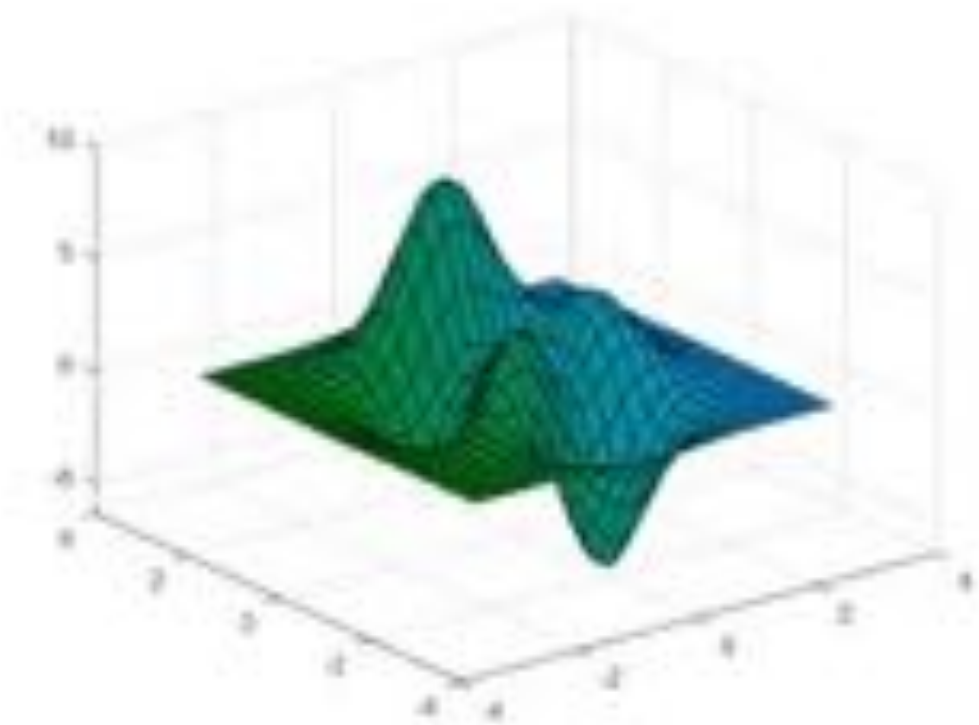




# Have We Changed? Enjoying the Symphony

- Measure Diversity to keep variation in our program.
- Association Mapping/Marker assisted Selection. Lining up the major genes.
- Better Selections of Phenotyped lines.
- Earlier Parent Selection for our crossing block (adding group 1 lines 1-2 years earlier).
- Preliminary Yield Trial is now a 2-rep alpha lattice trial at 4 locations (AL, NP, GR, LN) and an augmented unreplicated design at 4 locations (SD, MC, MD, CC)—hedging our bets.
- Genomic Selection and breeding populations are being targeted for:
  - Grain yield and adaptation.
  - Stem rust and Fusarium Head Blight resistance
  - End-use quality—particularly useful in the  $F_{3:5}$  generation.
  - Anther Extrusion for male hybrid parent selection, *Rf* gene selection for CMS hybrids.

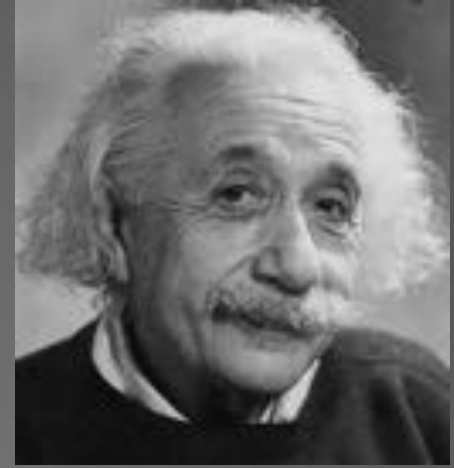
# Is Genomic Selection a Panacea



- Probably not—you are limited by your training populations. You are breeding using the rearview mirror.
- You cannot predict what you do not know/have in the program.
- How do you handle new genetic variation (are you working on the right peak)?
- There will always be room for good ideas.

The highest intelligence of mankind is  
not reason, but vision.

Albert Einstein



Be the change you want to see in  
the world!

Gandhi







# Why Hybrid Wheat, Why Now?

P. S. Baenziger, A. Easterly, N. Garst, H. Stoll, A. Adhikari, Geraldine Opena, **V. Belamkar**, I. S. El-Baysoni, A. M. H. Ibrahim, J.C. Rudd, B. Sade, B. Basnet, F. Longin, J. Reif, J.-B. Sarazin, and J. Poland.



United States  
Department of  
Agriculture

National Institute  
of Food and  
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International Maize and Wheat  
Improvement Center



**K-STATE**

Research and Extension

UNIVERSITY OF HOHENHEIM





# Short History of Hybrid Small Grains

- I started breeding wheat in 1976
- Very active hybrid programs in the 1970s and 1980s
- Most U.S. public and private programs were gone by the end of the 1990s
- Hybrid rice facing similar challenges continued—30 years in the wilderness. Yuan Longping died May 22, 2021
- 17,000,000+ hectares of hybrid rice
- Where would we be if we had continued to work on hybrid wheat?





# Need for rekindling Hybrid wheat efforts

Increase grain yield by 1.4 to 1.7% annually, but currently our rate of gain is considerably less (~0.9%)

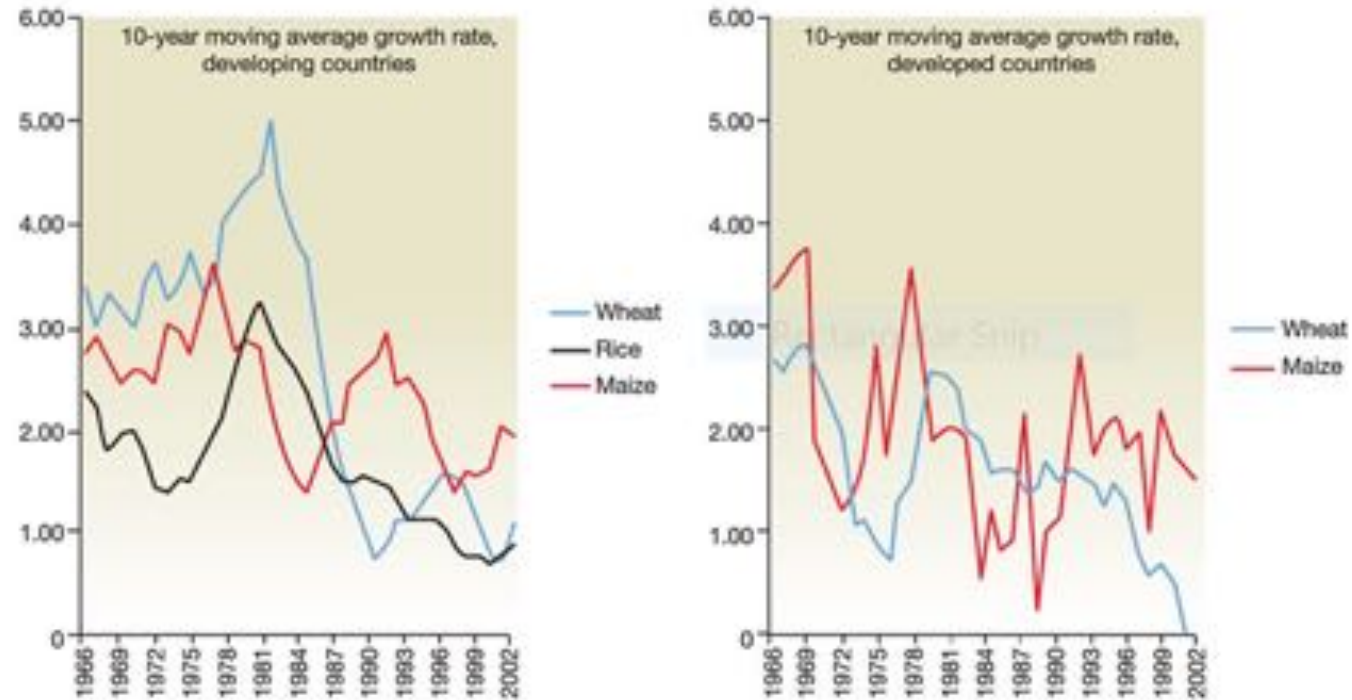
If you do not have a plan to raise grain yield by 1.4 to 1.7% annually, you have a plan to fail

Failure is not an option





# Current Rate of Yield Gain

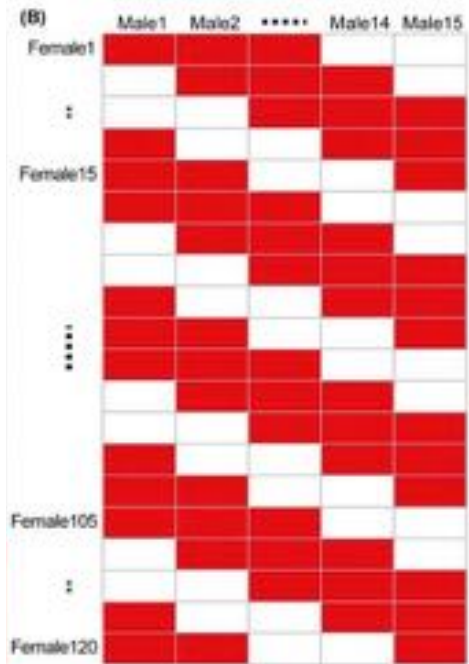
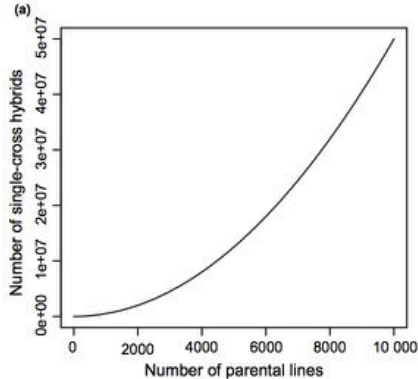


**Figure 1** For wheat and rice there was a boost in the annual rate of yield gain in the 1970s and 1980s, associated with the green revolution, but there has been a major decline in the rate of gain since then in both developing and industrial countries. (Data from Fischer *et al.*<sup>6</sup>.) Current global yield increases remain around 1% gain per year for rice and wheat, but with a large variation between countries<sup>28</sup>. Maize has retained a slightly higher rate of gain.

Flavell, 2016



# Hybrid Wheat: Heterotic Pools



Hybrid	GEBV
H1	M
H2	M
H3	P
H4	M
H5	P
...	M
...	M
...	P
...	M
H11175	M

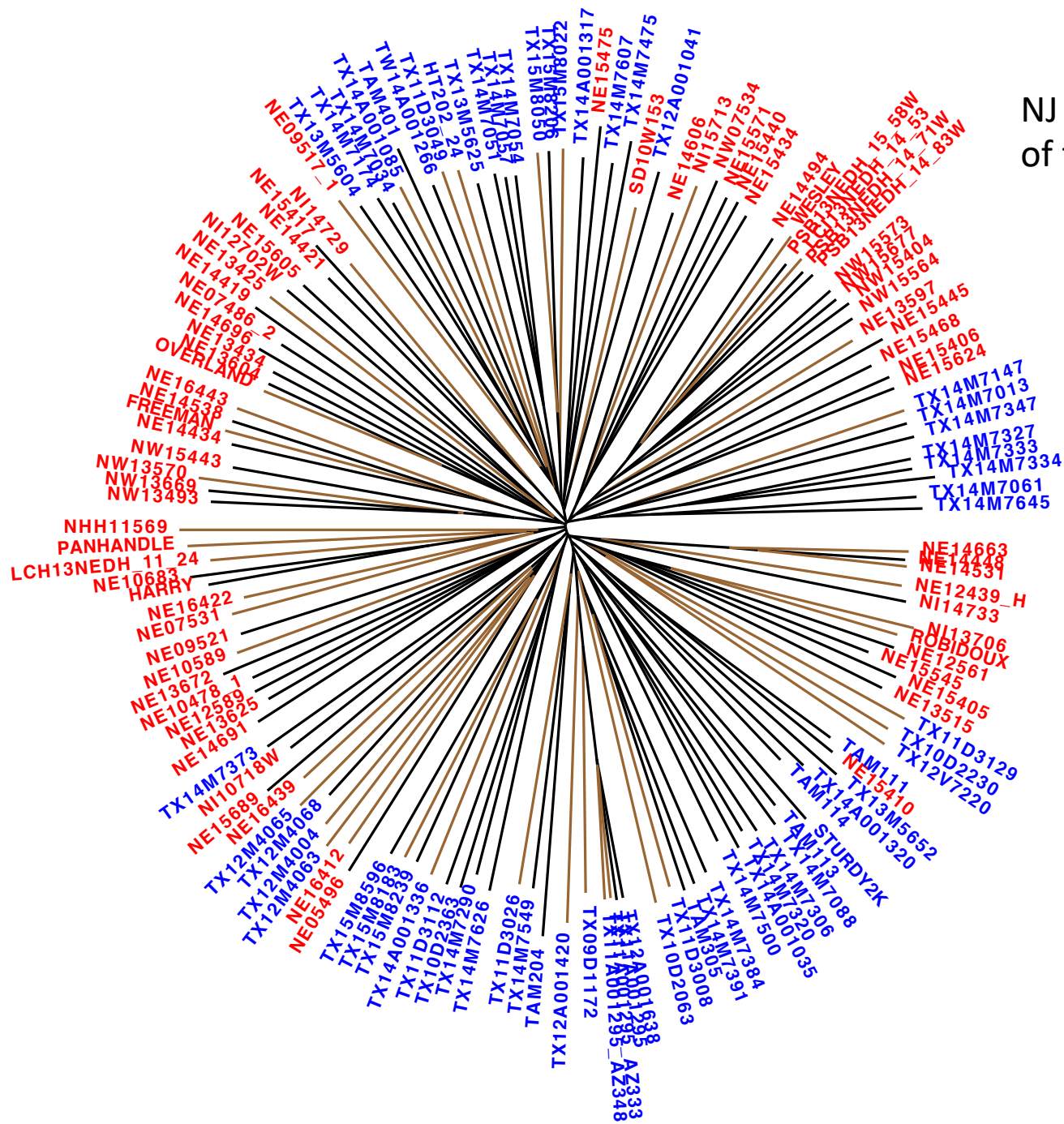


Heterotic groups and patterns

M: Hybrid made and phenotyped  
P: Hybrid performance predicted

- Crossing block design - Balanced Missing
- If you have dense marker data on the parents and phenotype a set of experimental hybrids, you can estimate/predict the rest of the hybrids.
- For example, UNL in collaboration with TAMU have developed a crossing block of 50 males and 100 females. You could make 11,175 hybrids.
- We create 700 hybrids ( 25 males x 14 females x 2 locations) and predict the performance of rest of the 10,475 hybrids.
- Using GEBV of 11,175 hybrids – we can start building heterotic groups and patterns that maximize heterosis.
- Even if we lose one crossing block location, we can estimate the performance of 7,750 hybrids.





NJ phylogeny mid-point rooted of the parent lines

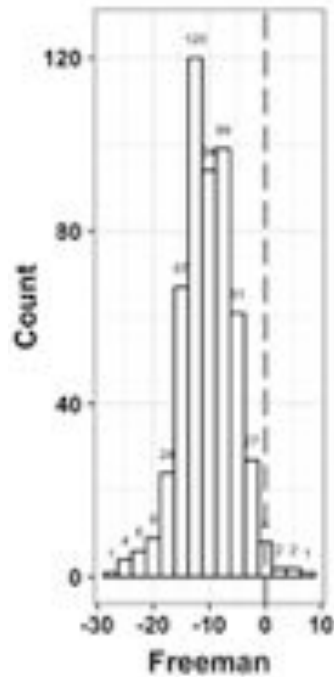
Mainly observe three types of clusters:

1. Nebraska lines
2. Texas lines
3. NE + TX lines

Male  
Female

# Commercial heterosis with respect to highest yielding check

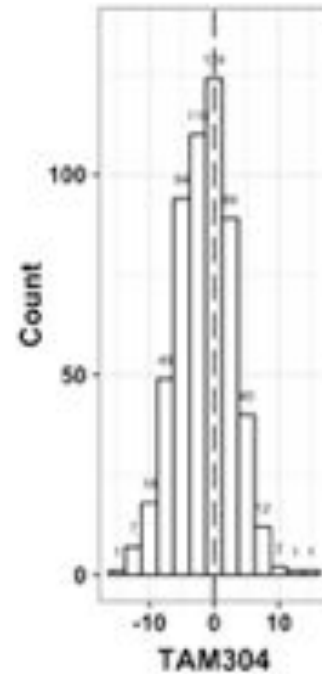
**Alliance**  
**-28.3 – 7.0**



**9 hybrids outperformed  
highest-yielding inbred check**

**0 hybrids in 2019**

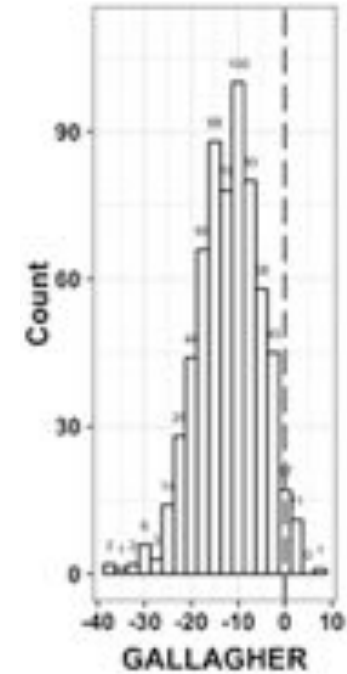
**North Platte**  
**-15.5 – 15.1**



**200 hybrids**

**7 hybrids in 2019**

**Lincoln**  
**-38.5 – 6.5**

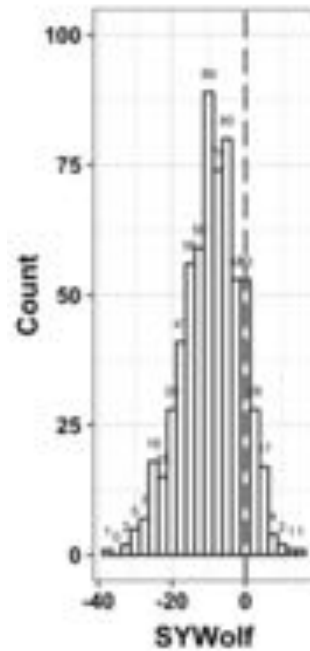


**18 hybrids**

**10 hybrids in 2019**

# Contd..

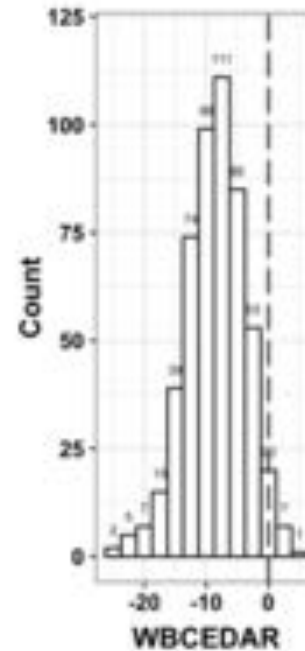
**McGregor**  
**-37.7% – 14.7%**



**75 hybrids outperformed  
highest-yielding inbred check**

**Not Applicable**

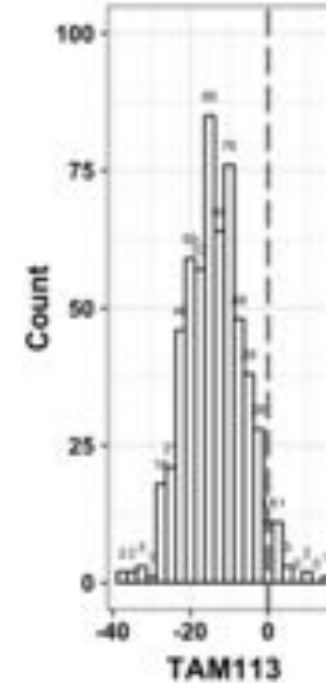
**Prosper**  
**-24.5% – 4.4%**



**19 hybrids**

**59 hybrids in 2019  
Pilot Point**

**Bushland**  
**-38.5% – 13.9%**



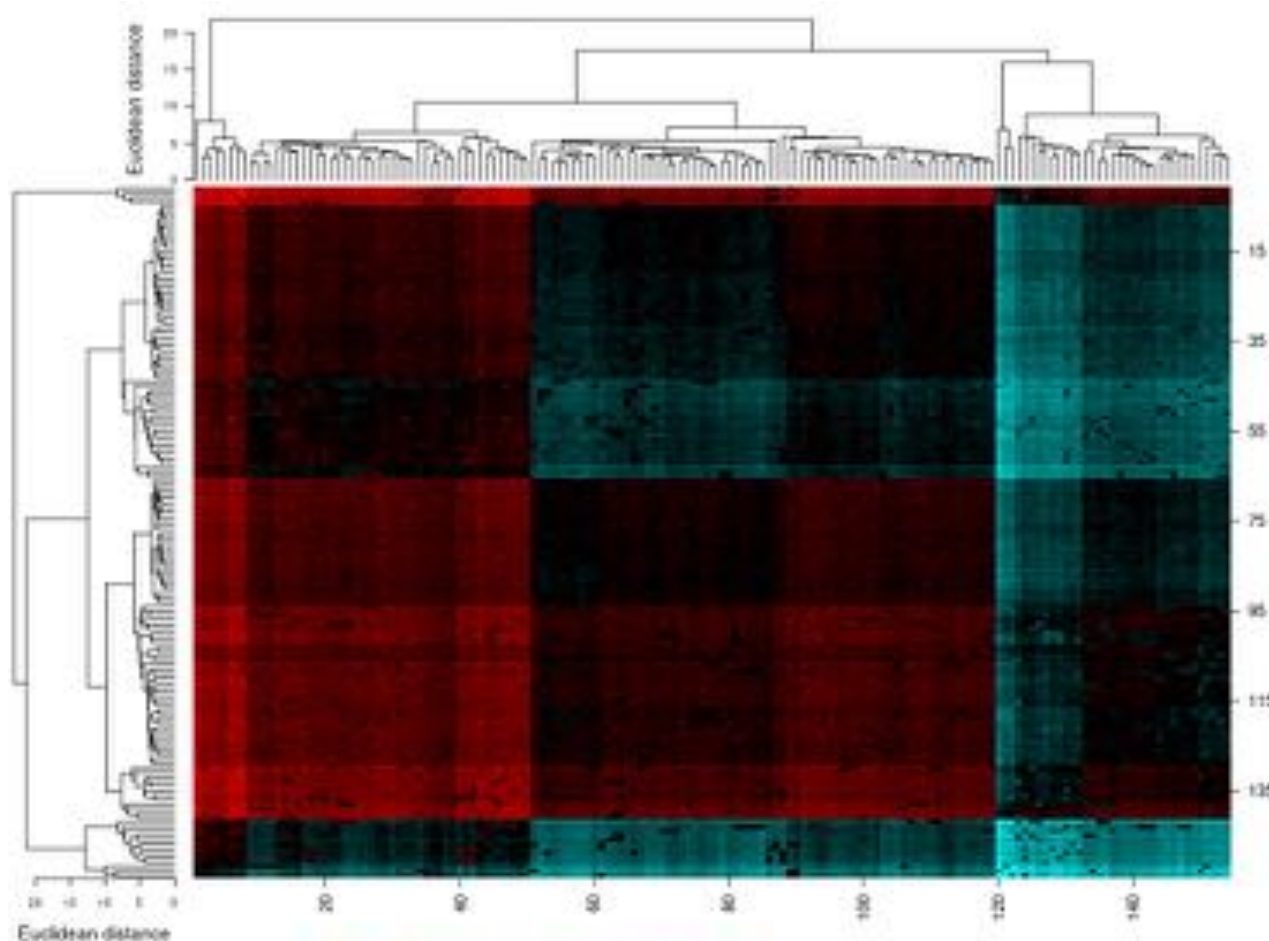
**18 hybrids**

**35 hybrids in 2019**



# **Predicting high-yielding crosses and building heterotic groups for hybrid cultivar development**

# Predicted yield of >11K hybrids for NE (Blackland and Bushland – completed – not shown)



~150 parental lines  
~700 hybrids made and tested  
~ >11K predicted hybrids

## Next steps:


Specific crosses (2020 and 2021 crossing blocks) – validate in yield trials in 2021 and 2022

Heterotic groups



Red – higher yield  
Blue – lower yield





*... a good past is positively dangerous  
if it makes us content with the present  
and unprepared for the future.*

Charles Eliot

# *Thank you*

Thanks go to the many students, postdocs, and collaborators that I have had over the years.

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