Genomes to Fields

Genotype by Environment Interaction in the 2014 and 2015 Inbred Study

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and the Genomes to Fields Consortium

G2F collaborator meeting

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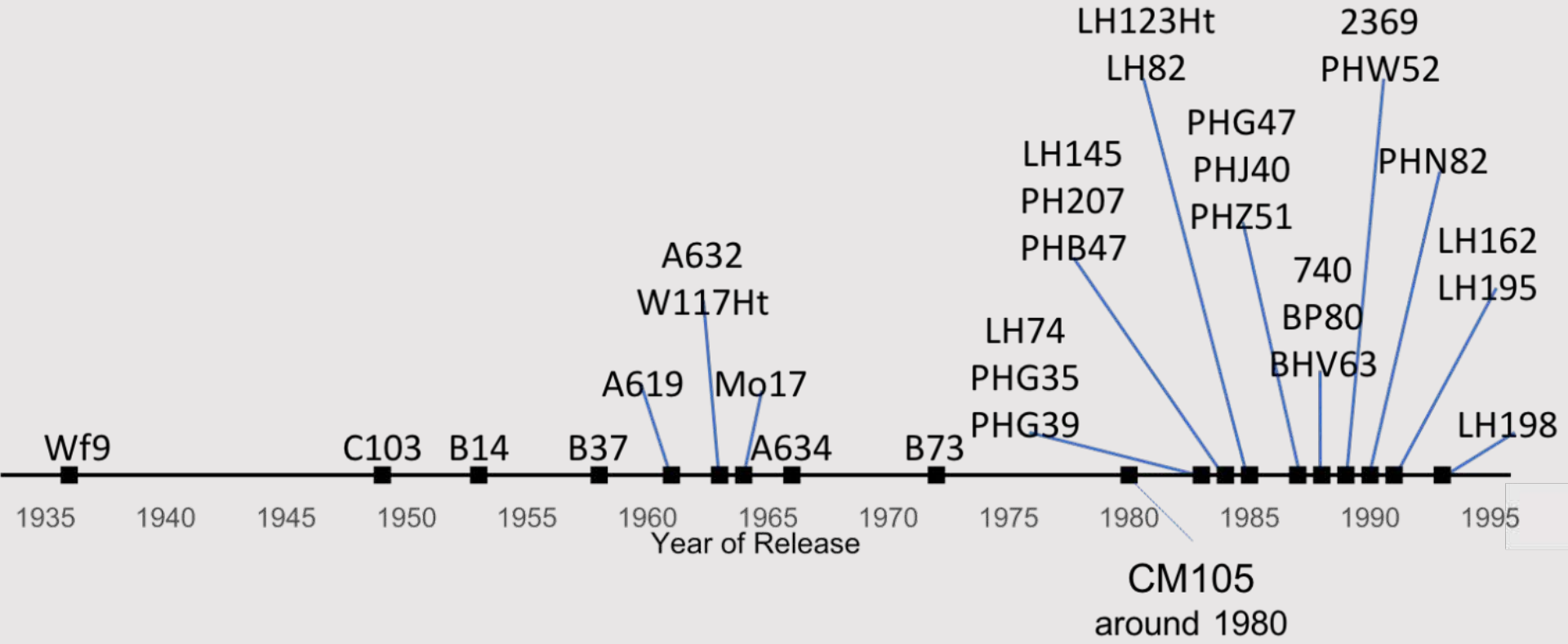
www.Genomes2Fields.org

Questions to explore

- ✧ How much does G × E influence each trait?
- ✧ Which environments are best at discriminating among genotypes?
- ✧ Which genotypes are the most stable?
- ✧ Which traits are good “indicator” traits for assessing G × E? (In other words, which traits are most sensitive to G × E interaction?)

Germplasm

31 inbred lines selected to represent range of locations & maturities and release date



Inbred trials

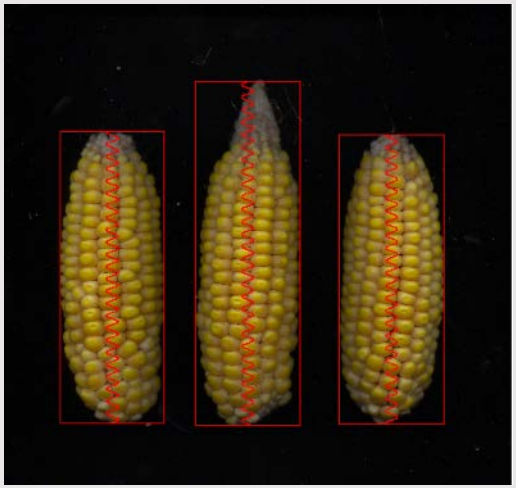
15 locations in 2014 ■ 21 locations in 2015

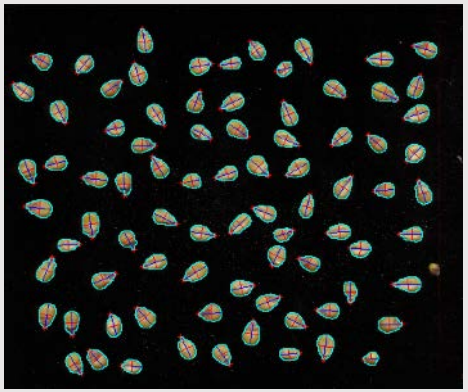
- ✧ 2 reps per environment
- ✧ Planting density ranged from ~12,000 to 50,000 plants per acre

Traits measured

- ✧ Anthesis date (GDU)
- ✧ Silking date (GDU)

- ✧ Plant height (cm)
- ✧ Ear height (cm)



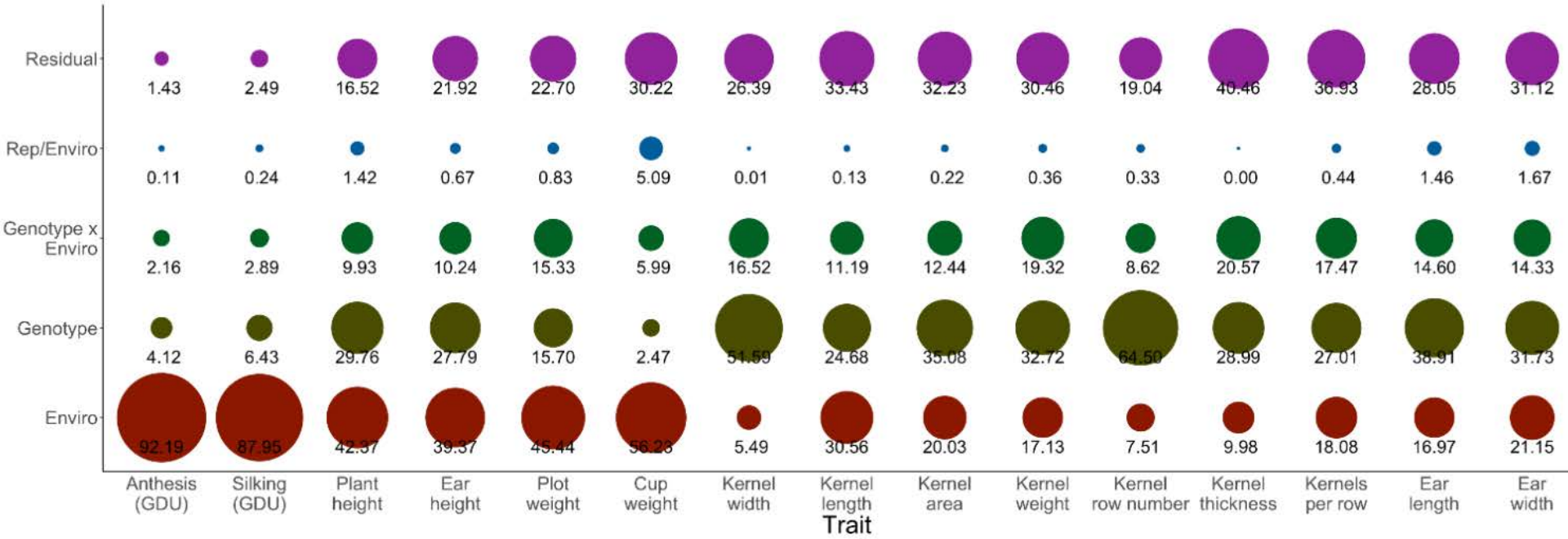


- ✧ Plot weight (g)

Miller et al. 2016 – The Plant Journal

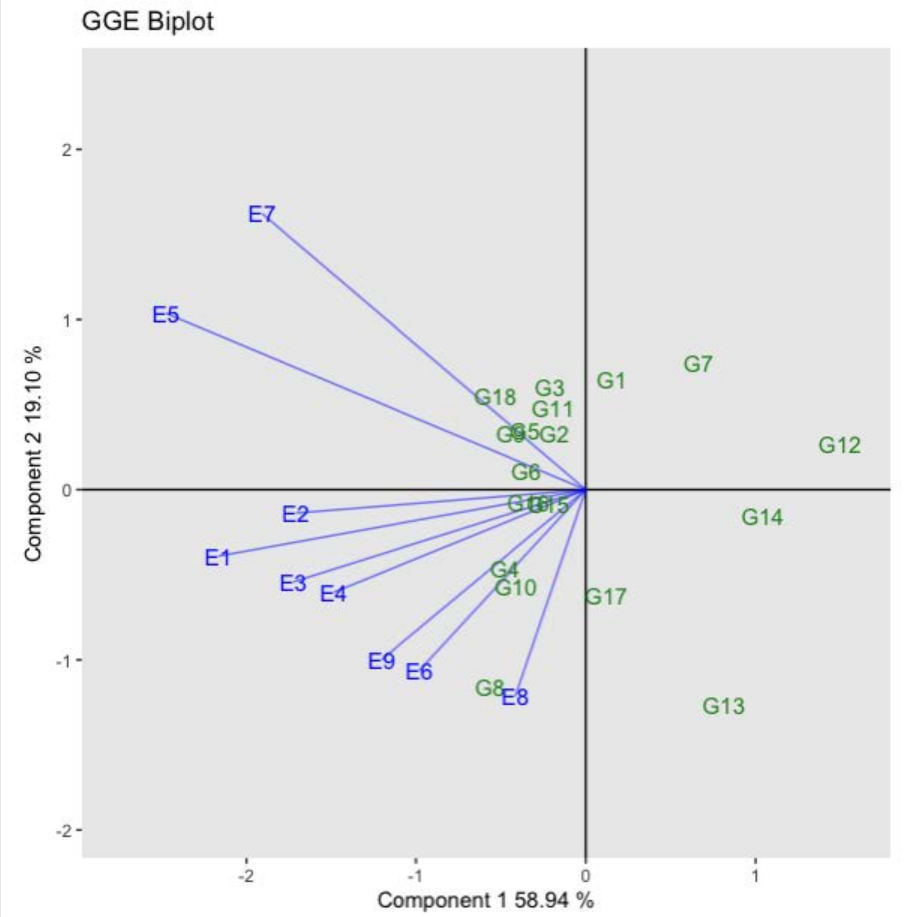
How much is each trait influenced by G × E?

How much is each trait influenced by G × E?



Which environments are best at discriminating among genotypes?

GGE analysis and biplot



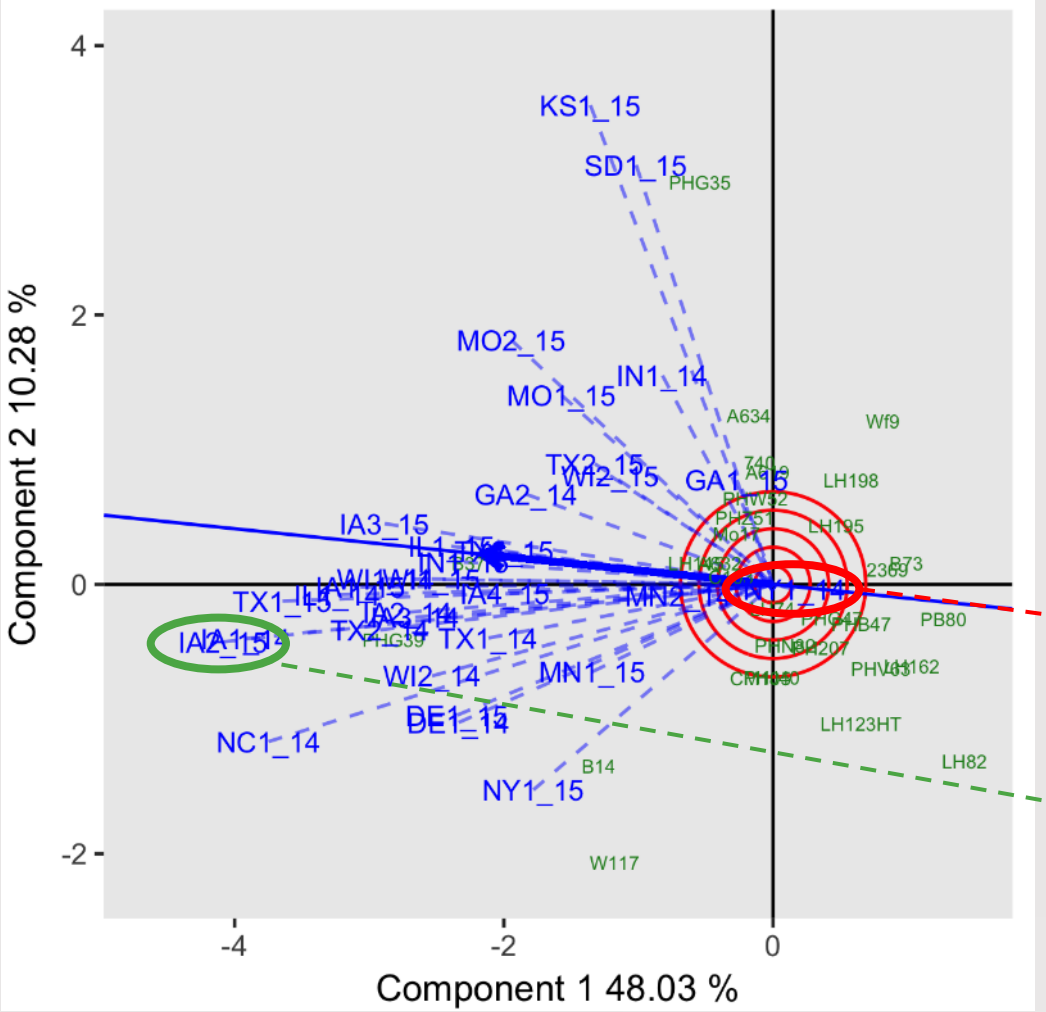
GGE Biplot showing components 1 and 2 explaining 78.04% of the total variation using Column Metric Preserving SVP and Tester-Centered G+GE with no scaling

- **G**enotypic main effects (x-axis) and **G**enotype x **E**nvironment interactions (y-axis)
- Useful for
  - Environment evaluation
    - Discriminability
    - Representativeness
  - Genotype evaluation
    - Mean
    - Stability

Yan and Kang 2002; Yan et al. 2007

Which environments are best at discriminating among genotypes?

Kernel thickness



- ✧ "Discriminating power vs. representativeness" view of GGE biplot
- ✧ Length of the <u>environment vector</u> (from environment to origin) corresponds to standard deviation of genotype means in the environment, a measurement of discriminability
- ✧ **NY1_14** (shortest environment vector) == least discriminable environment
- ✧ **IA2_15** (longest environment vector) == most discriminable environment

Yan et al. 2007

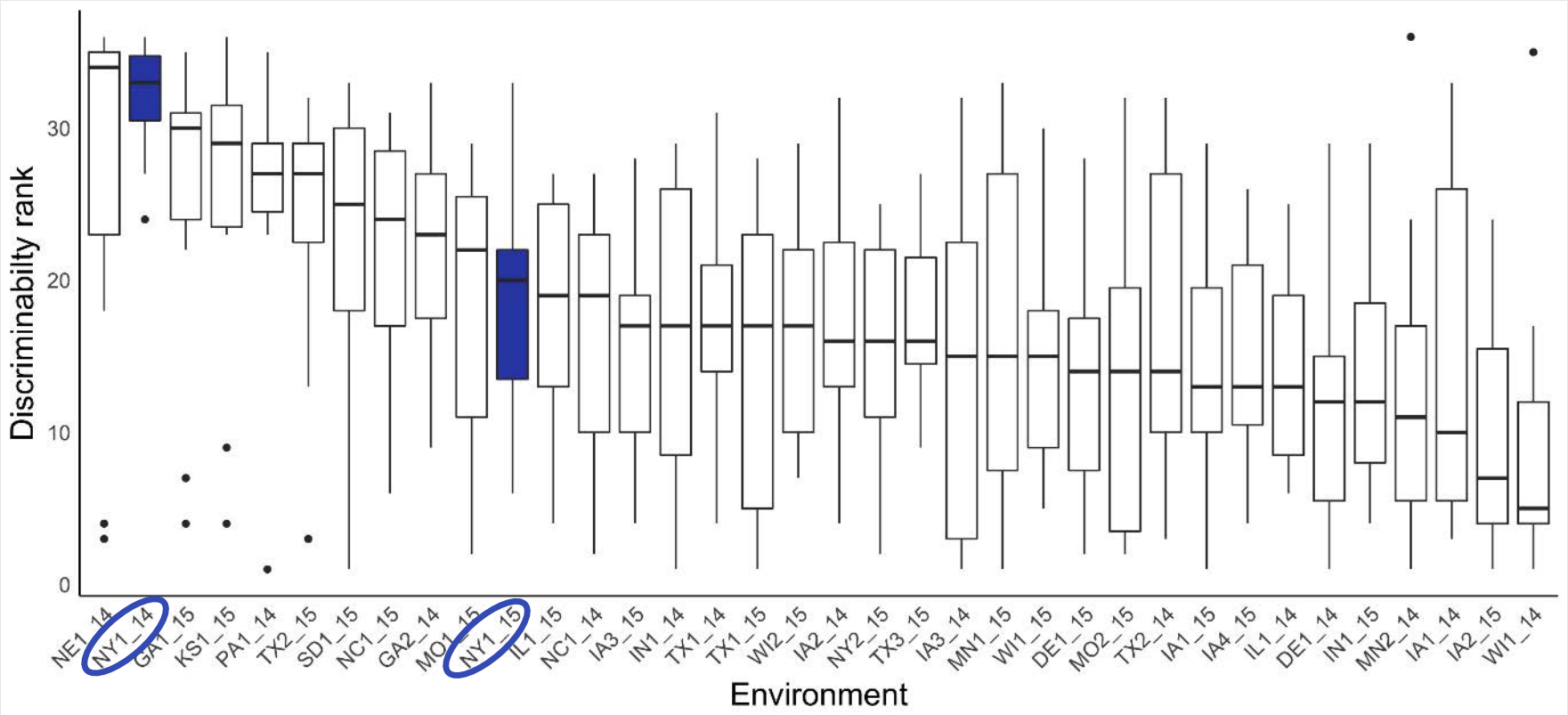
Which environments are best at discriminating among genotypes?

Enviro	Anthesis (GDU)	Silking (GDU)	Plant height	Ear height	Plot weight	Cup weight	Kernel width	Kernel length	Kernel area	Kernel weight	Kernel row number	Kernel thickness	Kernels per row	Ear length	Ear width	Median rank
WI1_14	12	17	12	8	2	35	1	5	2	4	6	12	4	4	5	5
IA2_15	23	22	1	15	24	6	16	3	7	3	5	1	7	5	13	7
IA1_14	27	25	31	31	8	33	6	4	3	5	10	3	6	10	11	10
MN2_14	16	15	18	13	21	36	11	1	5	7	24	6	5	6	2	11
DE1_14	10	14	13	12	3	29	28	2	8	14	22	16	3	12	1	12
IN1_15	8	5	8	11	29	26	7	22	10	12	14	20	15	17	4	12
IA1_15	19	20	5	1	17	8	21	11	29	19	11	9	11	13	26	13
IA4_15	20	21	6	6	4	10	13	12	15	21	26	25	13	11	23	13
IL1_14	21	19	14	23	13	25	9	8	6	11	16	8	12	19	7	13
DE1_15	14	18	15	20	7	28	14	9	4	10	28	17	2	3	8	14
MO2_15	2	2	2	2	20	5	19	14	14	13	32	14	17	21	22	14
TX2_14	NA	NA	3	14	10	19	27	27	30	32	18	10	8	7	14	14
IA3_14	22	23	24	21	6	32	3	6	1	2	1	15	24	20	3	15
MN1_15	15	11	16	4	15	11	33	33	32	1	3	30	18	2	24	15
WI1_15	11	10	7	5	11	15	25	7	23	30	8	18	16	15	18	15
IA2_14	25	26	32	32	18	16	10	20	13	15	4	13	14	16	10	16
NY2_15	18	13	21	16	25	23	2	23	9	16	9	NA	NA	NA	NA	16
TX3_15	NA	NA	NA	NA	16	27	15	19	19	24	12	24	9	14	15	16
IA3_15	17	16	11	7	5	4	20	18	27	18	17	11	20	9	28	17
IN1_14	1	1	17	9	28	13	8	25	16	6	21	27	29	28	19	17
TX1_14	NA	NA	4	19	14	20	24	17	21	31	15	23	10	8	16	17
TX1_15	NA	NA	23	27	9	17	5	24	20	28	2	5	1	1	21	17
WI2_15	NA	NA	9	10	12	22	17	10	18	26	7	29	26	18	12	17
IL1_15	NA	NA	25	17	27	18	4	21	12	8	13	19	21	25	27	19
NC1_14	7	8	19	25	19	9	18	15	11	20	23	2	25	27	25	19
NY1_15	NA	NA	NA	NA	33	14	12	13	17	22	20	21	30	22	6	20
MO1_15	5	12	10	3	26	2	29	26	25	17	27	22	22	24	20	22
GA2_14	9	9	20	24	23	21	32	16	31	33	19	26	28	26	9	23
NC1_15	6	6	22	28	31	12	22	29	24	27	29	NA	NA	NA	NA	24
SD1_15	NA	NA	NA	NA	22	1	30	32	33	25	25	7	19	30	17	25
PA1_14	26	24	29	29	1	31	26	35	28	23	NA	NA	NA	NA	NA	27
TX2_15	13	3	27	26	32	3	31	28	22	29	31	28	23	23	29	27
KS1_15	NA	NA	NA	NA	36	24	23	31	26	9	33	4	32	29	30	29
GA1_15	4	7	26	22	30	7	35	30	34	35	30	31	31	31	31	30
NY1_14	24	NA	30	30	35	34	34	36	35	34	35	32	27	32	32	33
NE1_14	3	4	28	18	34	30	36	34	36	36	34	NA	NA	NA	NA	34

Which environments are best at discriminating among genotypes?

✧ Year-to-year variation has much influence on G × E (perhaps more than location-to-location)

(Elgersma 1990, Yan and Hunt 2001, Singh et al. 2011)



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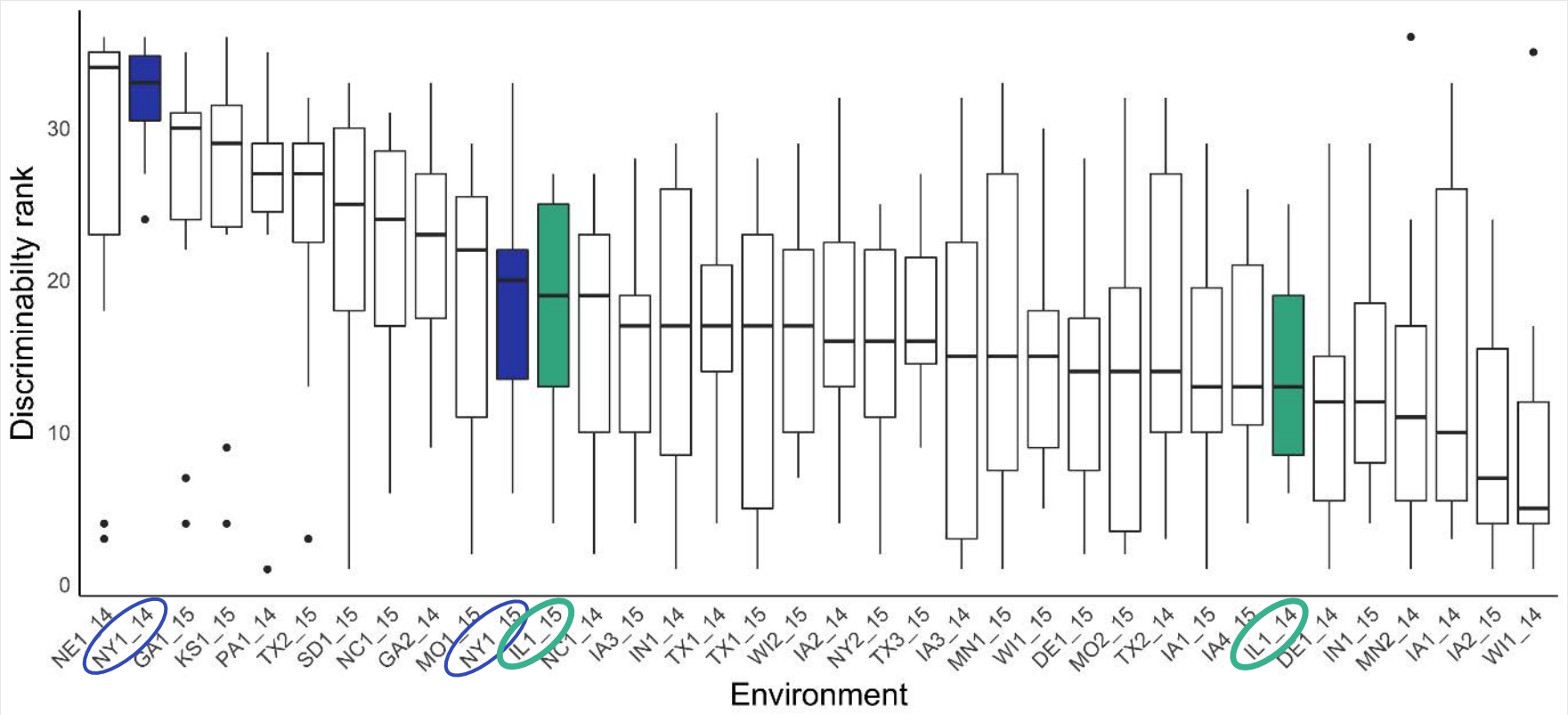
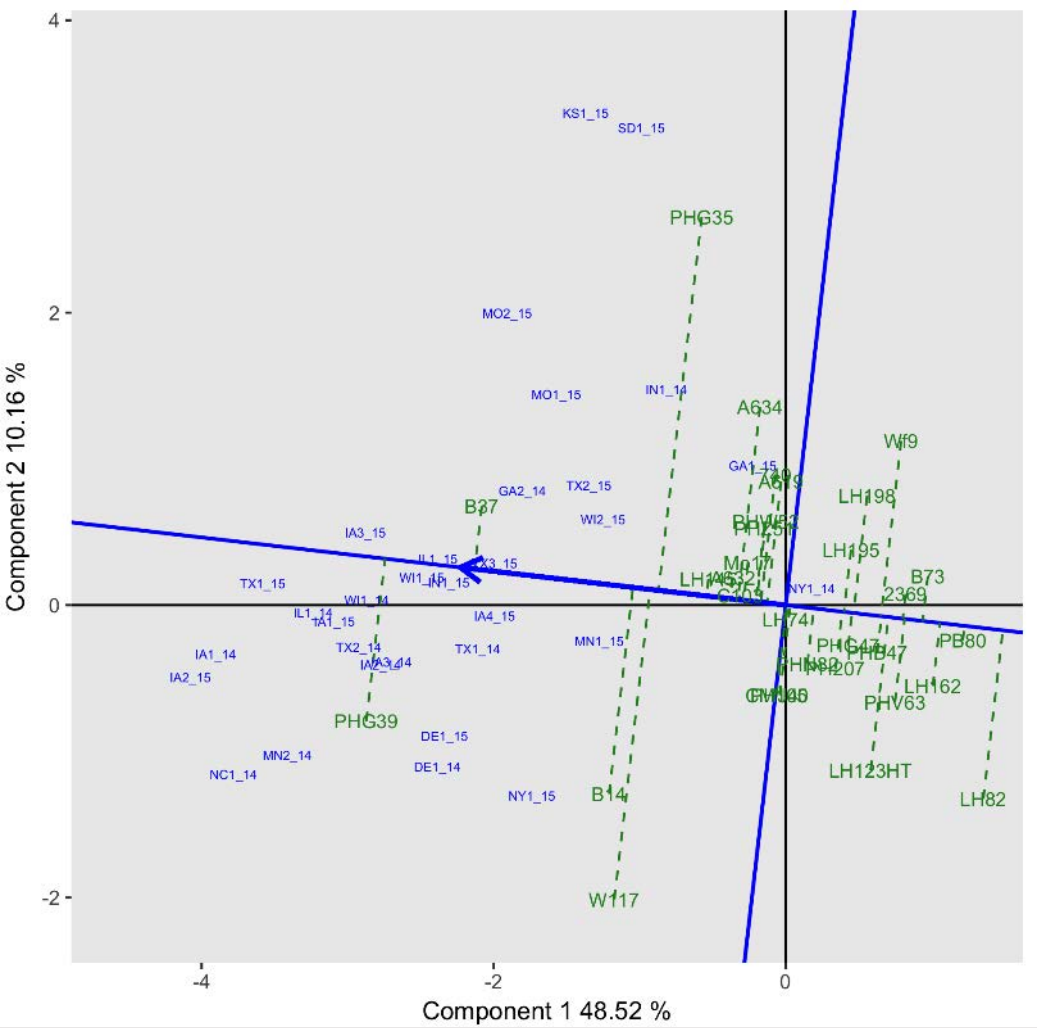


Which genotypes are the most stable?

Which genotypes are the most stable?

Kernel thickness

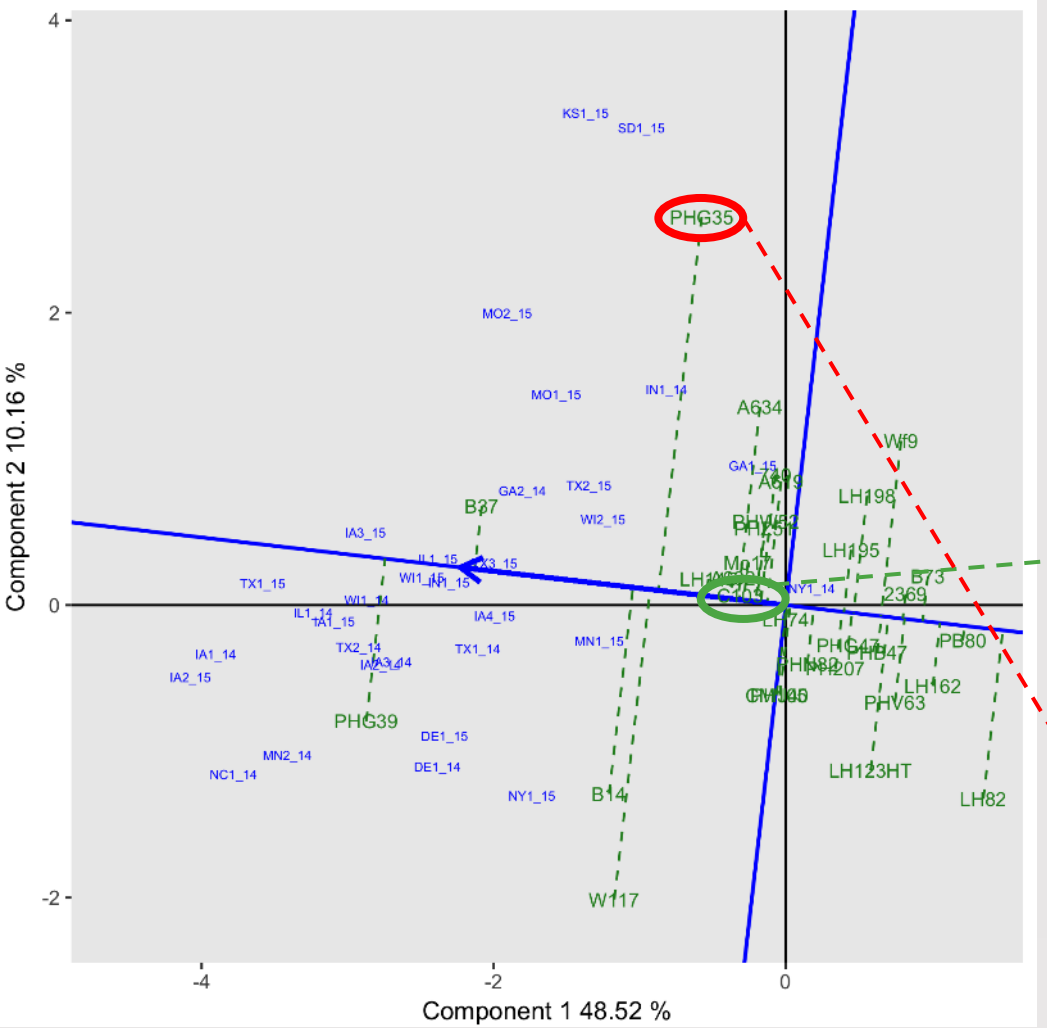


- “Mean vs. stability” view of GGE biplot
- AEC (average environment coordination) abscissa
  - drawn through the origin and an imaginary “average environment” calculated based on all environments

Yan et al.

Which genotypes are the most stable?

Kernel thickness



- G represented along AEC abscissa
- G × E represented along AEC ordinate
  - Genotypes near the AEC abscissa= more stable than those far from it
- **C103** (shortest distance from AEC abscissa) == most stable genotype
- **PHG35** (greatest distance from AEC abscissa) == least stable genotype

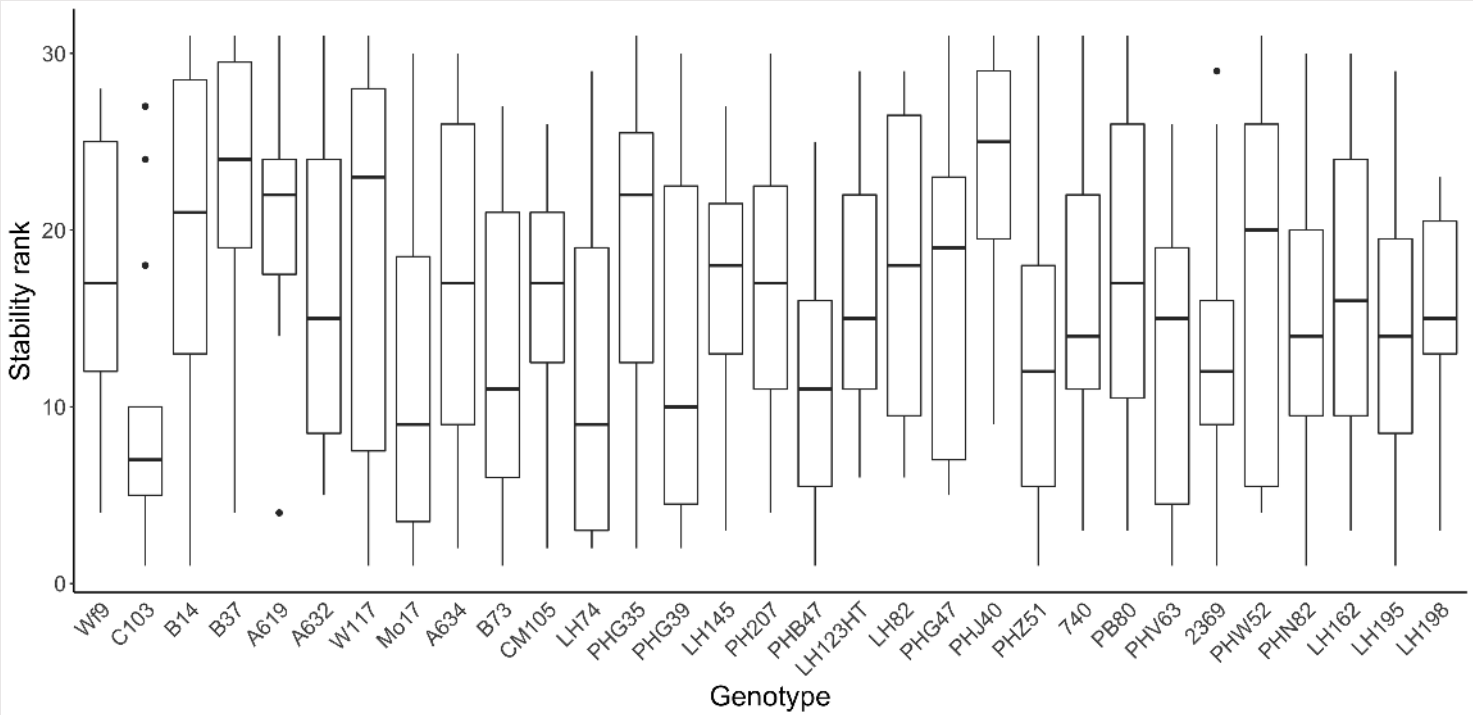
Yan et al.

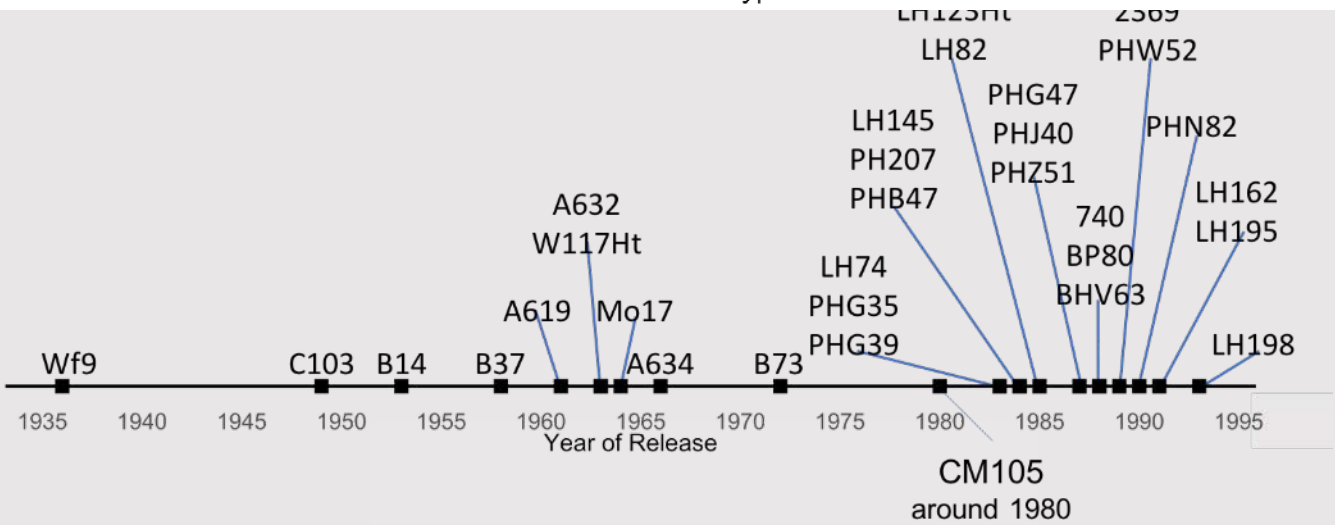
Which genotypes are the most stable?

Genotype	Anthesis (GDU)	Silking (GDU)	Plant height	Ear height	Plot weight	Cup weight	Kernel width	Kernel length	Kernel area	Kernel weight	Kernel row number	Kernel thickness	Kernels per row	Ear length	Ear width	Median rank
C103	6	27	2	24	5	18	8	5	7	10	9	1	21	10	5	8
LH74	29	2	17	2	9	6	5	10	15	21	4	2	19	23	2	9
Mo17	30	29	4	1	24	9	3	18	9	12	18	9	10	3	3	9
PHG39	4	3	7	12	8	4	23	22	10	2	5	25	27	20	30	10
B73	10	11	26	27	4	3	13	21	2	8	11	10	20	24	1	11
PHB47	9	16	16	3	25	2	18	2	11	14	1	8	5	11	21	11
2369	16	7	11	11	15	12	16	1	13	3	12	6	23	29	19	12
PHZ51	20	19	6	6	3	5	29	12	31	17	7	16	2	1	12	12
LH123HT	17	6	27	20	10	13	6	29	12	13	16	24	7	27	9	13
LH195	12	8	1	14	14	29	19	9	26	27	20	13	14	7	7	14
PHN82	14	28	21	5	1	15	17	13	21	19	30	11	11	13	8	14
740	26	13	12	31	7	21	15	11	19	24	6	23	18	14	11	15
A632	31	30	10	10	23	25	7	8	6	26	23	5	12	15	18	15
LH198	3	14	22	7	12	19	12	20	14	15	14	21	25	19	23	15
PHV63	19	22	3	15	26	1	9	4	5	18	19	18	24	2	10	15
LH162	27	26	15	16	30	16	4	3	8	4	26	15	4	18	22	16
A634	2	10	19	8	2	24	30	16	17	29	8	28	28	21	15	17
CM105	25	20	20	17	16	8	22	14	16	11	2	20	1	25	26	17
PB80	11	9	31	30	22	23	24	15	28	28	10	3	17	8	16	17
PH207	18	17	5	4	19	27	10	27	20	30	25	12	15	4	17	17
Wf9	15	4	24	28	17	7	11	26	18	9	22	27	26	16	13	17
LH145	22	23	13	18	21	26	21	19	3	16	3	4	6	17	27	18
LH82	8	18	29	13	11	11	28	7	25	6	27	26	22	6	29	18
PHG47	7	21	25	19	20	10	31	6	27	5	13	7	16	28	20	19
PHW52	5	5	23	26	28	20	26	24	30	31	15	17	8	5	6	20
B14	21	25	14	21	31	30	1	23	1	7	21	29	31	12	28	21
A619	23	31	28	22	18	28	20	17	22	25	17	22	9	22	4	22
PHG35	13	12	8	29	13	14	2	25	23	22	28	31	3	26	24	22
W117	1	1	9	23	6	31	14	28	24	1	24	30	30	30	14	23
B37	24	24	18	9	27	22	27	30	4	20	29	14	29	31	31	24
PHJ40	28	15	30	25	29	17	25	31	29	23	31	19	13	9	25	25

Which genotypes are most stable?

✧ earlier vs. more recent releases

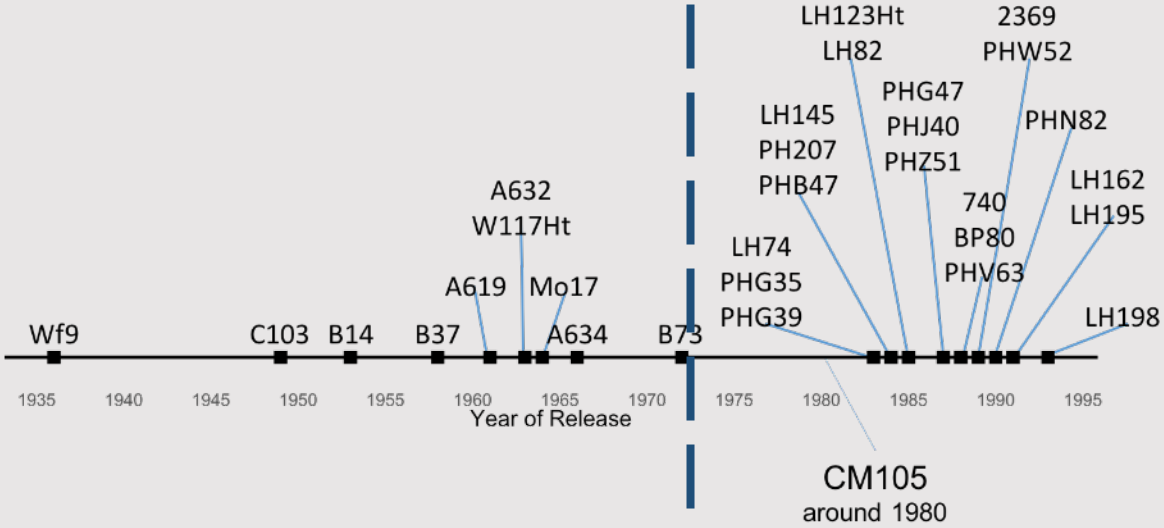




Which genotypes are most stable?

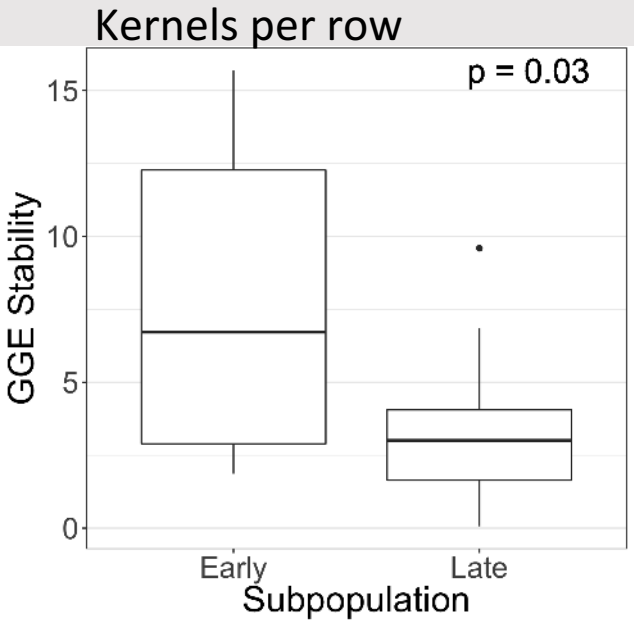
✧ earlier vs. more recent releases

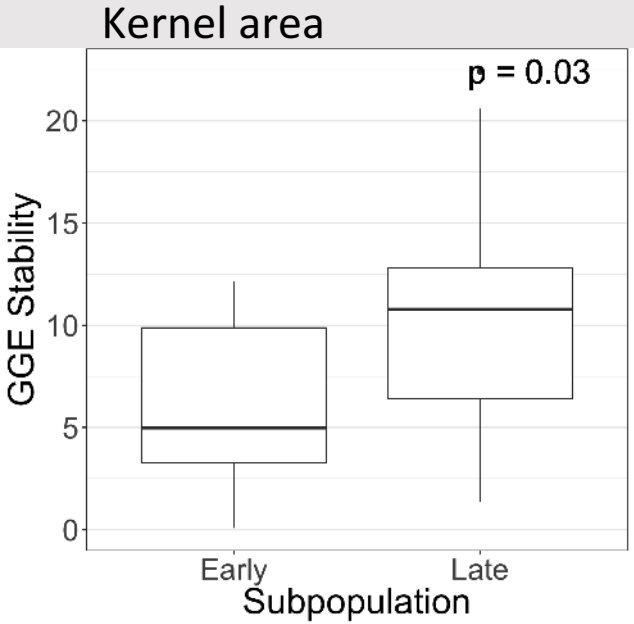
- ✧ Kernels per row
  - ✧ More recent releases are more stable
- ✧ Kernel area
  - ✧ Earlier releases are more stable



Earlier releases
(in or before 1972)

Recent releases
(after 1972)

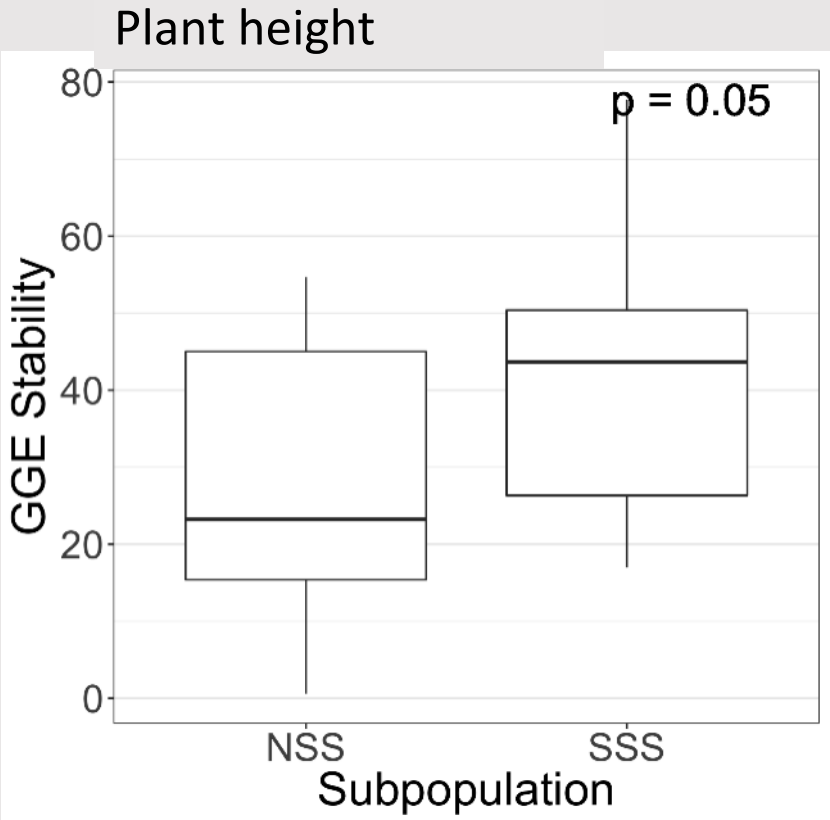




Which genotypes are most stable?

✧ NSS vs. SSS

- ✧ Plant height
  - ✧ NSS subpopulation is more stable (marginal significance)

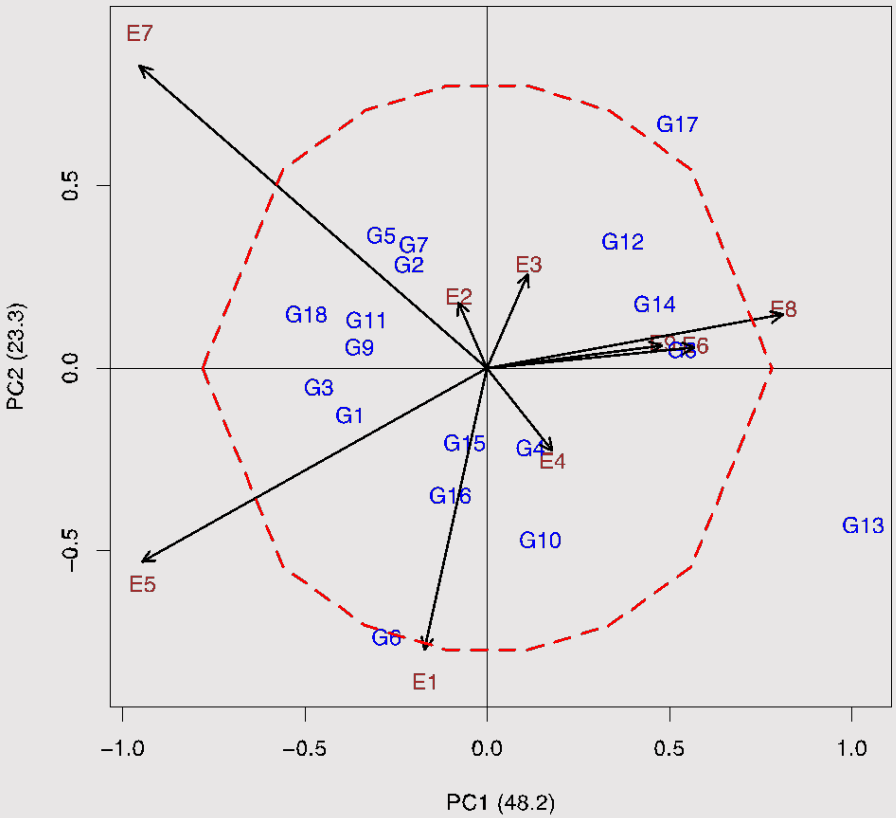


Which traits are good “indicator” traits for assessing G × E?

AMMI analysis and biplots

- **A**dditive **M**ain effects and **M**ultiplicative **I**nteractions
- Useful for
  - Identifying genotypes with similar G × E
  - Identifying similar environments
  - Detecting outlying genotypes and environments
  - Investigating genotype adaptation
- In contrast to GGE, AMMI focuses solely on the G × E interaction (not G + GE)

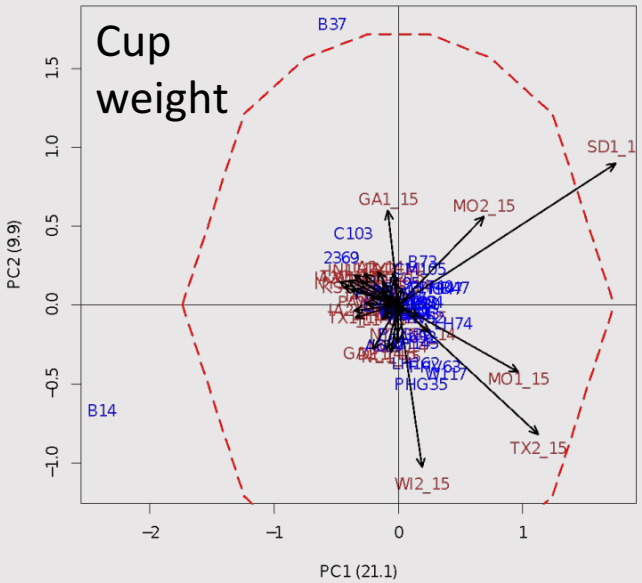
AMMI2 plot

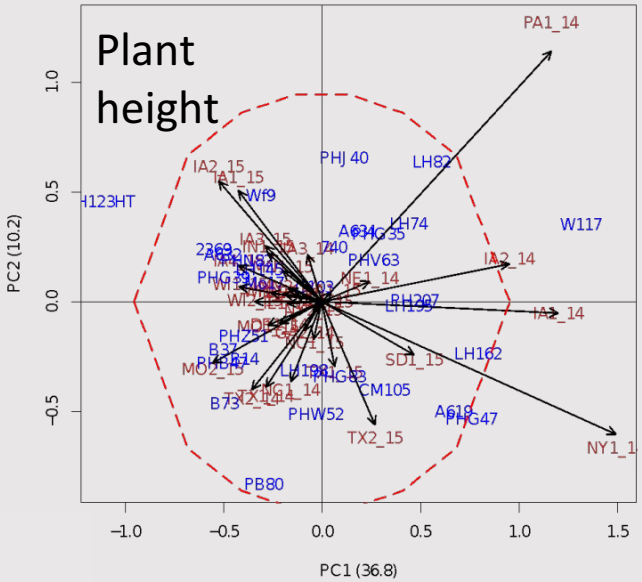


Gauch 1988; Gauch 1992

Which traits are good "indicator" traits for assessing G × E?

- Traits for which G × E explains more variation are "sensitive" to G × E
- Visually inspect AMMI PC1 *vs.* PC2 biplots for clustering or spreading points
- To quantify
  - Standardize traits
  - Conduct AMMI analysis
  - Calculate Euclidean distance between pairs of genotype points and pairs of environment points





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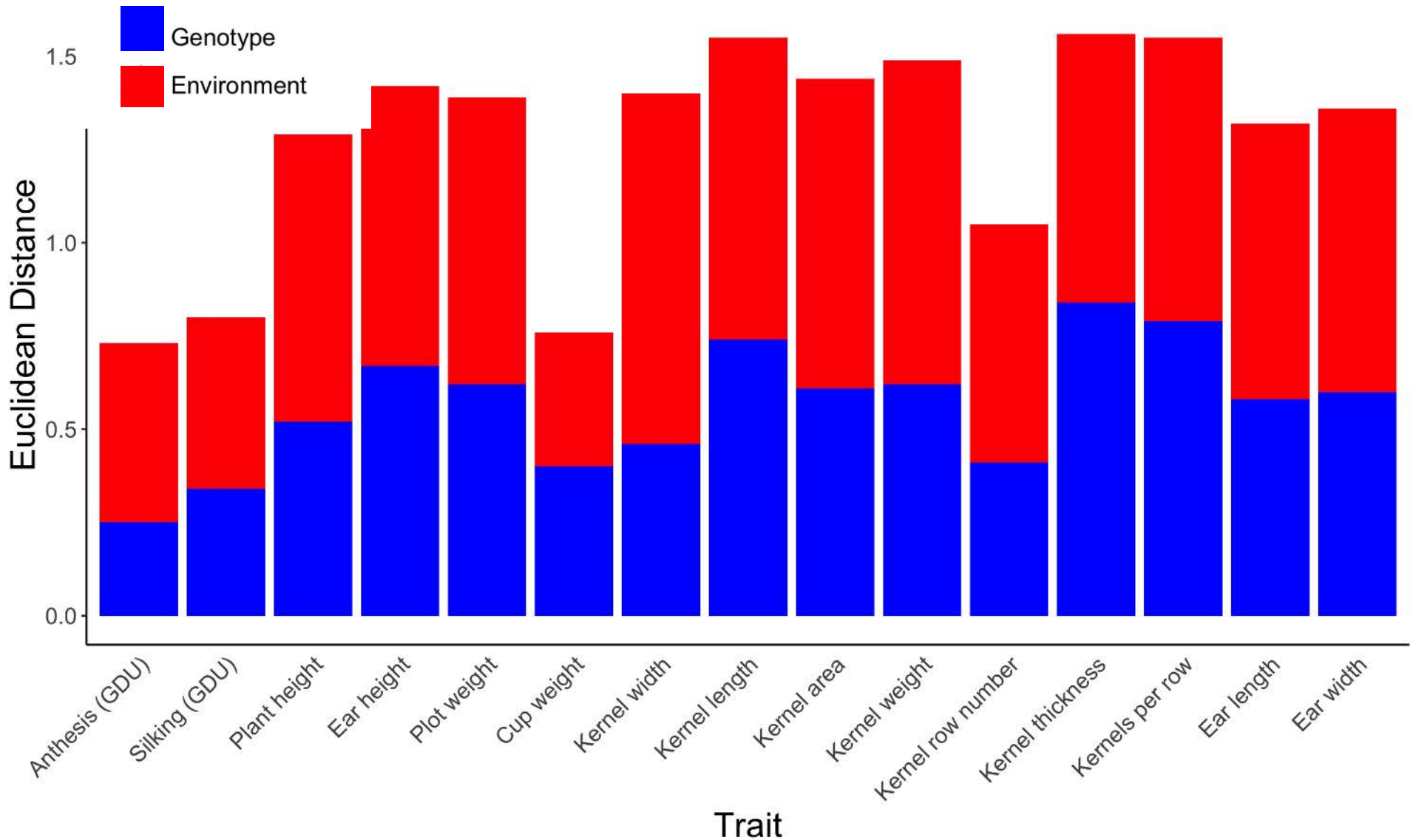

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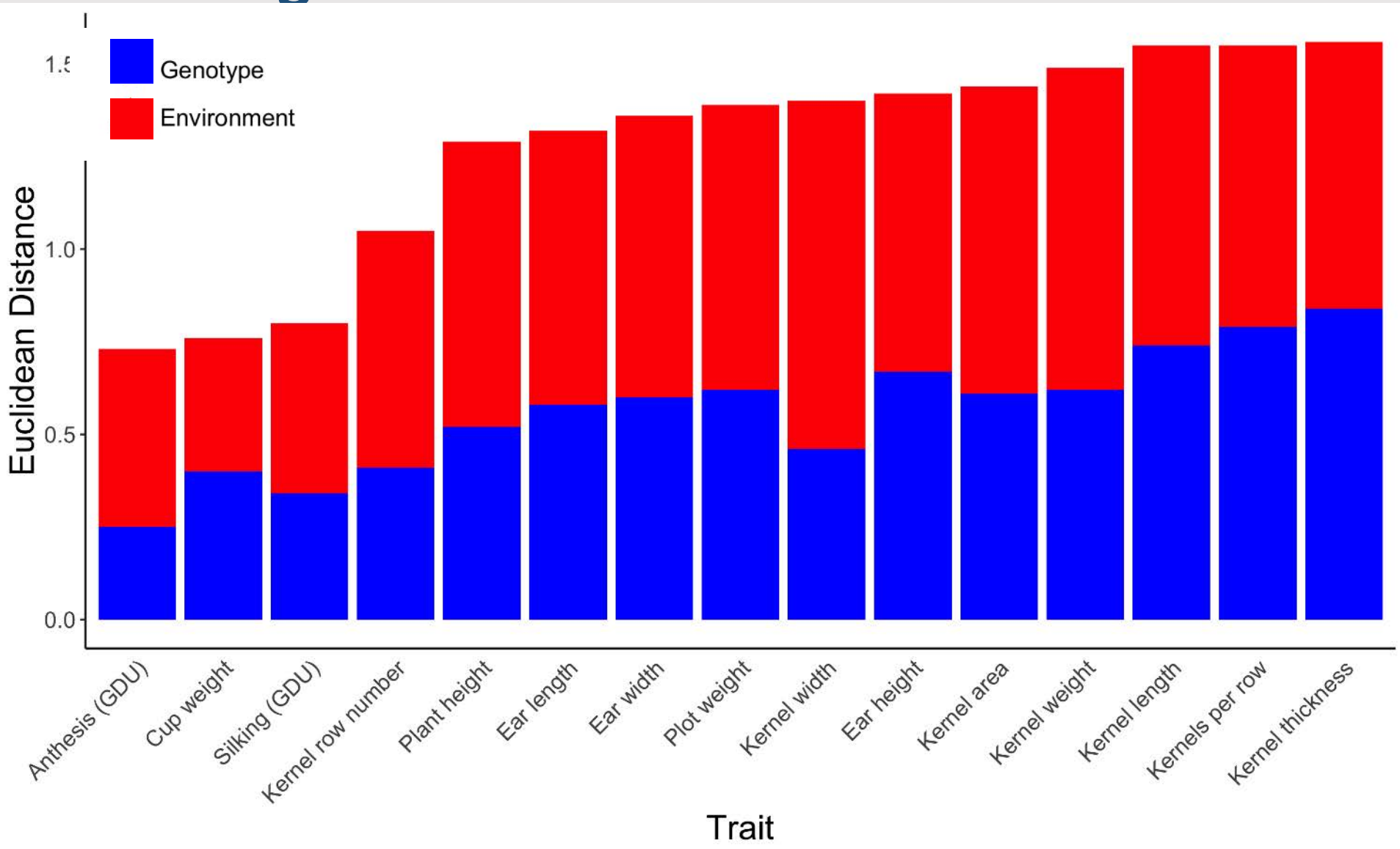

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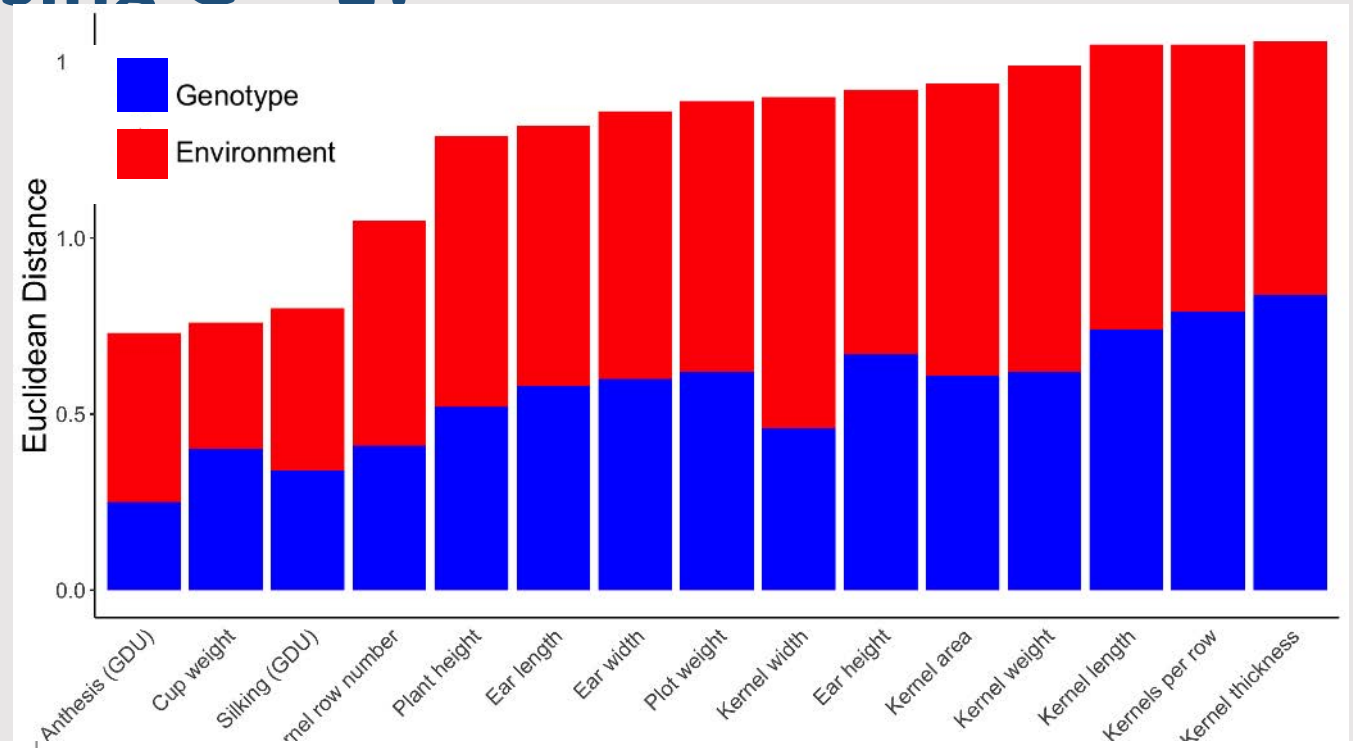

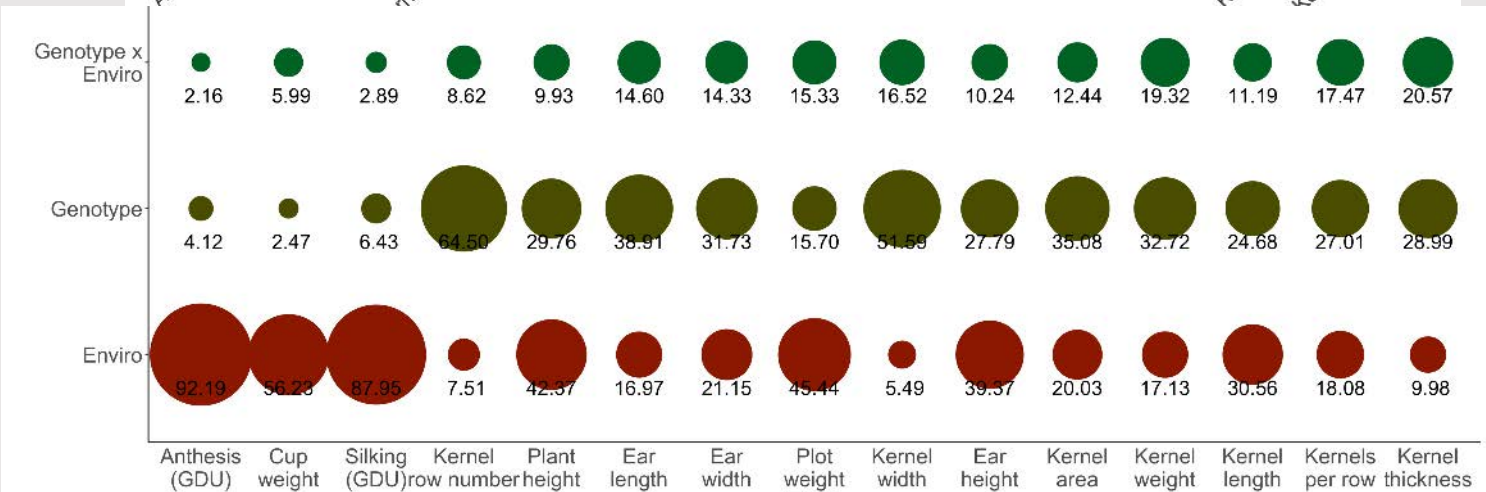

Concluding remarks

- How much is each trait influenced by G × E?
  - G x E interaction explains sizeable portion of variation

- Which environments are best at discriminating among genotypes?
  - Notice patterns in the discriminability of each location: some locations discriminate well for most traits while others are poor discriminators for most traits

  - The top locations for discriminability are in the Midwest…
    - as is the majority of the inbreds' origins

  - Continue experiments discriminating locations
    - Difficult to determine because, for many locations, discriminating ability changes between 2014 and 2015
    - Should also update to include a measure of representativeness /

Concluding remarks

- Which genotypes are the most stable?
  - Stability patterns among genotypes are less defined: most genotypes are stable for some traits and unstable for others
  - For the most part, early- vs. recent-release germplasm and NSS vs. SSS are not significantly different in terms of stability
  - While plant breeders usually seek stable performance, for this experiment, we want to see G × E so keep using the less stable lines (e.g. PHJ40, B37, A619) as well

- Which traits are useful for assessing G × E interaction?
  - Kernel traits (area, length, thickness, weight) showed greater sensitivity to G × E—good "indicator traits" for future studies
  - Flowering time (anthesis and silking) showed the least sensitivity to G × E

GxE 2014 and 2015 Inbred Trials

- Jonathan Lynch
- Randy Wisser
- Joe Knoll
- Nick Lauter
- Pat Schnable
- Torbert Rocheford
- Sherry Flint-Garcia
- Jim Holland
- Aaron Lorenz
- Ed Buckler
- Margaret Smith
- Rebecca Nelson
- Mike Gore
- Wenwei Xu
- Natalia de Leon
- Shawn Kaeppler
- Candy Hirsch

University of Wisconsin

- Nathan Miller
- Edgar Spalding
- Naser AlKhalifah
- Emily Rothfusz
- Jane Petzoldt
- Jonathan Renk
- Andy Stuebs

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- Jode Edwards (ARS)
- David Ertl (IA Corn)
- Celeste Falcon (UW)
- Sherry Flint-Garcia (ARS)
- Joseph Gage (UW)
- Jack Gardiner (ISU)
- Fiona Goggin (Univ AR)
- Byron Good (Guelph)
- Mike Gore (Cornell)
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- Joe Knoll (ARS)
- Judith Kolkman (Cornell)
- Greg Kruger (UNL)
- Nick Lauter (ARS)
- Carolyn Lawrence-Dill (ISU)
- Liz Lee (Guelph)
- Zhizhai Liu (TAMU)
- Natalia de Leon (UW)
- Alex Lipka (UIUC)
- Argelia Lorence (AR-State)
- Aaron Lorenz (UMN)
- Jonathan Lynch (PSU)
- Bridget McFarland (UW)
- John McKay (CSU)
- Nathan Miller (UW)
- Steve Moose (UIUC)
- Seth Murray (TAMU)
- Rebecca Nelson (Cornell)
- Torbert Rocheford (Purdue)
- Oscar Rodriguez (UNL)
- Cinta Romay (Cornell)
- Emily Rothfusz (UW)
- James Schnable (UNL)
- Pat Schnable (ISU)
- Brian Scully (ARS)
- Rajandeep Sekhon (Clemson)
- Maninder Singh (MSU)
- Kevin Silverstein (UMN)
- Margaret Smith (Cornell)
- Bob Snyder (PSU)
- Edgar Spalding (UW)
- Nathan Springer (UMN)
- Srikant Srinivasan (ISU)
- Yiwei Sun (ISU)
- Kurt Thelen (MSU)
- Peter Thomison (OSU)
- Kelly Thorp (ARS)
- Mitch Tuinstra (Purdue)
- Jason Wallace (UGA)
- Renee Walton (ISU)
- Rick Ward (UA)
- Bill Widdicombe (MSU)
- Rod Williamson (IA Corn)
- Randy Wisser (UDel)
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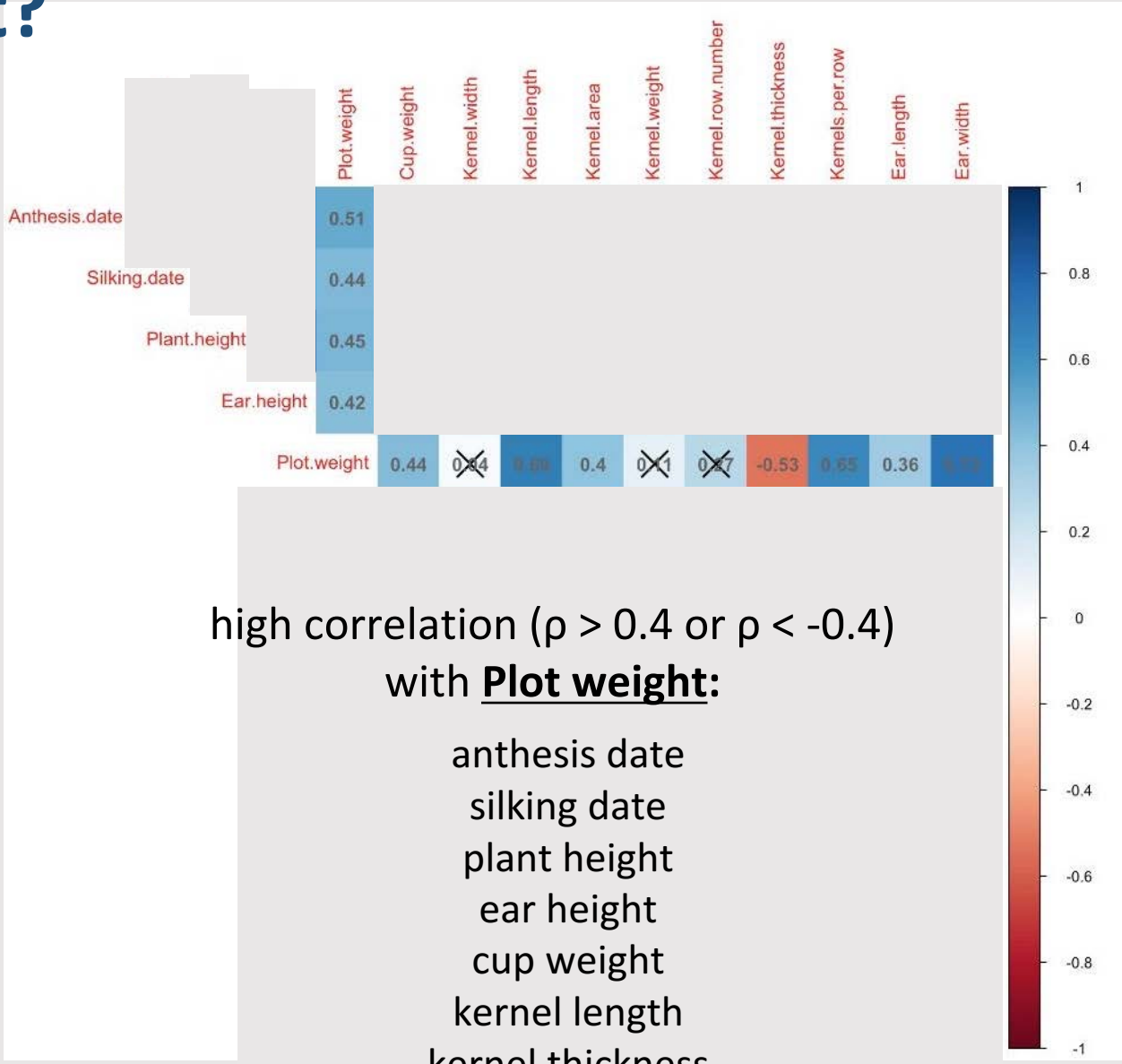
Thank you for your attention!

Questions?

Concluding remarks

- How much is each trait influenced by G × E?
  - G x E interaction explains sizeable portion of variation
- Which environments are best at discriminating among genotypes?
  - Notice patterns in the discriminability of each location: some locations discriminate well for most traits while others are poor discriminators for most traits
  - The top locations for discriminability are in the Midwest…as is the majority of the germplasm
  - Continue experiments discriminating locations
    - Difficult to determine because, for many locations, discriminating ability changes between 2014 and 2015
    - Should also update to include a measure of representativeness/uniqueness of each enviro
- Which genotypes are the most stable?
  - Stability patterns among genotypes are less defined: most genotypes are stable for some traits, unstable for others
  - For the most part, early- vs. recent-release germplasm and NSS vs. SSS are not significantly different in terms of stability
  - While plant breeders usually seek stable performance, for this experiment, we want to see G × E so keep using the less stable lines (e.g. PHJ40, B37, A619) as well
- Which traits are useful for assessing G × E interaction?
  - Kernel traits (area, length, thickness, weight) showed greater sensitivity to G × E—good "indicator traits" for future studies
  - Flowering time (anthesis and silking) showed the least sensitivity to G × E

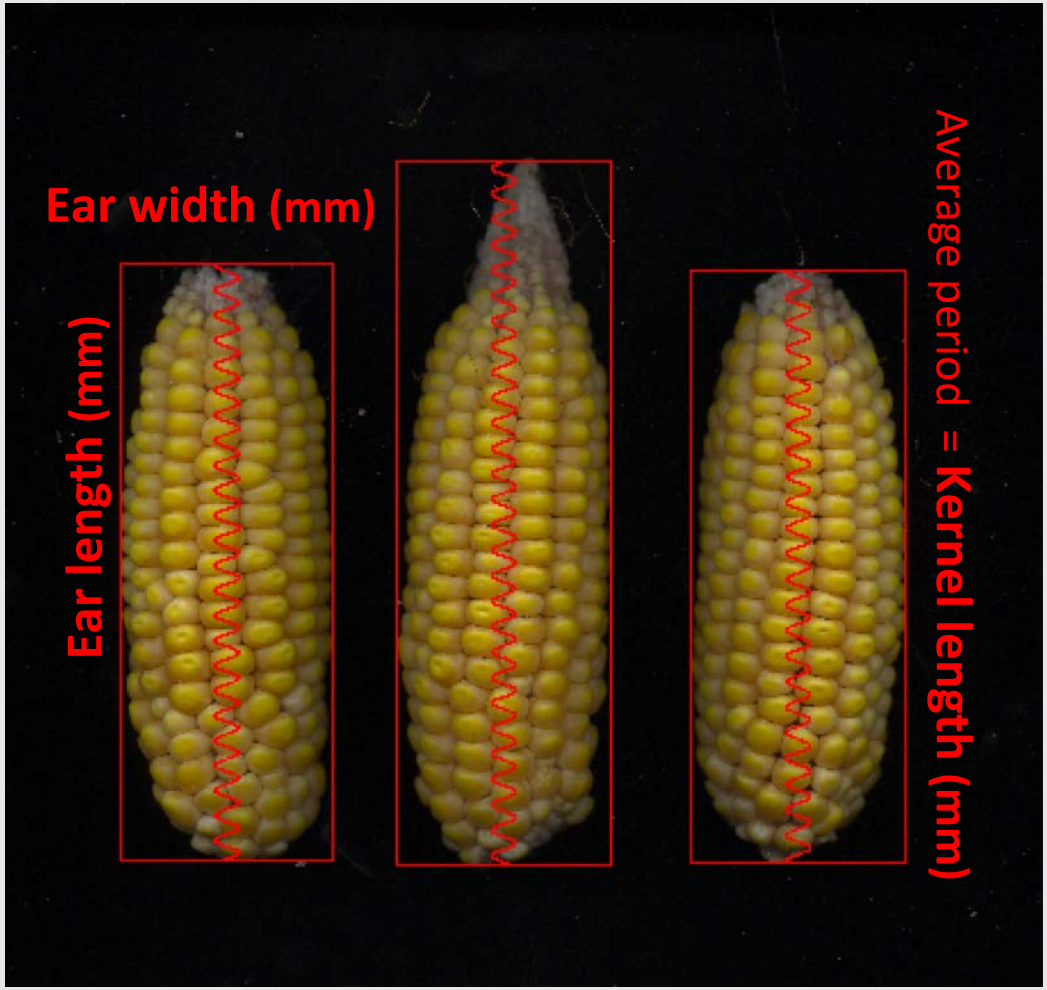
Which traits are correlated with plot weight?



high correlation (ρ > 0.4 or ρ < -0.4)
with **<u>Plot weight</u>:**

anthesis date
silking date
plant height
ear height
cup weight
kernel length
kernel thickness
kernels per row

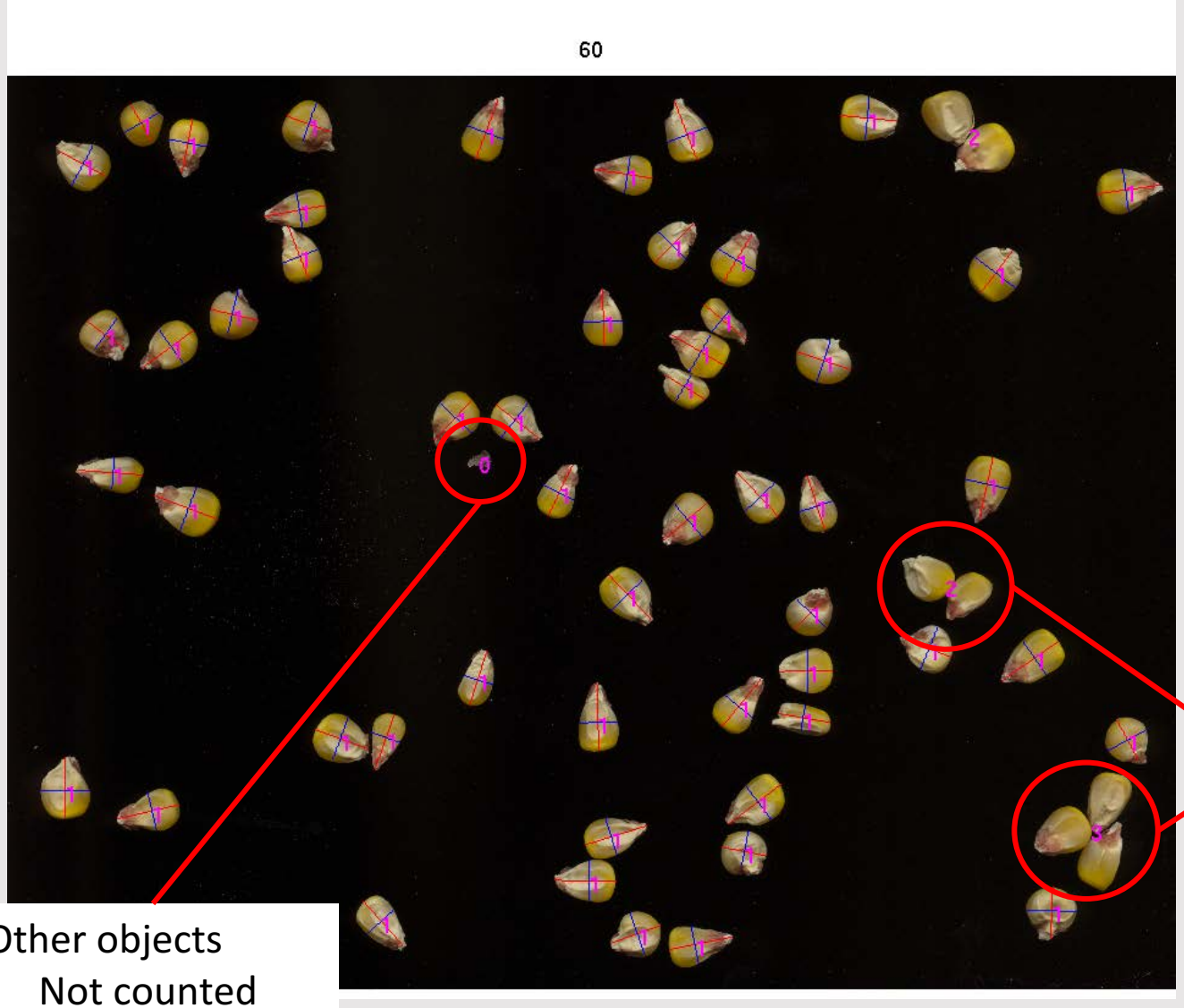
Imaging Output: Ears



- ✧ **Kernel row number**: counted manually
- ✧ **Kernels per row** = Ear length / Kernel length

Miller et al. 2016 – The Plant Journal

Imaging Output: Kernels



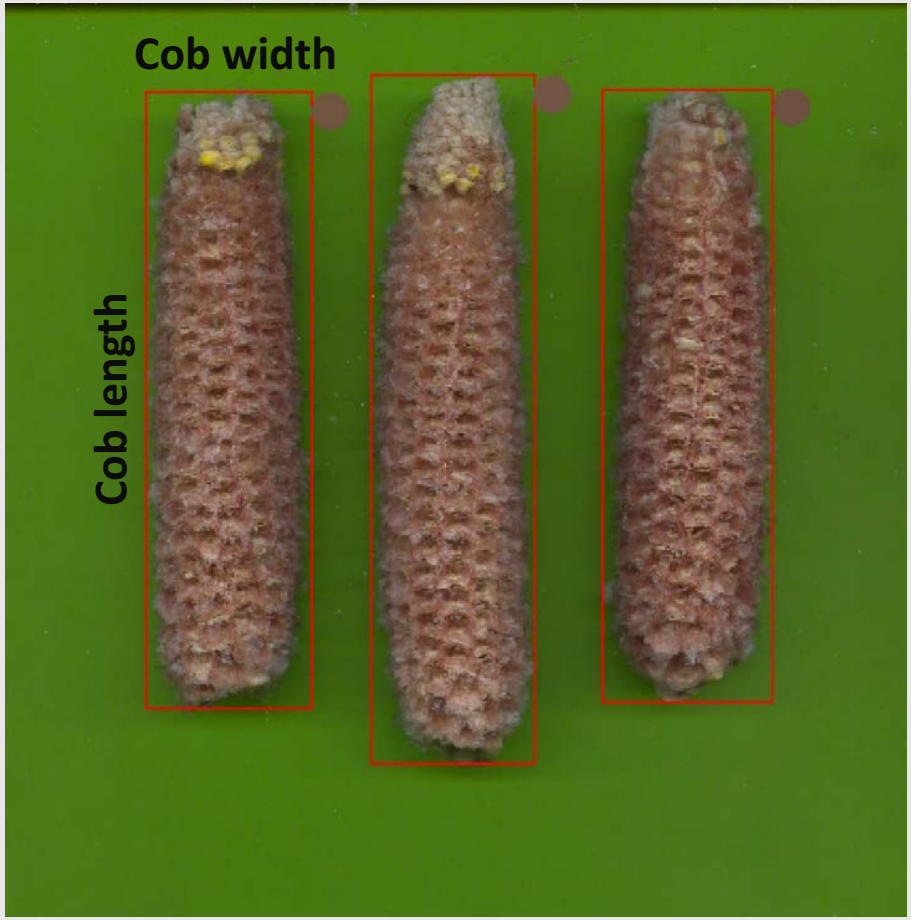
- **Kernel weight** = Cup weight (g) / kernel count

Grouped kernels:
- Counted accurately
- No measurements recorded

Other objects
- Not counted
- Not measured

Miller et al. 2016 – The Plant Journal

Imaging Output: Cobs



Average RGB value of middle third of cob

Miller et al. 2016 – The Plant Journal

GxE Consortium: Data Usage Disclaimer

This presentation includes data analysis and interpretation conducted by the presenter and does not necessarily reflect the observations and conclusions of the GxE Consortium.