University of Minnesota

Characterizing the Profile of Allele-by-environment Interactions Using B73-Mo17 Introgression Lines

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Chicago

Background

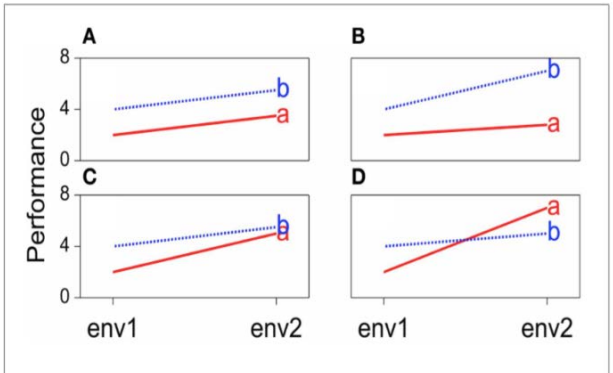
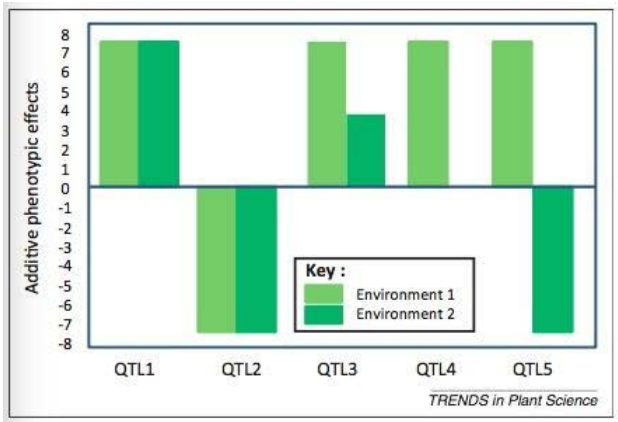


FIGURE 1 | Genotype-by-environment interaction in terms of changing mean performances across environments: (A) additive model, (B) divergence, (C) convergence, (D) cross-over interaction.

Molosetti et al., 2013



El-Soda et al., 2014

Conventional G by E study:

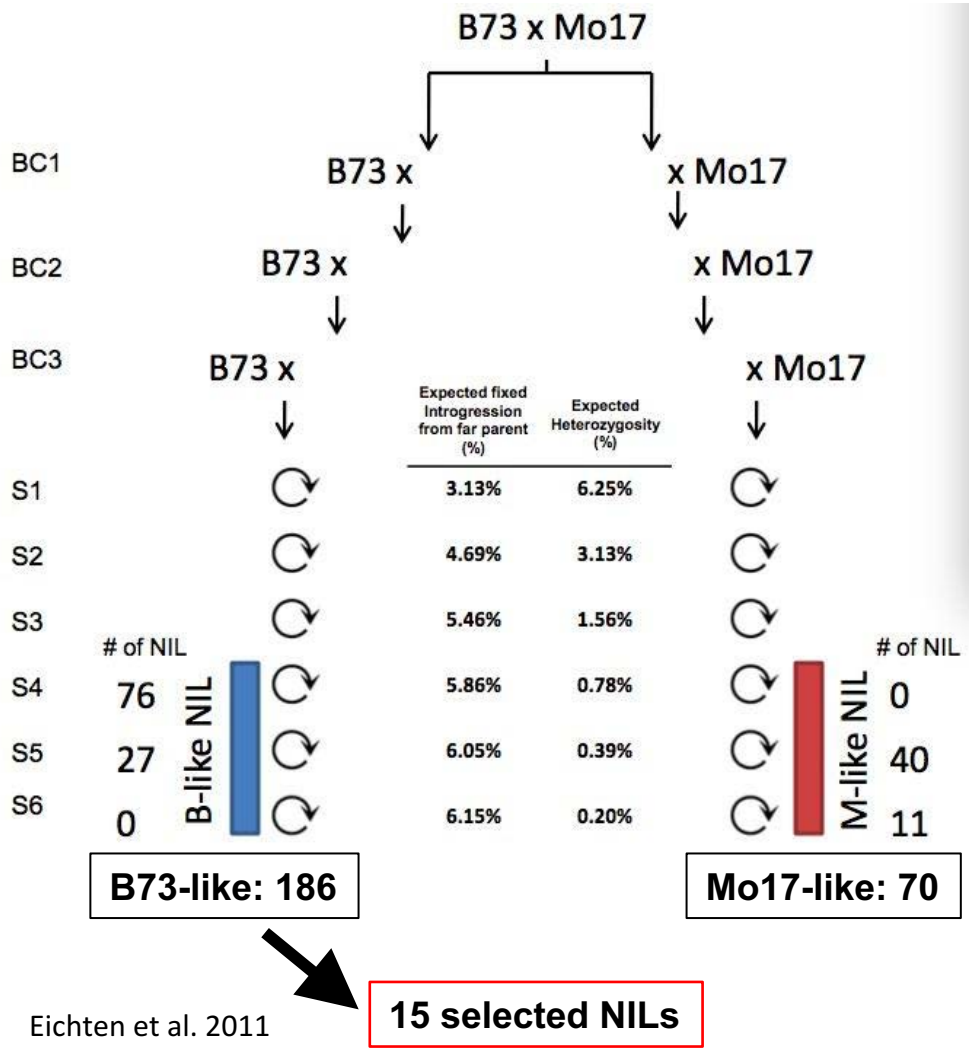
- Mapping G X E QTL in segregation populations: like F_2, RIL…
- Using hybrids or inbred to study genotype-by-environment interaction
- Studying single gene-by-environment effect

Big questions on GE

- **Do random introgression segments throughout the genome have variation in GE sensitivity? To what extent?**
- **What does the allele-by-environment interaction profile look like under natural planting conditions for multiple traits?**

In this study, we use NILs with limited genomic introgression proportion evaluated in multiple natural environments to study the profile of allele-by-environment interactions.

NIL population and Field experiment



Eichten et al. 2011

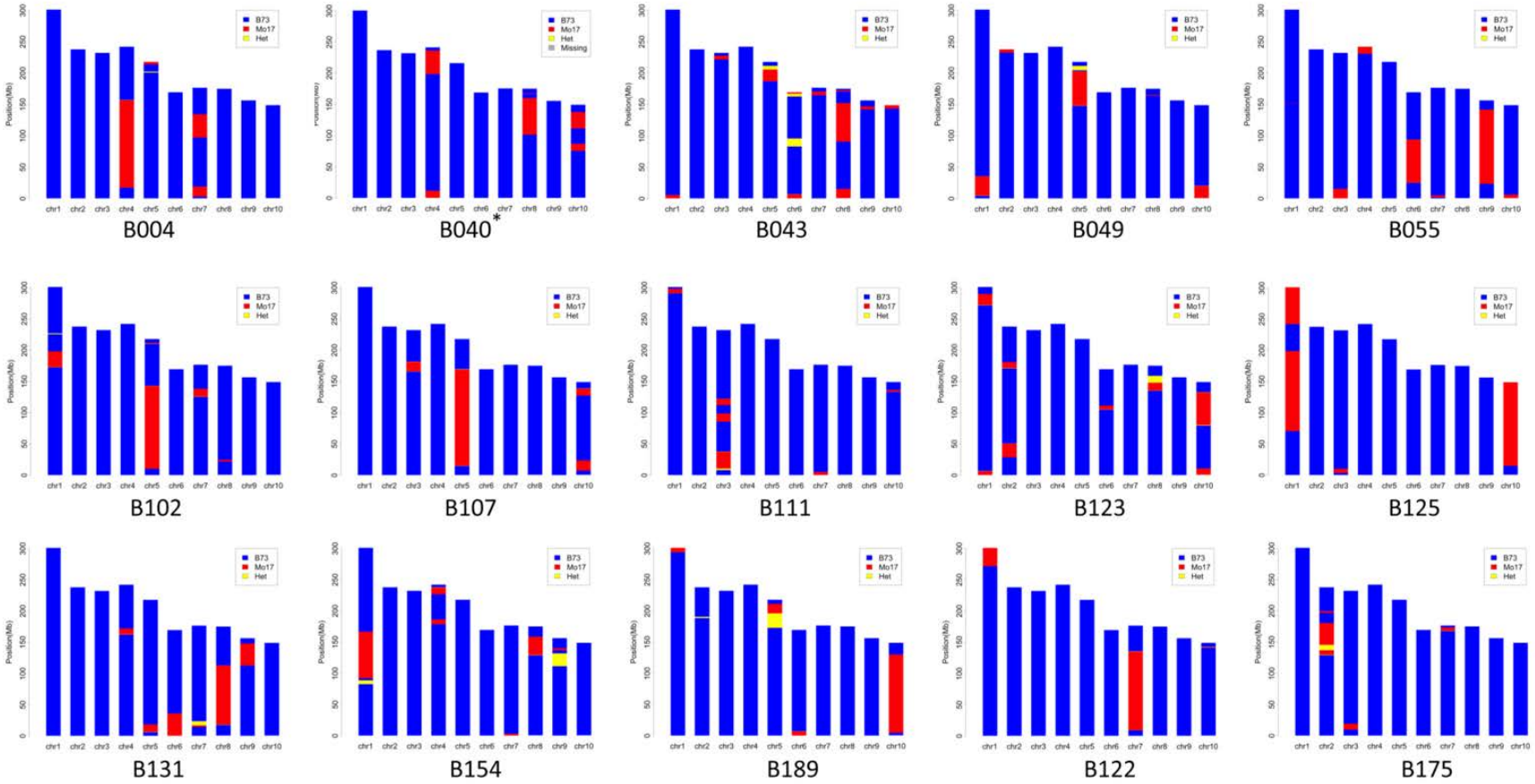
All the 256 NILs were planted in MN during 2015 summer season in two replications.

Selected 15 NILs that showed variation for at least one trait

Distribution of introgression segments in the genome of 15 selected NILs

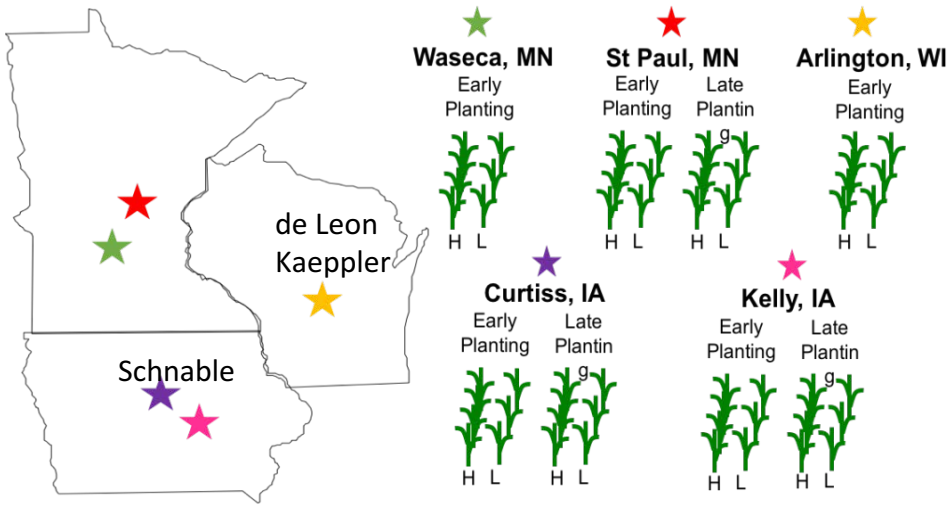
4~11 introgression segments
66.7~311.6Mb, average 182.5Mb (~8.87%)

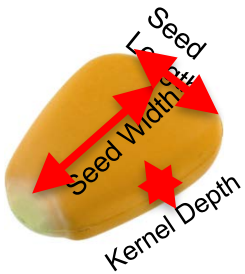
Heterozygous: 7.24Mb (0.35%)
Genes: 989~4,754, average 2789



Experimental Design

16 Environments





Traits measured: 26 traits total!

Vegetative traits: 15 in total

- Weekly plant heights ~14 to ~70 DAP
- Days to mid-pollen shed and mid-silk
- Plant height at maturity
- Ear height at maturity
- Leaf number (above/below ear)

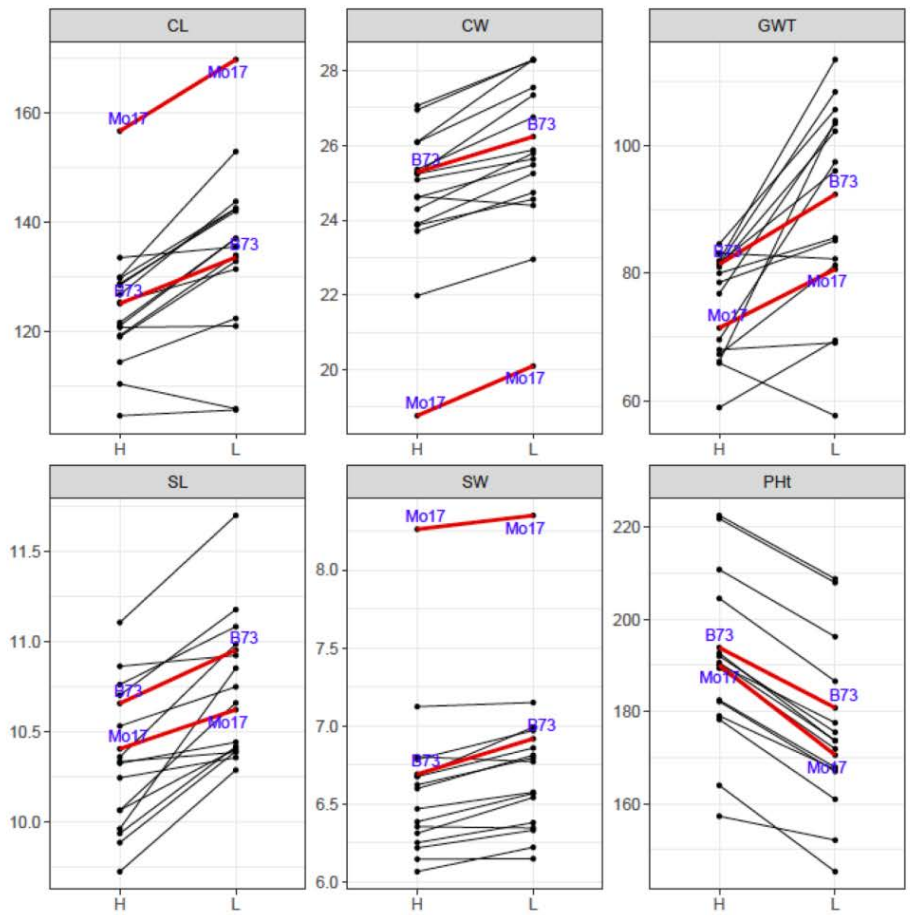
Yield related traits: 11 in total

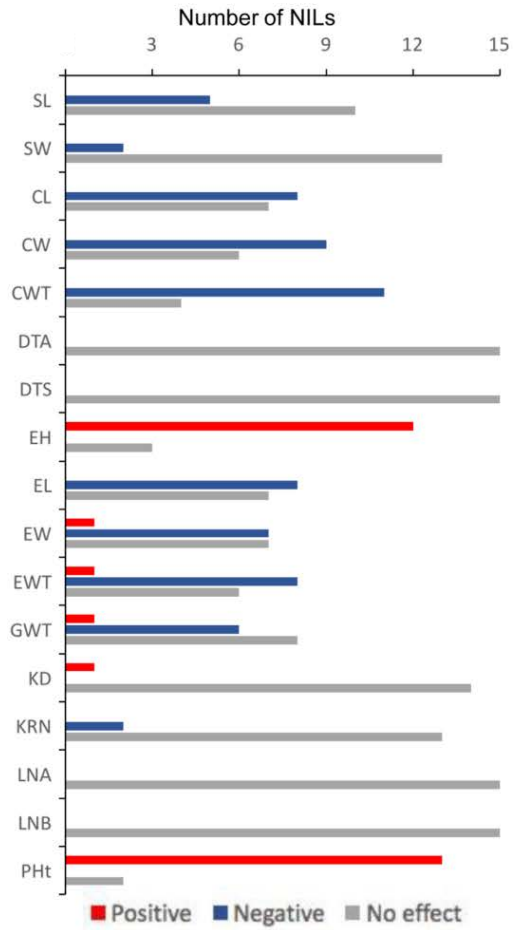
- Ear_Weight; Ear_Width; Ear_Length
- Cob_Weight; Cob_Width; Cob_Length
- Seed Length; Seed Width; Kernel_Depth
- Grain_Weight; Kernel_Row_Number

Significant genotype, environment and GE effects are observed across traits within selected NILs

Trait	Genotype	Environment	Genotype x Environment
PHt14	***	***	N.S.
PHt21	***	***	N.S.
PHt28	***	***	N.S.
PHt35	***	***	N.S.
PHt42	***	***	N.S.
PHt49	***	***	**
PHt56	***	***	**
PHt63	***	***	N.S.
PHt70	***	***	N.S.
PHt	***	***	N.S.
EH	***	***	*
DTA	***	***	***
DTS	***	***	***
LNA	***	***	N.S.
LNB	***	***	N.S.
SW	***	***	**
SL	***	***	**
CW	***	***	***
CL	***	***	***
CWT	***	***	***
EW	***	***	**
EL	***	***	***
EWT	***	***	***
KRN	***	***	N.S.
KD	***	***	***
GWT	***	***	***

Small proportion of the genome can drive significant GE interactions





CL, cob length; CW, cob width;
GWT, grain weight per plant;
SL, seed length; SW, seed width;
PHt, plant height at maturity.

Reaction norm of the selected NILs under high and low planting densities for various traits.

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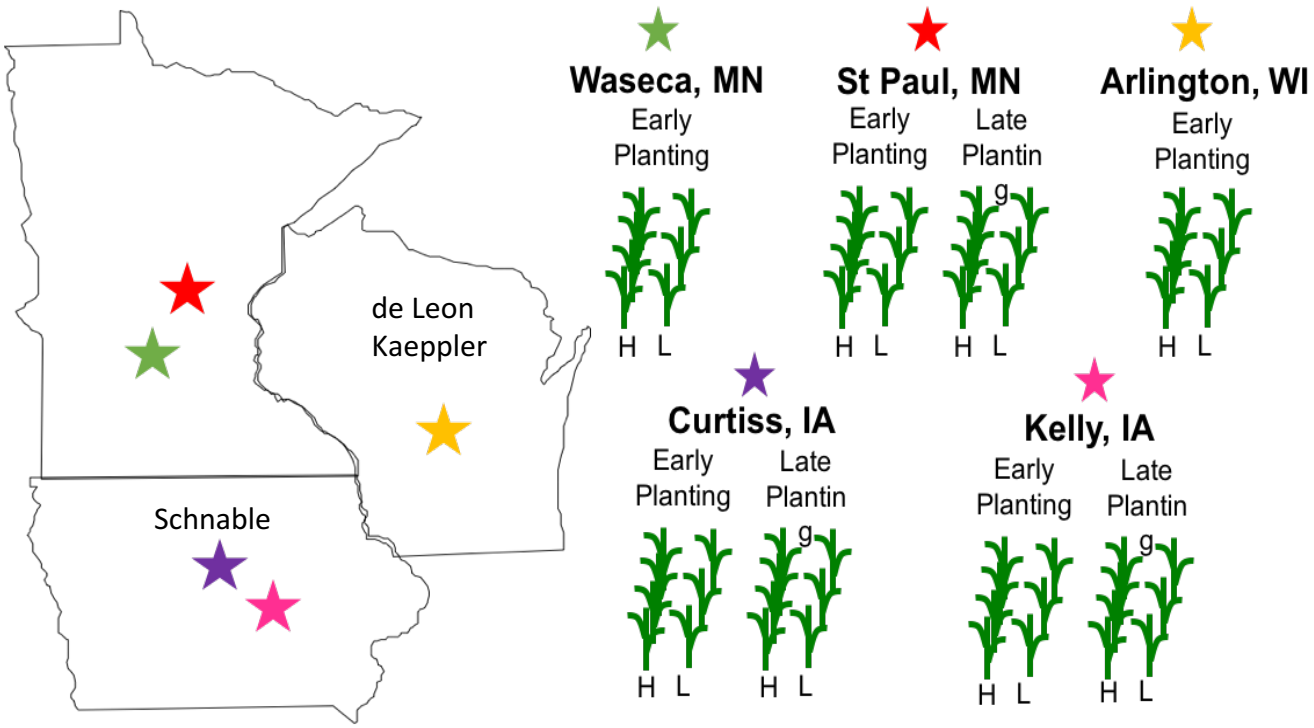
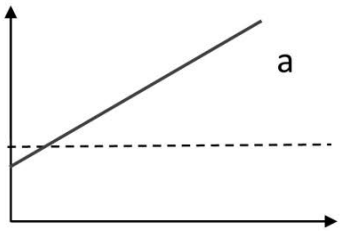
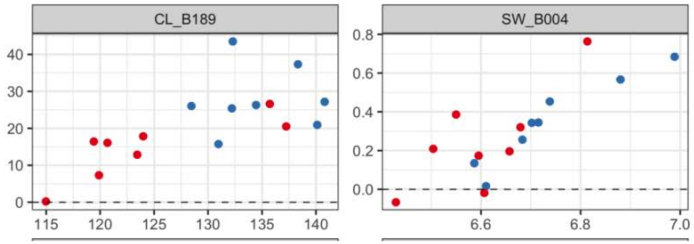


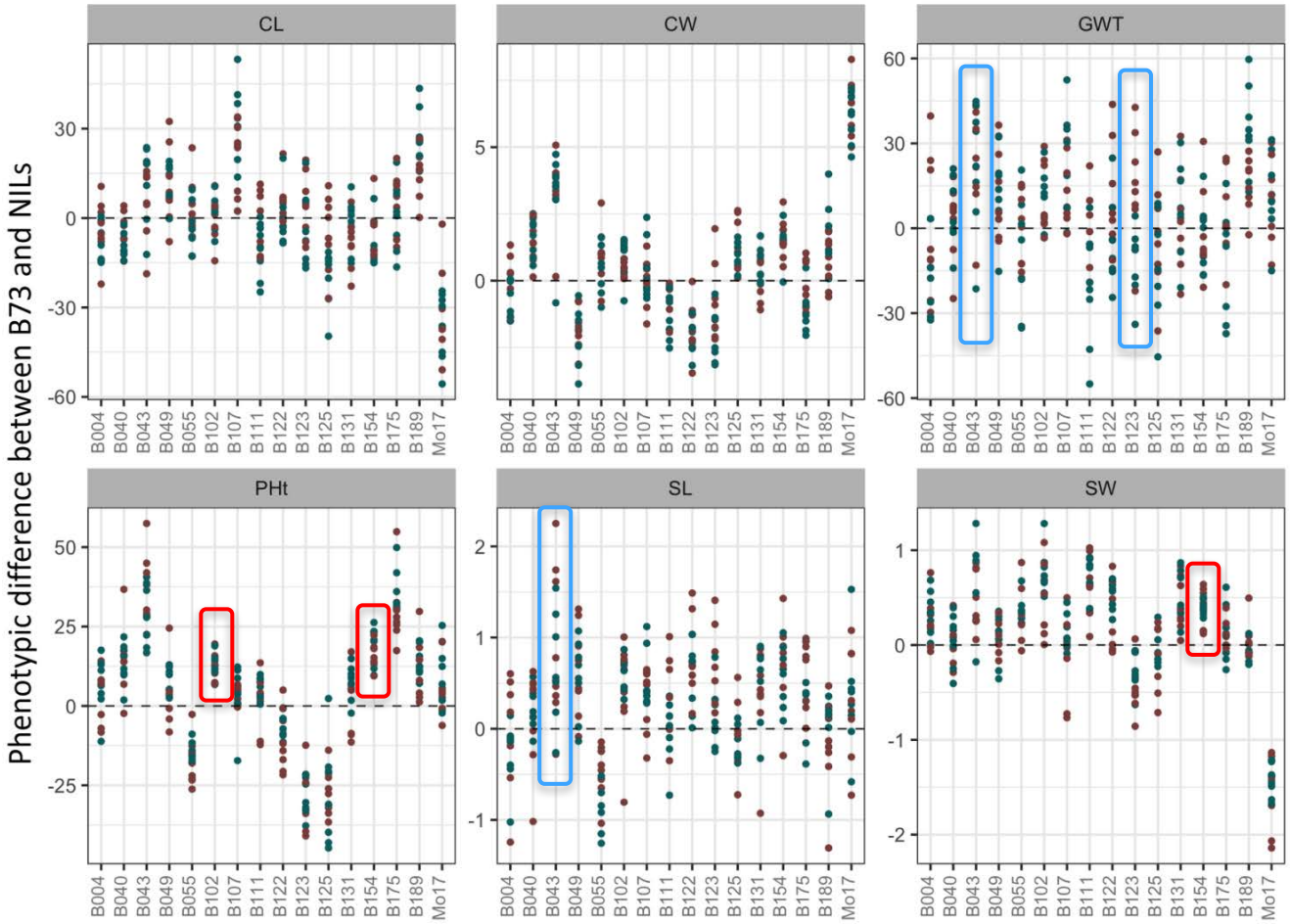
Small proportion of the genome can drive different patterns of GE interactions





Typical distribution pattern of NILs in different environments against environmental quality for various traits.

NILs with different introgression segments respond variously against micro-environmental factors



Phenotypic difference between B73 and the selected NILs across environment.

Red and blue dot indicate high and low planting densities respectively

Experimental Design

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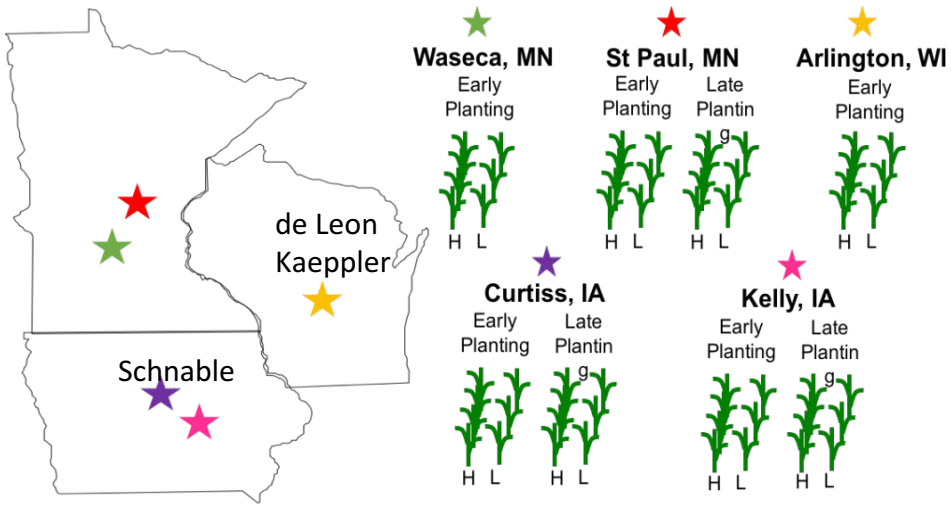

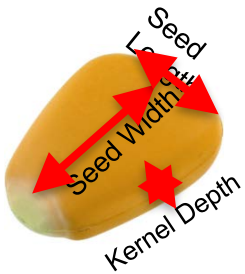

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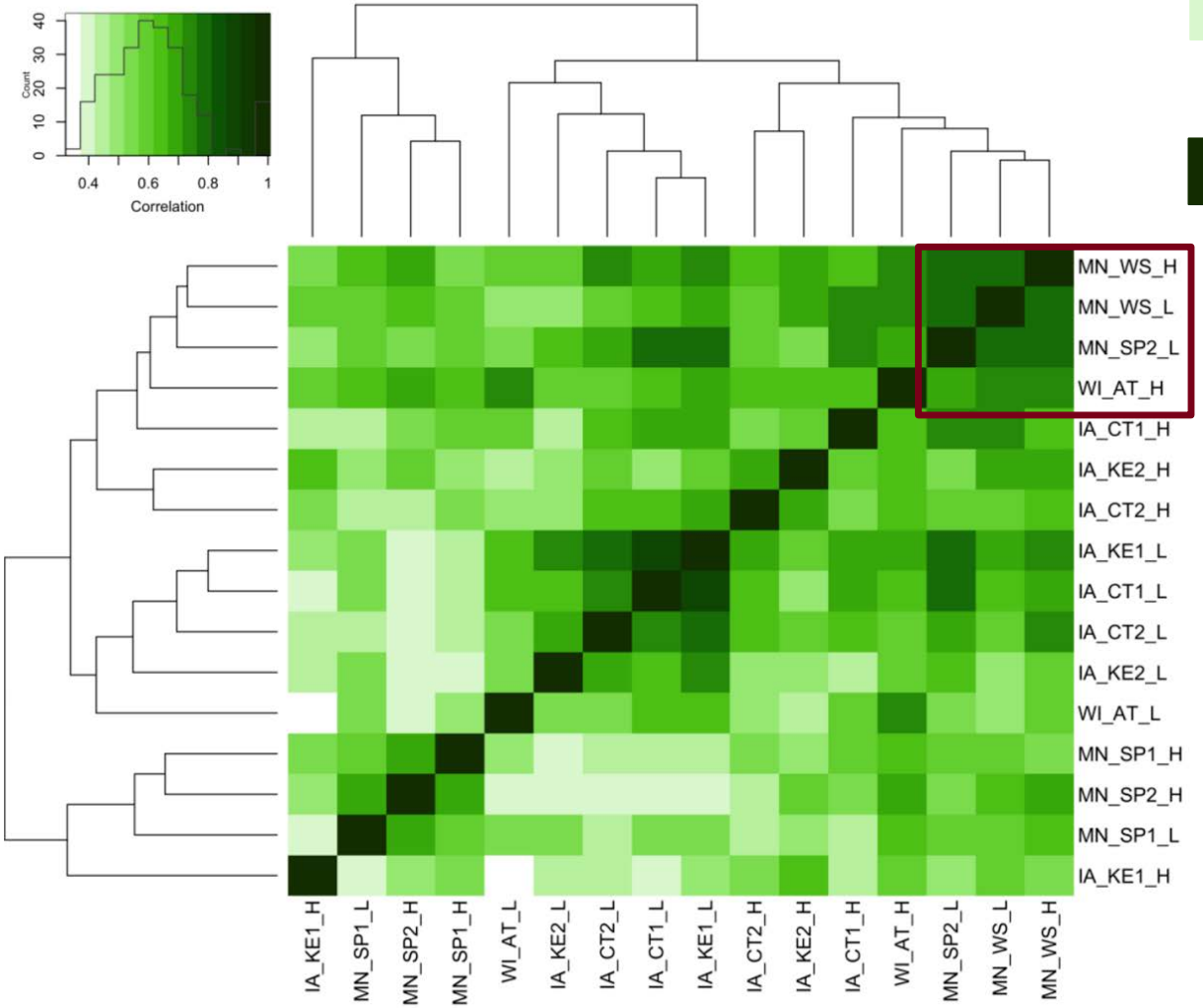
Environments do not group only by density or location on a whole plant phenotypic basis

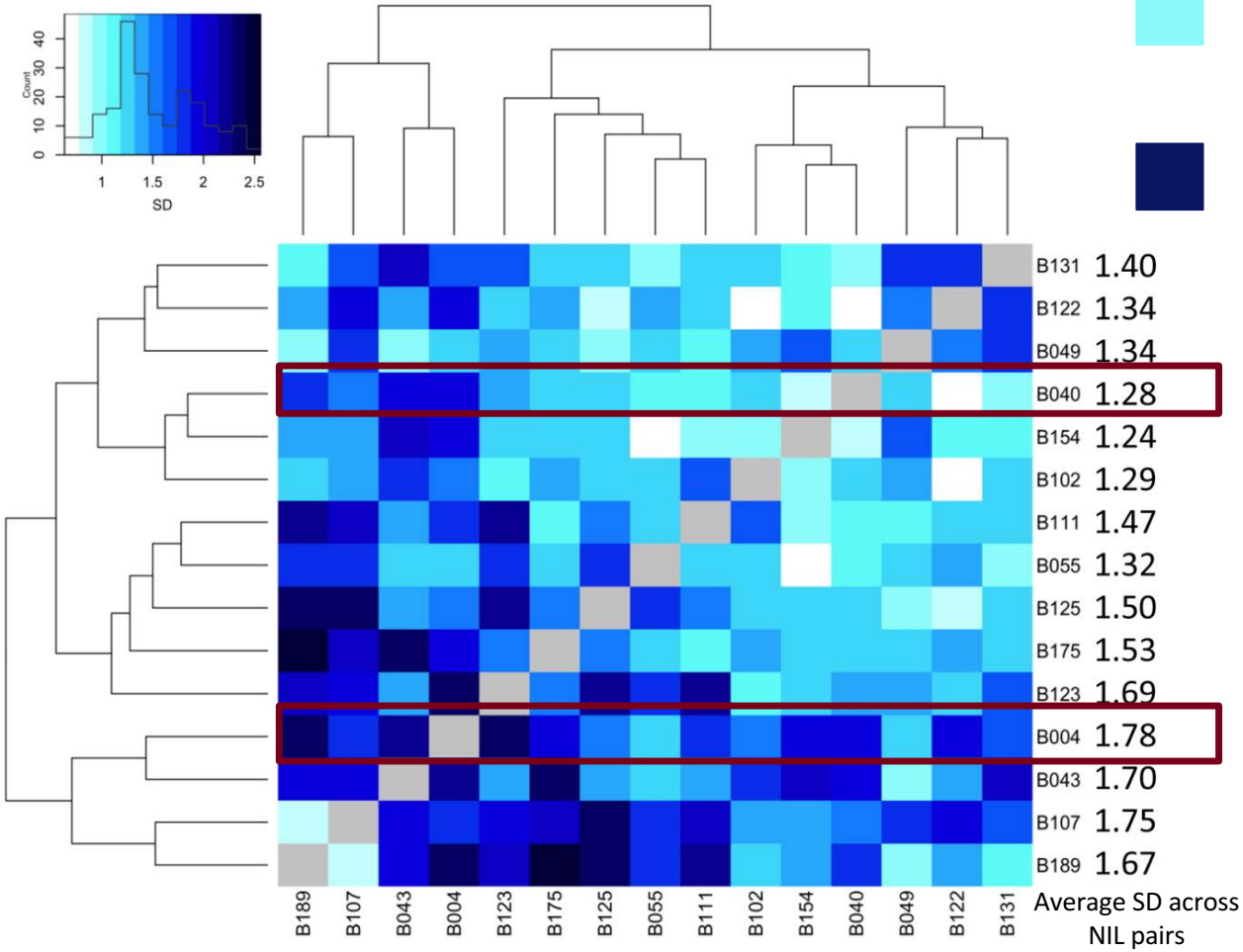


Matrix of genotype x trait shows low similarity between environments

Matrix of genotype x trait shows high similarity between environments

Relationship between environments on the whole plant bases detected by the Mantel test.

Random introgressions show variable stability on a whole plant basis

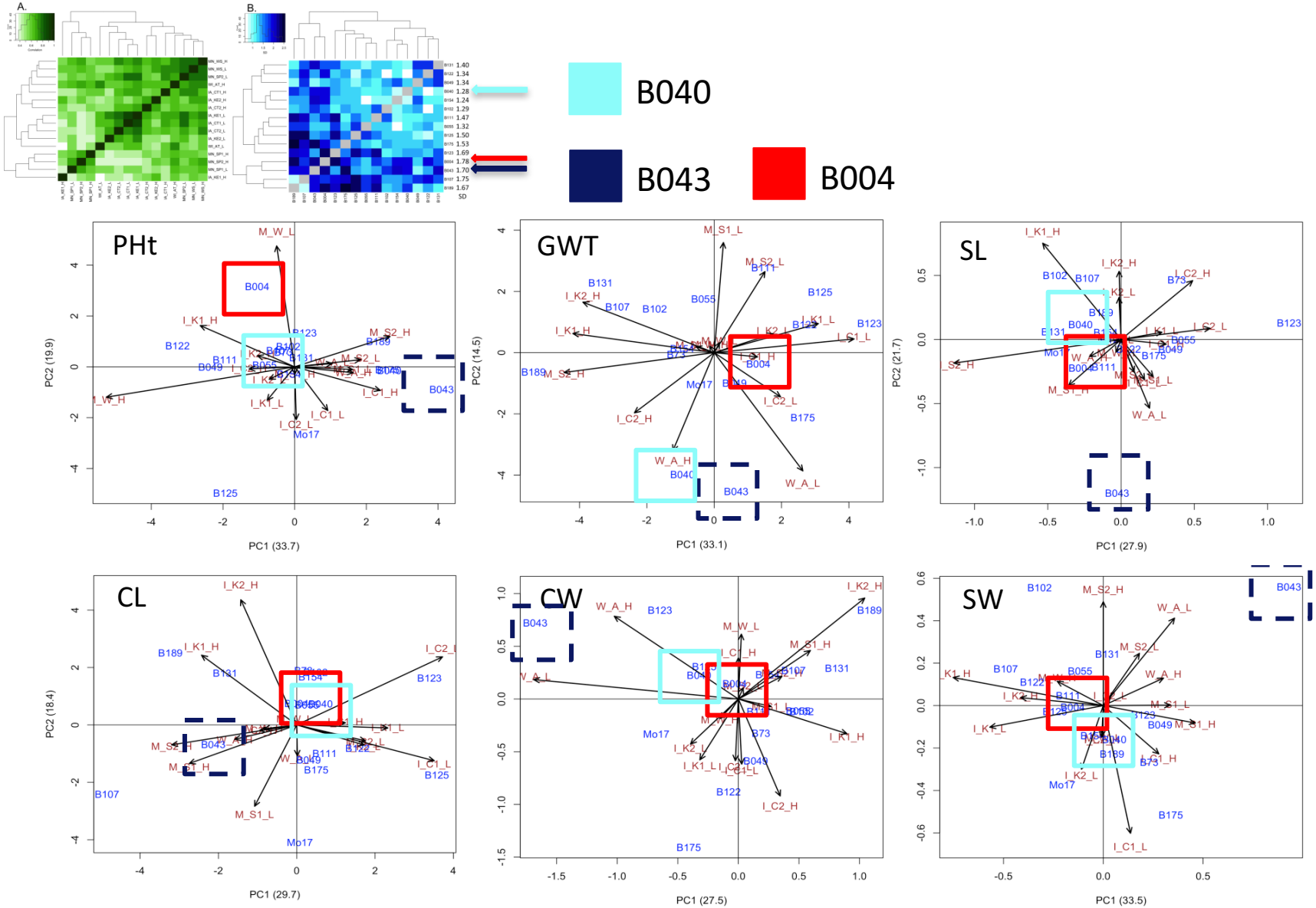


Low variation across environments on a whole plant basis

High variation across environments on a whole plant basis

Each cell is the variation (standard deviation) of distance between each pair of NIL across 16 environments

GE evaluated on a whole plant or individual trait basis can show inconsistencies



Summary

- ✓ **Significant genotype, environment and GE effects are observed across traits for the selected NIL set**
- ✓ **Small proportion of the genome can drive significant and various Allele-by-environment interactions**
- ✓ **Some random introgressed segments in maize genome are more prone to GE interaction than others on the whole plant bases. And the magnitude of the allele-by-environment interaction may vary across specific traits**
- ✓ **NILs enable us to look at QTL or allele by environment interaction in the context of a small portion of the genome**
- ✓ **Next step is to look at GE of NILs in a hybrid context from G2F 2016 and 2017 data**

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