The effects of artificial selection on phenotypic plasticity in maize

Joseph Gage, Diego Jarquin, Cinta Romay, G2F Consortium, Edward S. Buckler, Aaron Lorenz, Shawn Kaeppler, and Natalia de Leon
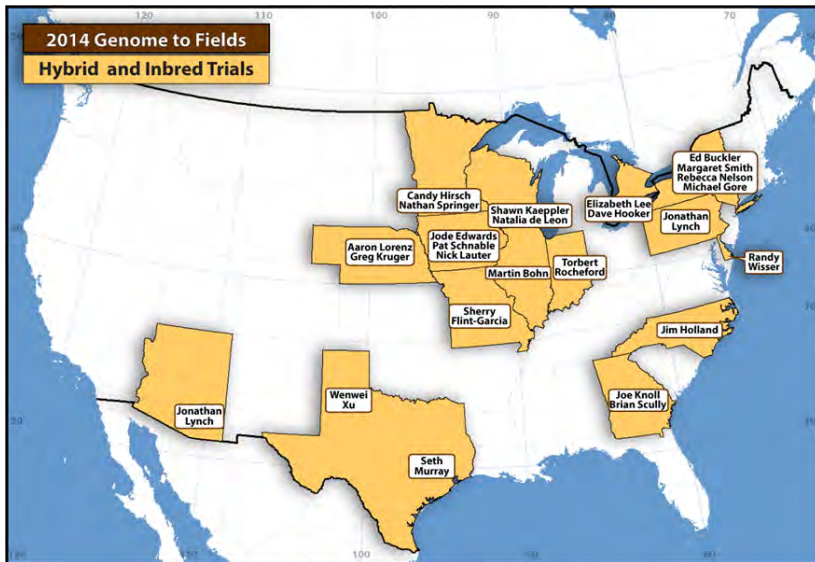
8 December 2016

Using the 2014 G2F data to ask:

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1 How do selected loci contribute to GxE variation?

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1. How do selected loci contribute to GxE variation?
2. What parts of the genome control GxE variation?

- >800 Hybrids
- 21 Locations

Core Set of Phenotypes:

- Days to anthesis
- Days to silk
- Ear height
- Plant height
- Plot weight
- Test weight
- Moisture
- Grain yield
- Stand count
- Root Lodging
- Stalk Lodging

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Hypothesis: Regions under selection for fitness in new environments can ultimately show reduced contribution to plasticity.

Identify regions selected for temperate climates based on Fst between Temperate and Tropical materials:

Credit: Cinta Romay

Use genotypic scores in high and low Fst loci to calculate GxE attributable to those regions:

$$\mathbf{y} = \mu + \mathbf{L} + \mathbf{E} + \mathbf{g} + \mathbf{g_H} \times \mathbf{E} + \mathbf{g_L} \times \mathbf{E} + \varepsilon$$

μ: overall mean
$\mathbf{y}$: phenotpe: Grain Yield and Plant Height
$\mathbf{L}$: line (hybrid) effect
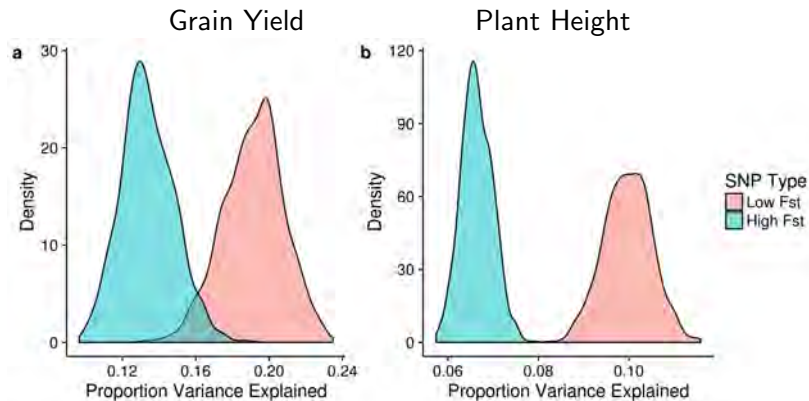$\mathbf{E}$: environmental effect
$\mathbf{g}$: overall genotypic effect
$\mathbf{g_H} \times \mathbf{E}$: High Fst by Environment effect
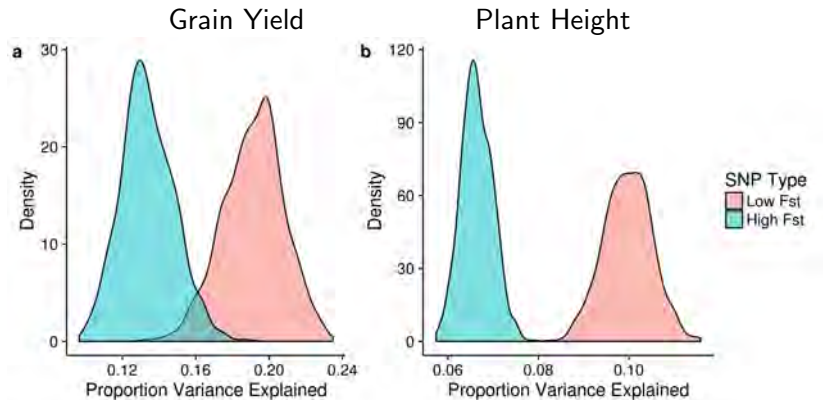$\mathbf{g_L} \times \mathbf{E}$: Low Fst by Environment effect
ε: residual error

Low Fst SNPs ($n \approx 200k$) sampled to eq. low High SNPs ($n \approx 9k$)

Credit: Diego Jarquin

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Grain Yield   Plant Height

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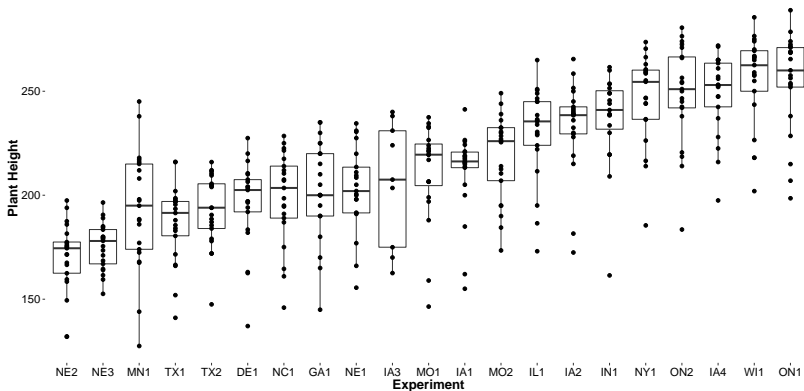
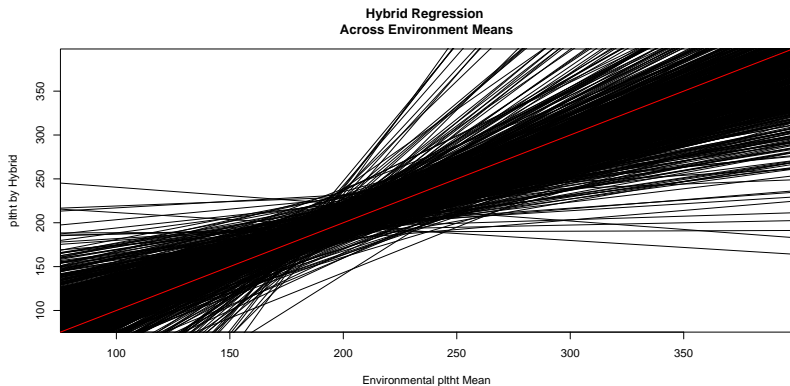**Hypothesis:** GE is controlled disproportionately by numerous regulatory mechanisms.

Performed Finlay-Wilkinson regression:

- Regress phenotypes of hybrids on environmental index

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Hybrid Regression
Across Environment Means

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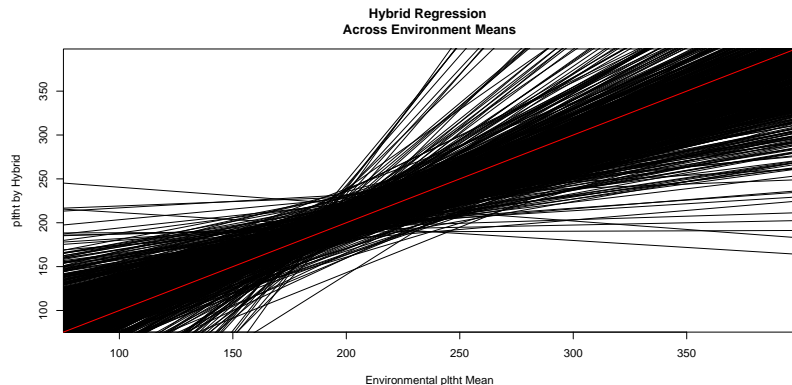
Calculate slope and MSE for each hybrid, for each of five traits:

Plant & Ear Height, Male & Female Flowering, Grain Yield

Perform GWAS using slope, MSE, and traits per se for each phenotype

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- slope: Type II stability
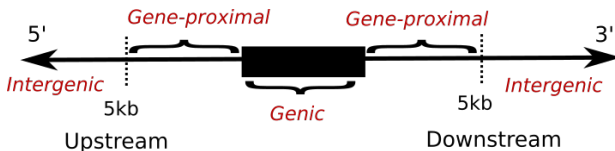- MSE: Type III stability
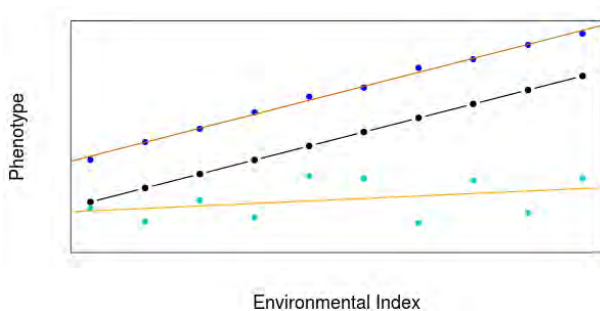
Pool 50 most significant SNPs for each trait/parameter combination:

- 250 slope SNPs
- 250 MSE SNPs
- 250 Per Se SNPs

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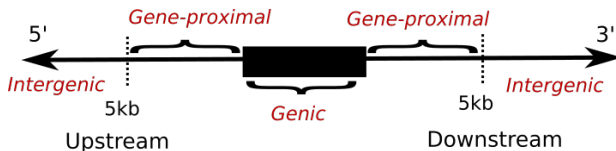- 250 slope SNPs
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Classify associated SNPs as Upstream/Downstream, Intergenic/Gene-proximal/Genic

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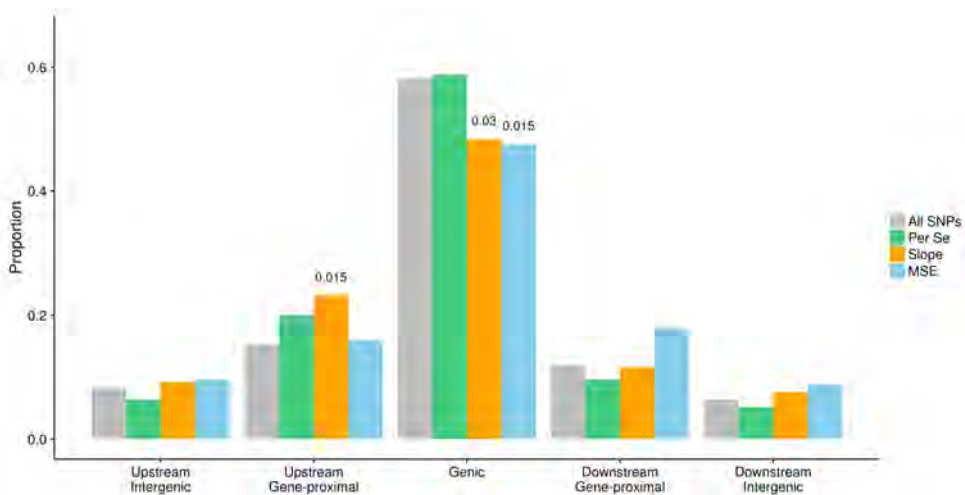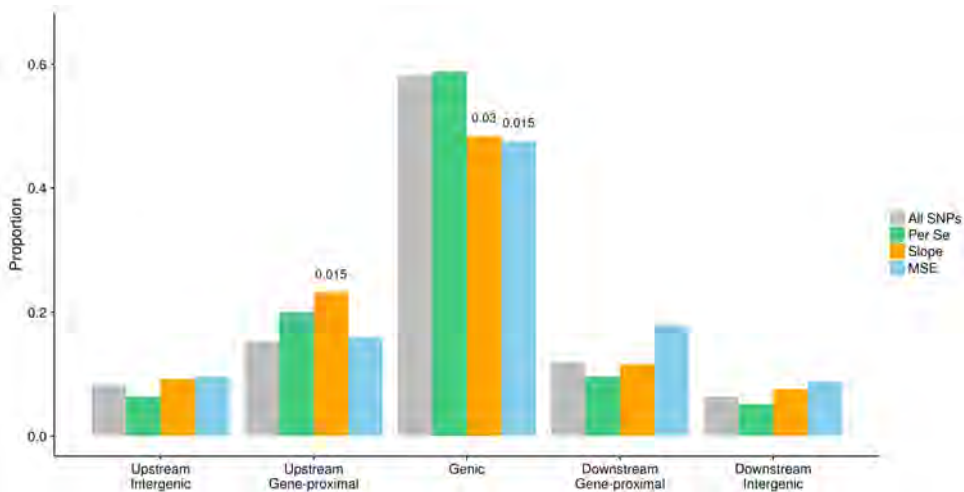Compare to null distribution of classification for all SNPs ($\approx$ 400k)

Hypothesis: GE is disproportionately controlled by numerous regulatory mechanisms.

Conclusions

High Fst loci contribute less GxE variance

- Loci selected for during temperate breeding may now limit plasticity
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- May contribute to stability and wide adaptation

Loci associated with stability are enriched in upstream gene-proximal regions, depleted in genic regions

- Regulatory control of linear environmental response, but not variance
- Evidence for decreased influence of genic variants on stability

Thank You!

- Diego Jarquin
- Cinta Romay
- Ed Buckler
- Aaron Lorenz
- Shawn Kaeppler
- Natalia de Leon

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Questions?