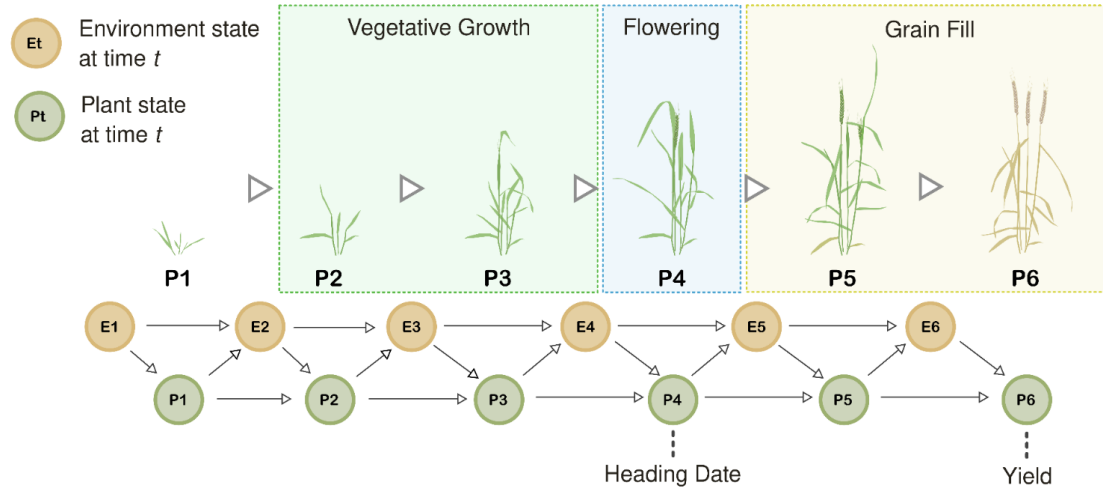
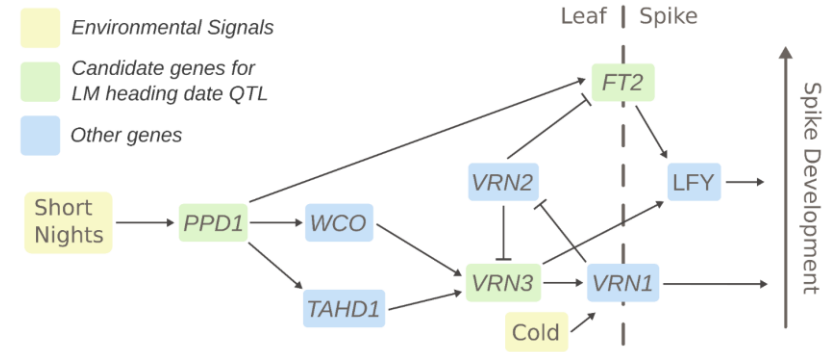


# Mining, Understanding, and Utilizing Adaptive Alleles

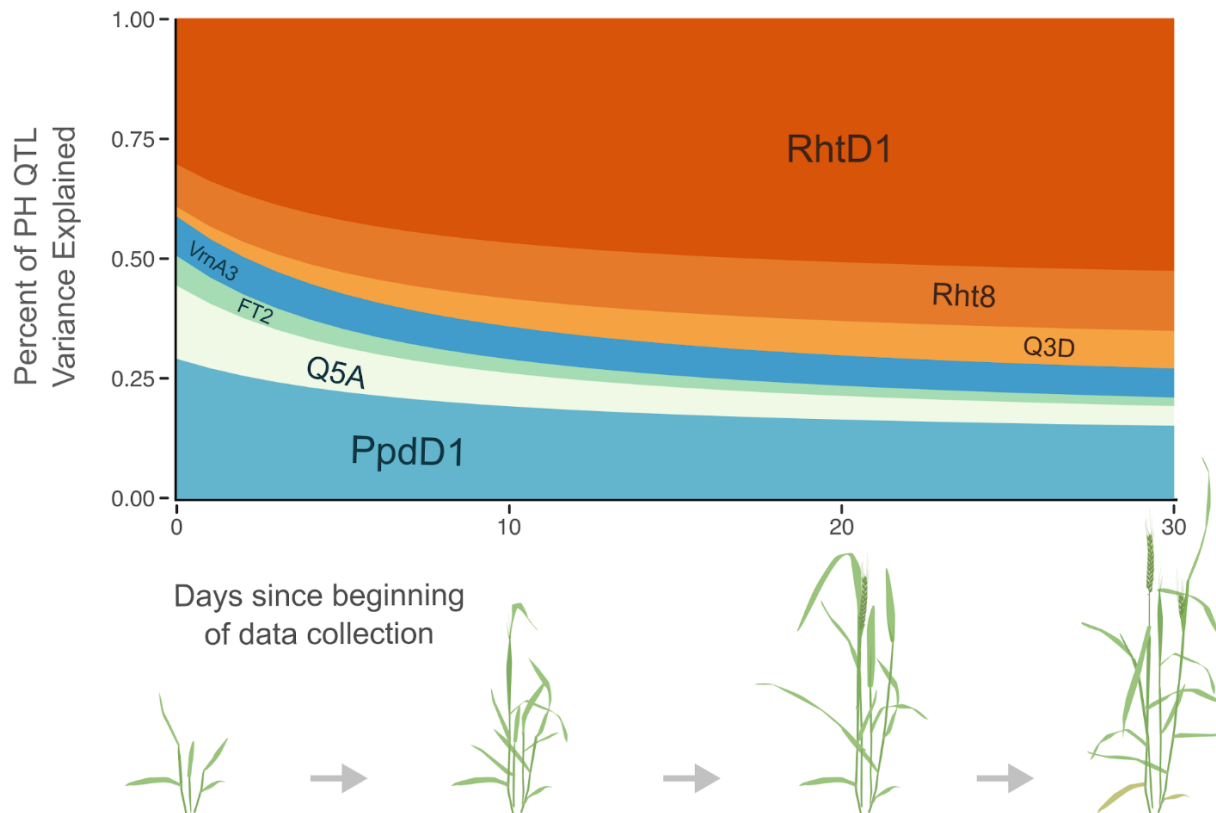
# Heading Date

- Heading date variation - indicator of variation in plant development rate
- RIL population LA96135 x MPV57 to seg for PH/HD genes
  - Large population: 348 RILs
  - Known HD gene *Ppd-D1*
  - Novel variants in *FT-2A* and *Vrn-A3*
  - Mature PH genes *Rht-D1* and *Rht8*

Mohammed Guedira

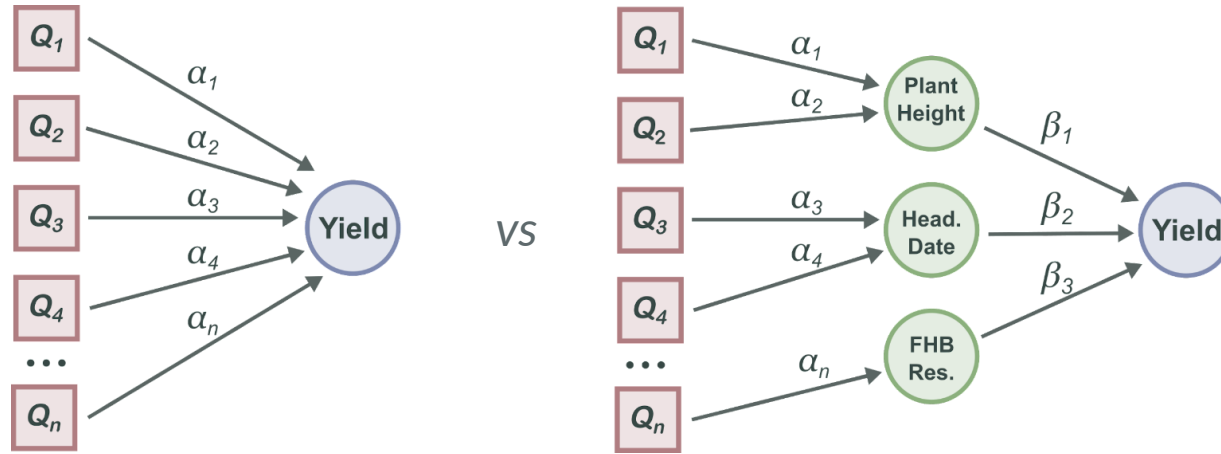


# QTL Effects on Plant Growth



- Plant height on each day for each row plot estimated, variance associated with QTL
- Both sets of variants affect plant height in the observed range
- In general, heading date variants explain a comparatively larger proportion of phenotypic variation early on, and plant height variants more later on

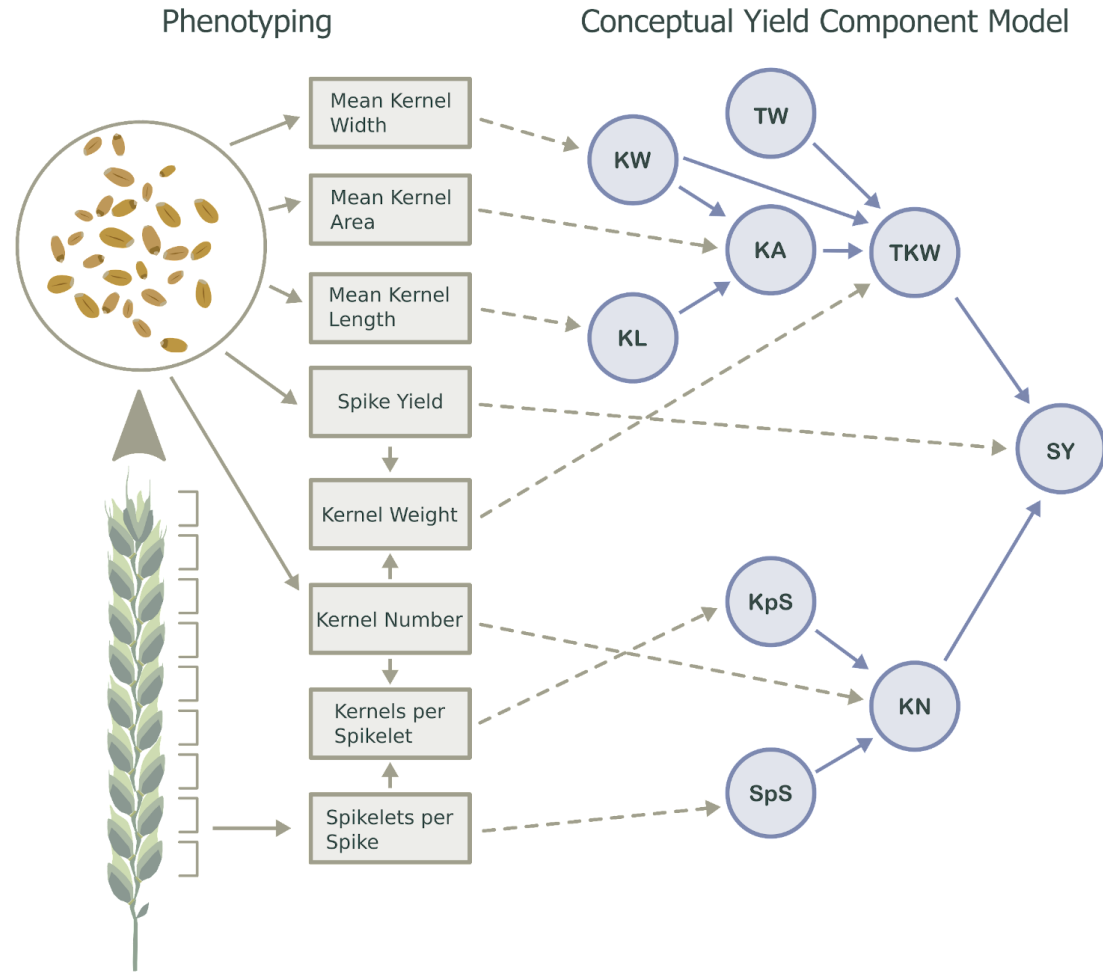
# Framework - Break Yield QTL Up



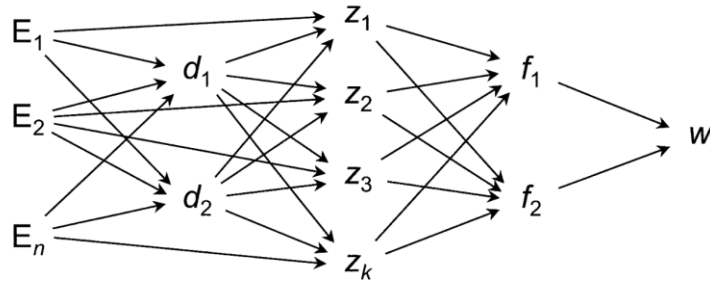
- Estimate a reasonable number of parameters per trait
- Understand mechanisms of yield QTL to use in breeding
  - E.g. some yield QTL are disease resistance QTL, which require strategy for use
- $\beta$ s can represent correlations, "real" models (e.g. crop models), or environmental interactions (covariance between GxE of QTL effects for QTL affecting same trait)

# Phenotyping Yield Components

- Focus on total per-spike yield
  - Easier to collect, tiller number has large management effect
- Spike yield broken up into kernel weight (TKW) and kernel number (KN); these both have components

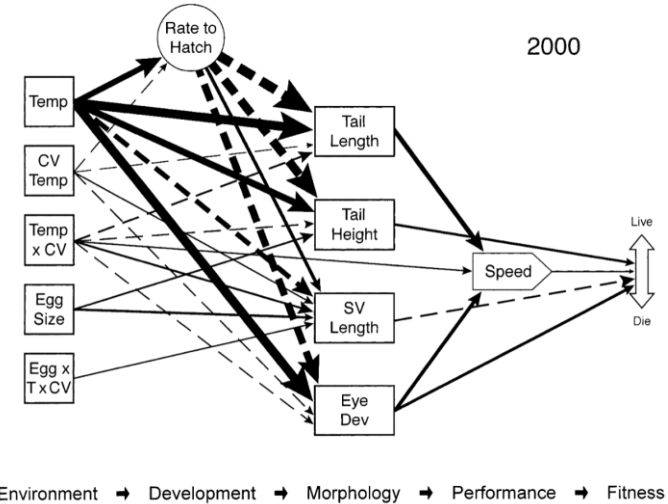


# Path Analysis and Structural Equation Modeling



Environment → Development → Morphology → Performance → Fitness

- Path coefficients as regression coefficients linking traits
- Fitness results from set of collected phenotypes, genotypes, and environmental variables meant to represent underlying causal processes.
- Variables can have direct effects, and indirect effects mediated by their effects on other variables



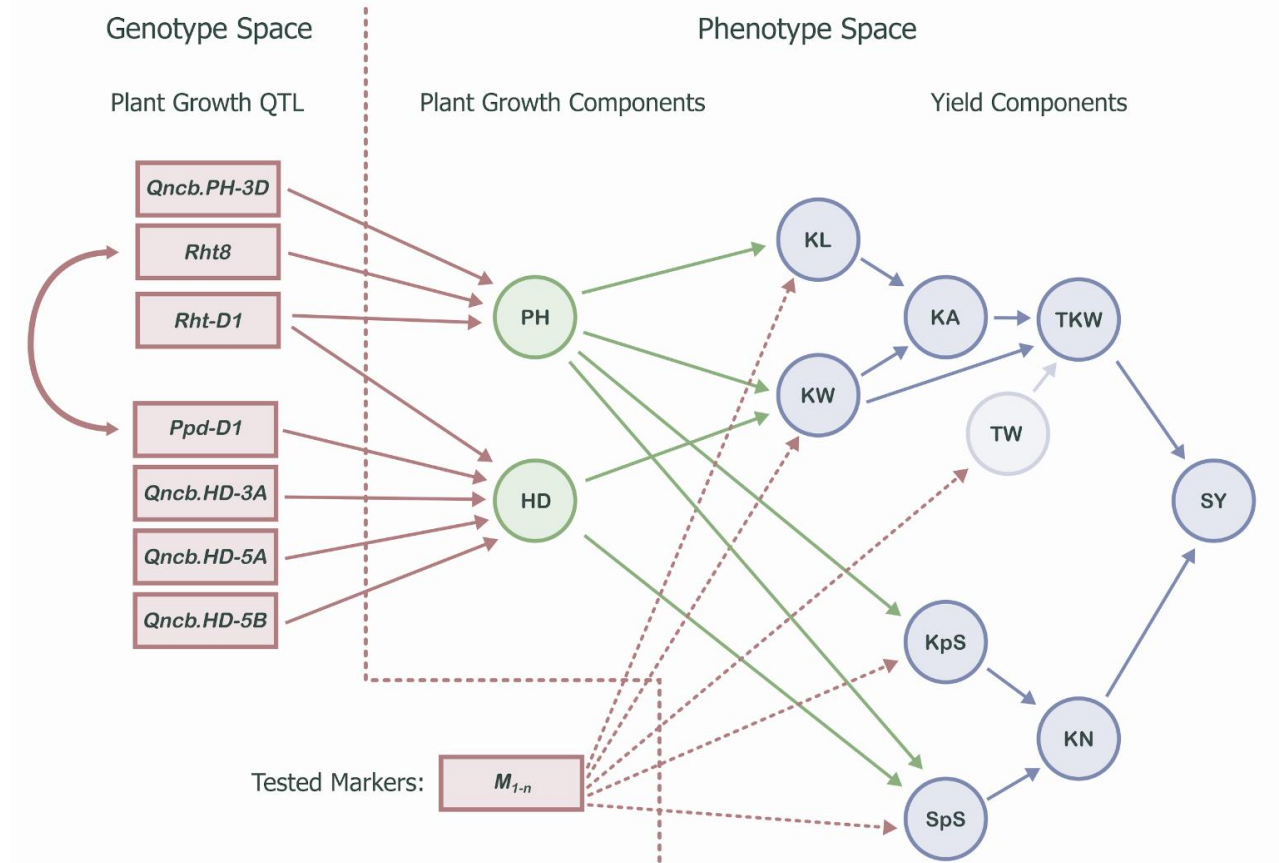
Environment → Development → Morphology → Performance → Fitness

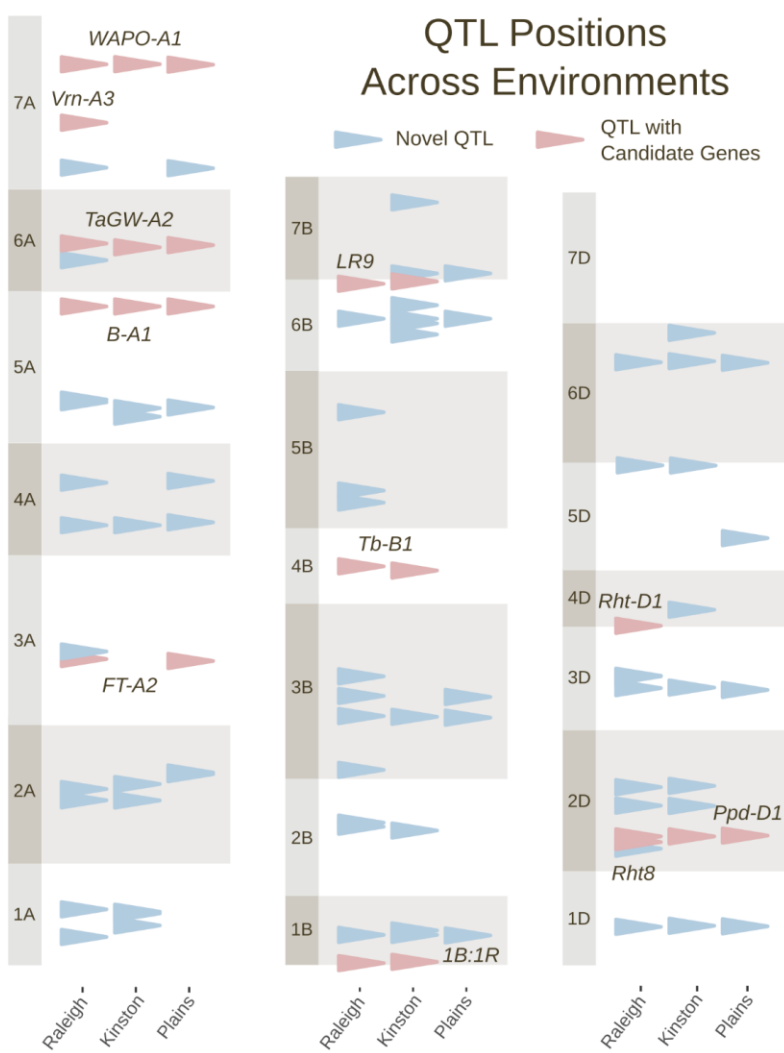
$$Y \sim \begin{bmatrix} 0 & \beta & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \beta & \beta & 0 & 0 & \beta & 0 \\ 0 & 0 & 0 & \beta & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \beta & \beta & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & \beta & \beta & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \beta & \beta \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & \beta \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix} Y + e$$



# Mapping Model

- Know causal relationships between phenotypes
- Genetic and non-genetic sources of correlations
- Test weight (kernel density) not observed (so test directly)



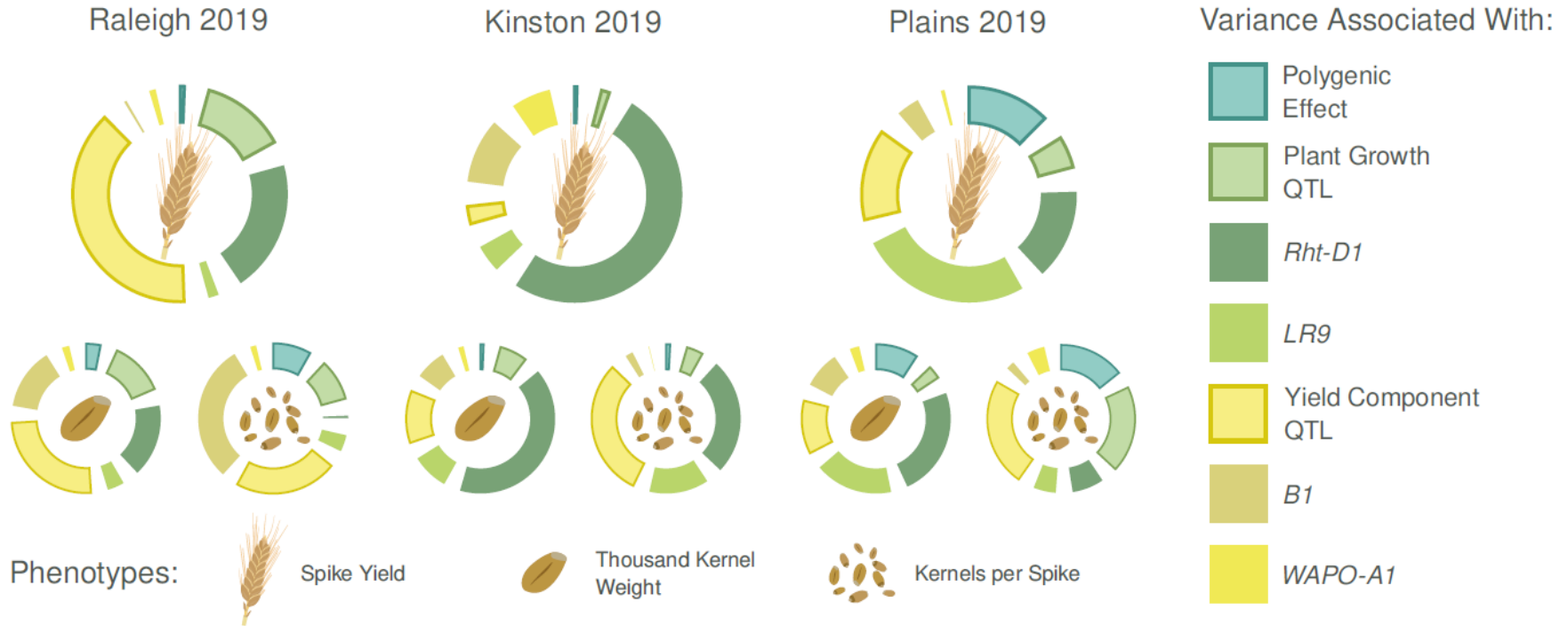


# Allele Mining with Multivariate Mapping

- Positions of mapped QTL mostly consistent across environments
- QTL largely evenly distributed across genome
- Heading date/plant height QTL mapped in all three locations, but vary
  - Suggests direct in addition to mediated effects for some major QTL
- Some QTL “clusters” - 2D, 6B



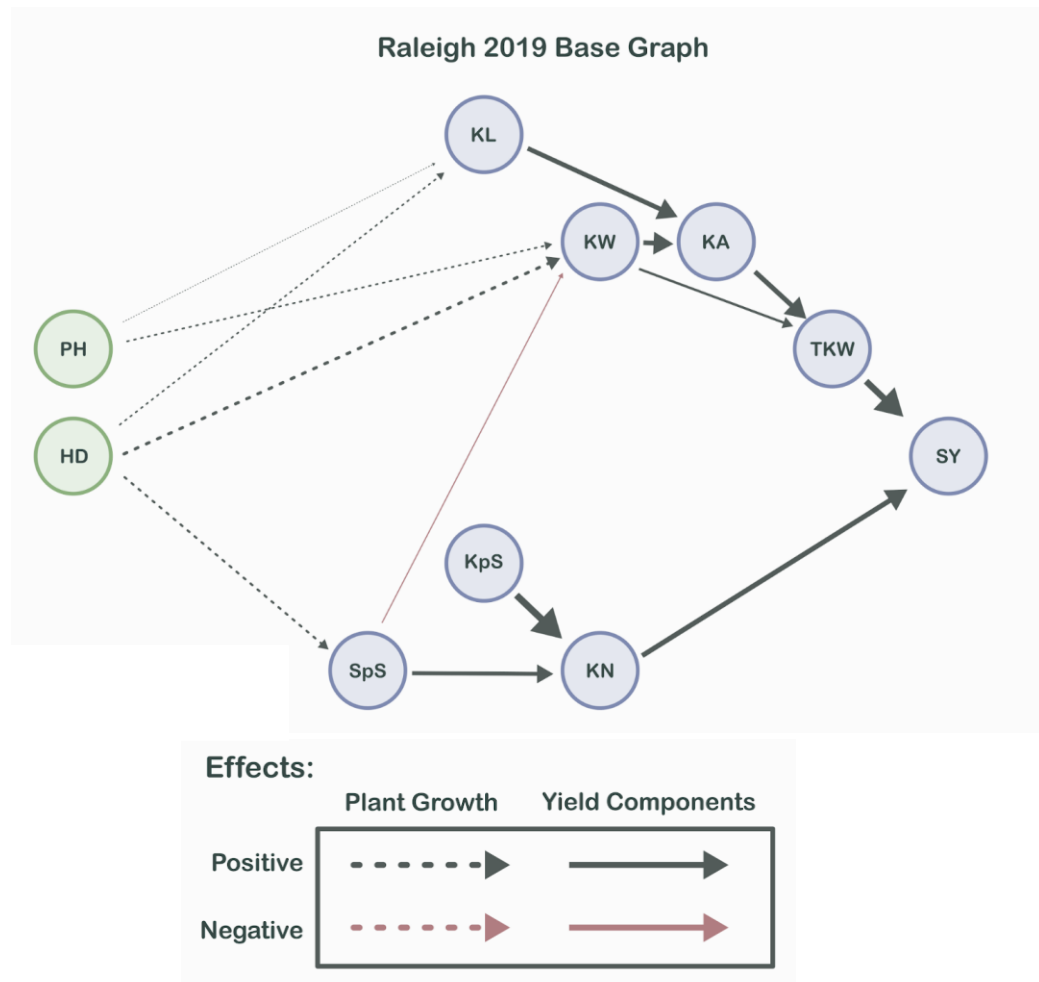
# QTL Affect Spike Yield and Components



- Prediction accuracy in LASSO model for spike yield nearly doubles when only use mapped QTL
  - $r = 0.50$  with only mapped QTL vs  $r = 0.28$  when including all markers

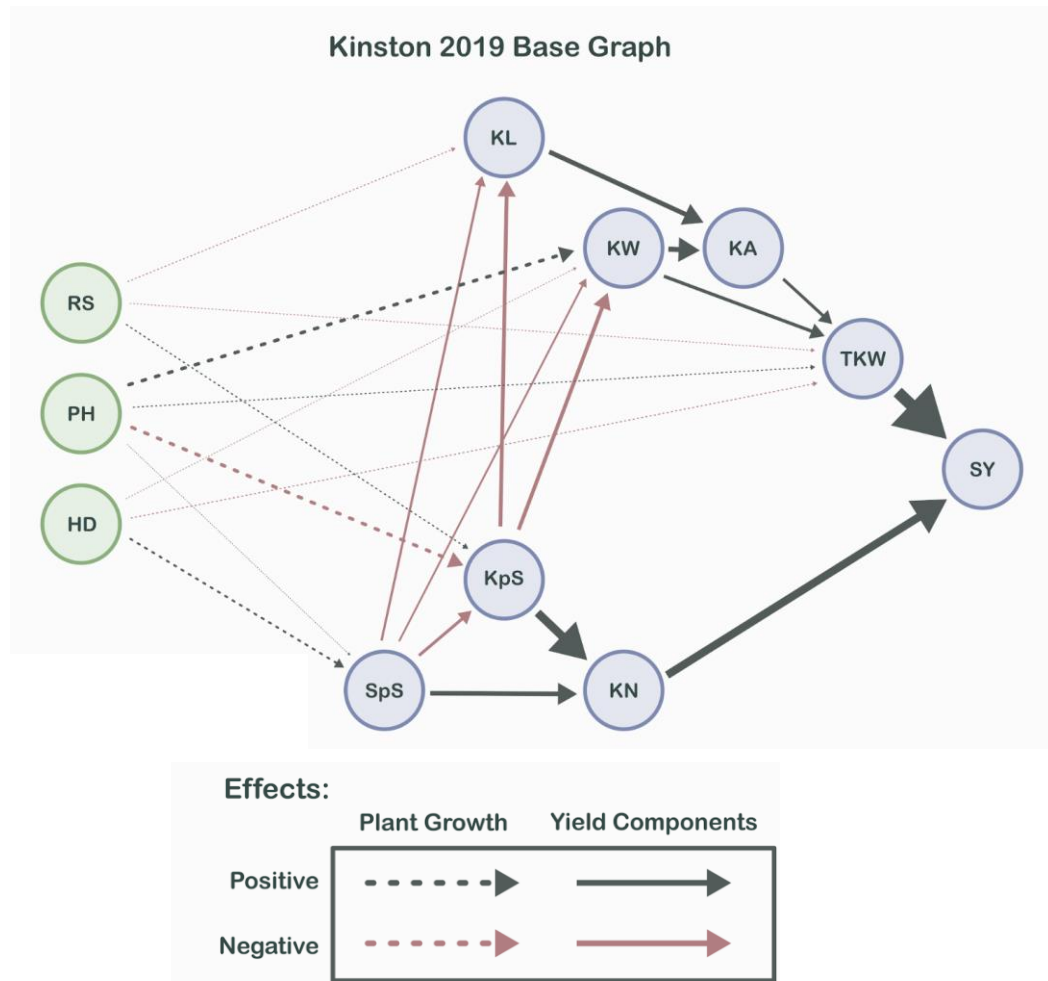
# Base Graph

- Raleigh model fit with 10 phenotypes, 11 plant growth QTL, and 14 yield component QTL
- Only phenotype relationships shown here
- Size and color of arrows indicate size and direction of effect, respectively
- In Raleigh, little negative correlations between yield component traits



# Base Graph

- Same model fit in Kinston, with addition of leaf rust score (RS) disease resistance phenotype
- Less effect of heading date on yield components, but greater effect of plant height
- More negative correlation between base yield components
- With source constraints, increasing kernel number decreases kernel size

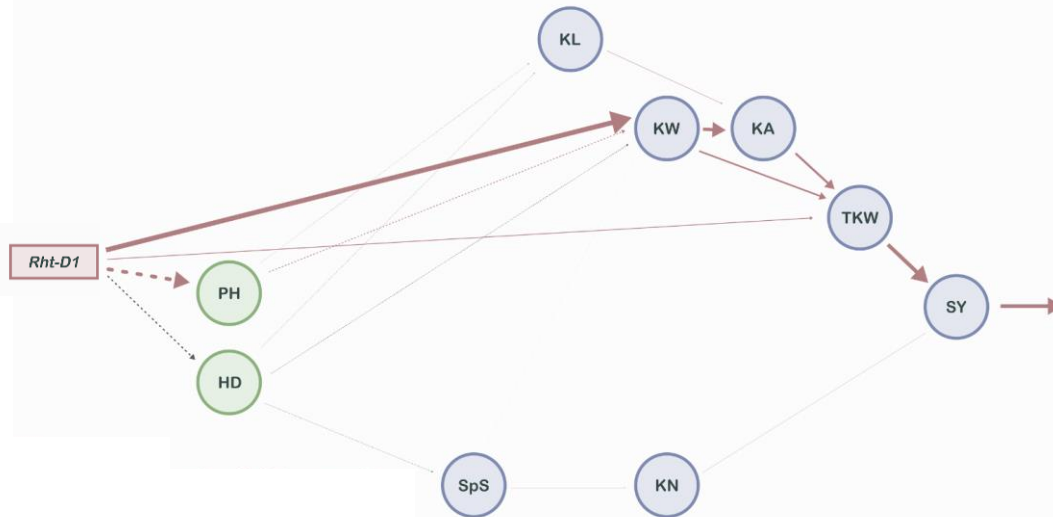


# Rht-D1b

## Raleigh 2019

- Small effect on spike yield
- Large direct effect on kernel width
- Plant height has a minimal effect on kernel width

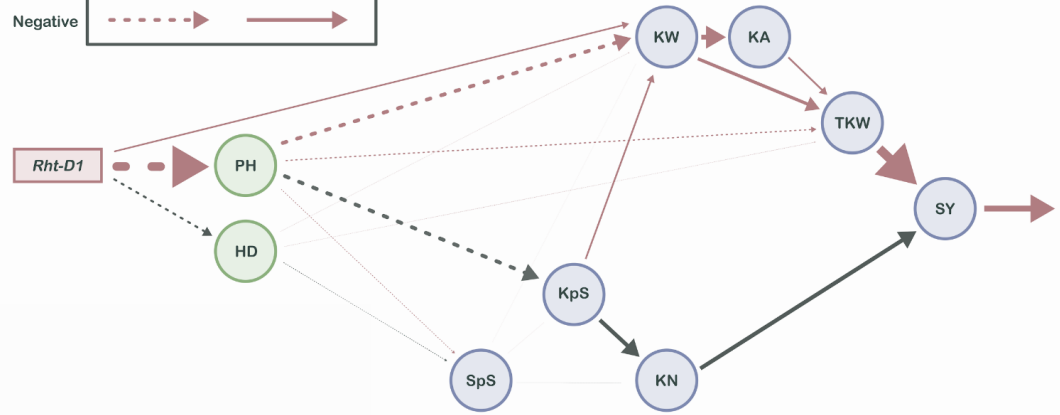
Raleigh 2019



Effects:



Kinston 2019

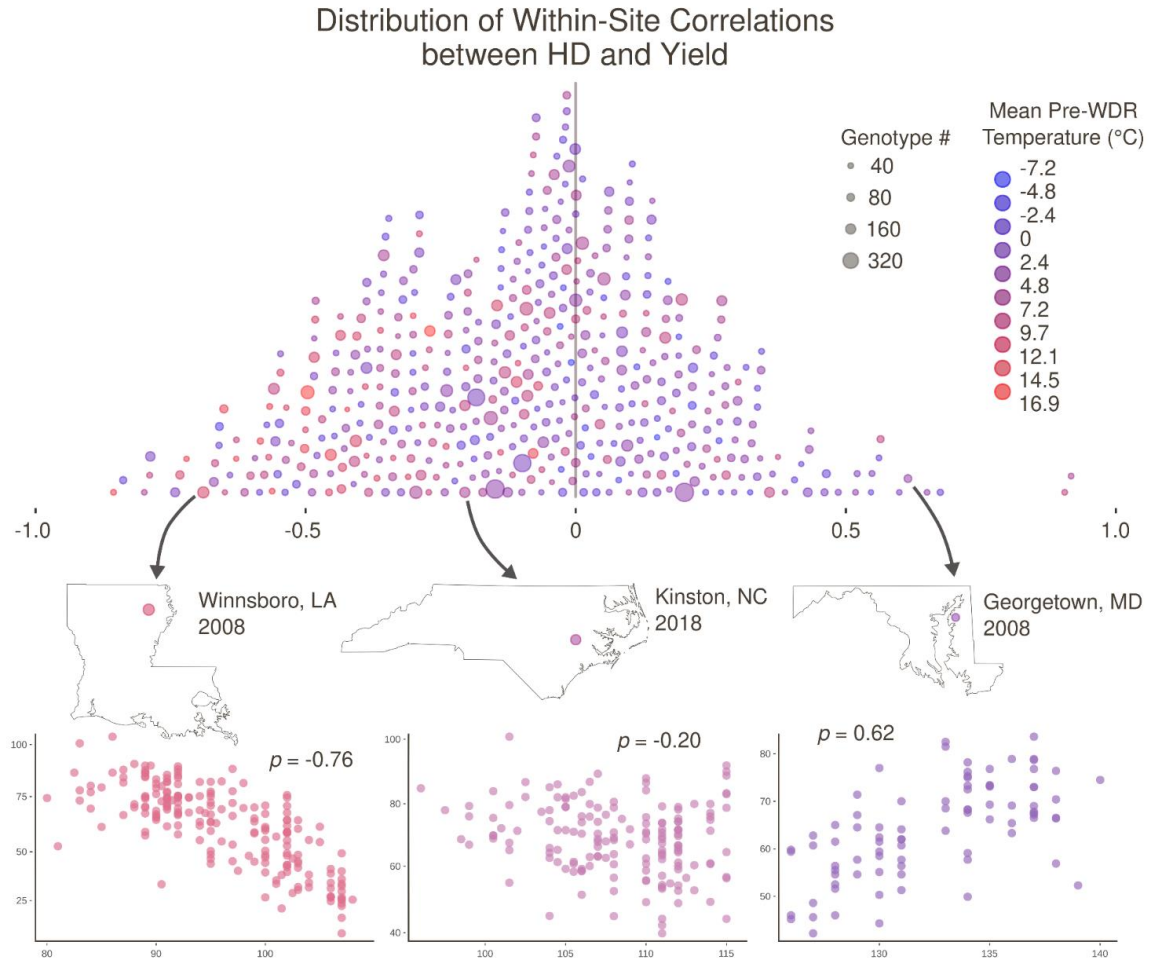


## Kinston 2019

- Large effect on spike yield
- Direct effect on kernel width
- Effect of plant height on kernel width
- Compensatory effect on KN

# Understanding Mined Alleles

- Across > 350 siteyears, within-siteyear correlation between heading date and yield varies based on environmental factors
- Significantly higher variance in correlations than would be expected by random chance
- Suggests heading date underlies some GxE
  - How do we make use of mined alleles to predict GxE as function of env?

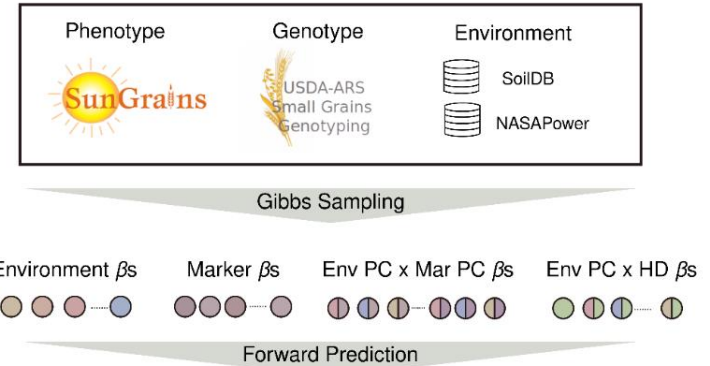




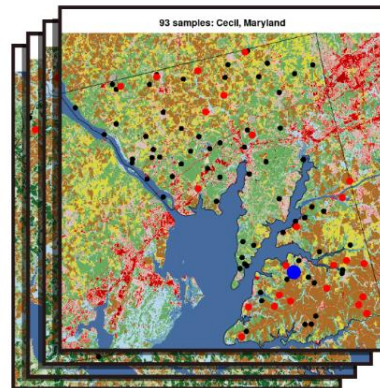
# County-Level GxE Prediction

- Target population of environments is farmland (brown) within counties
- Sample soil and weather for forward prediction from SunGrains data

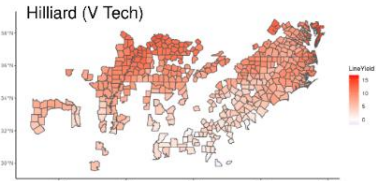
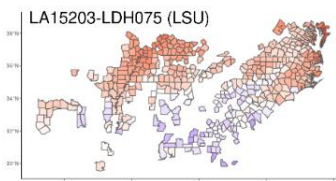
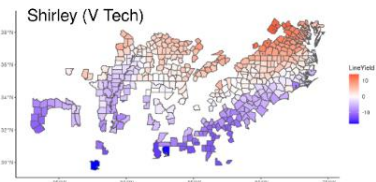
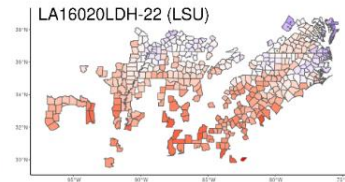
GxE Modeling of Heading Date + Yield



County Sampling and Land Use Characterization

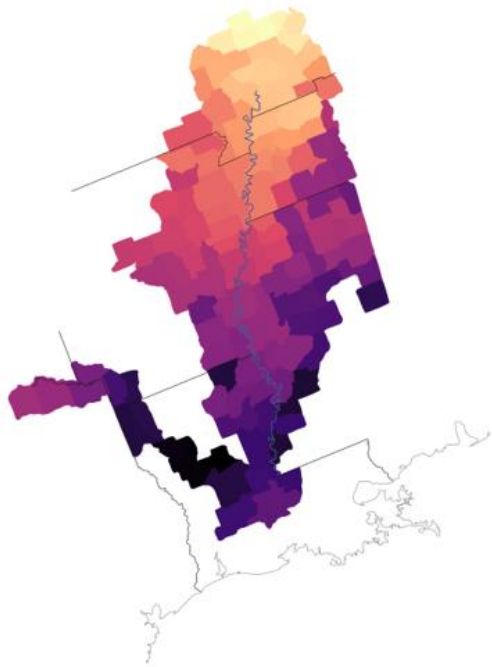


County-Level Yield Prediction

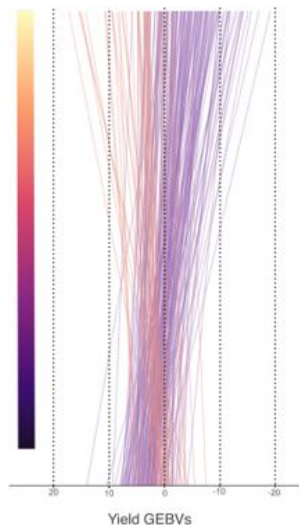


# How Do Alleles Drive GxE?

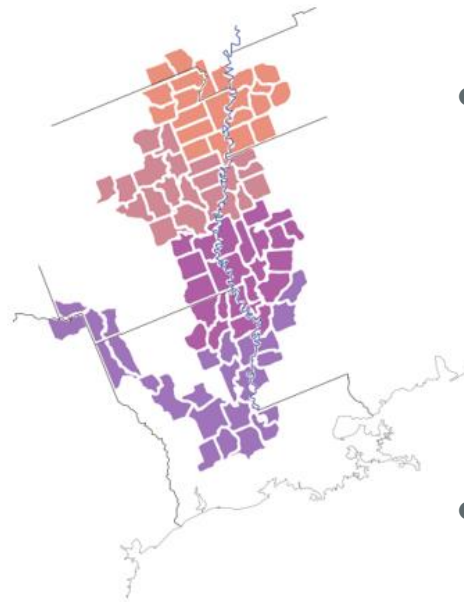
PC1 of Yield GEBV Covariance Matrix



Genomic Estimated Reaction Norms of Louisiana Lines on PC1



Informed Subjective Mega Environments for Delta Region

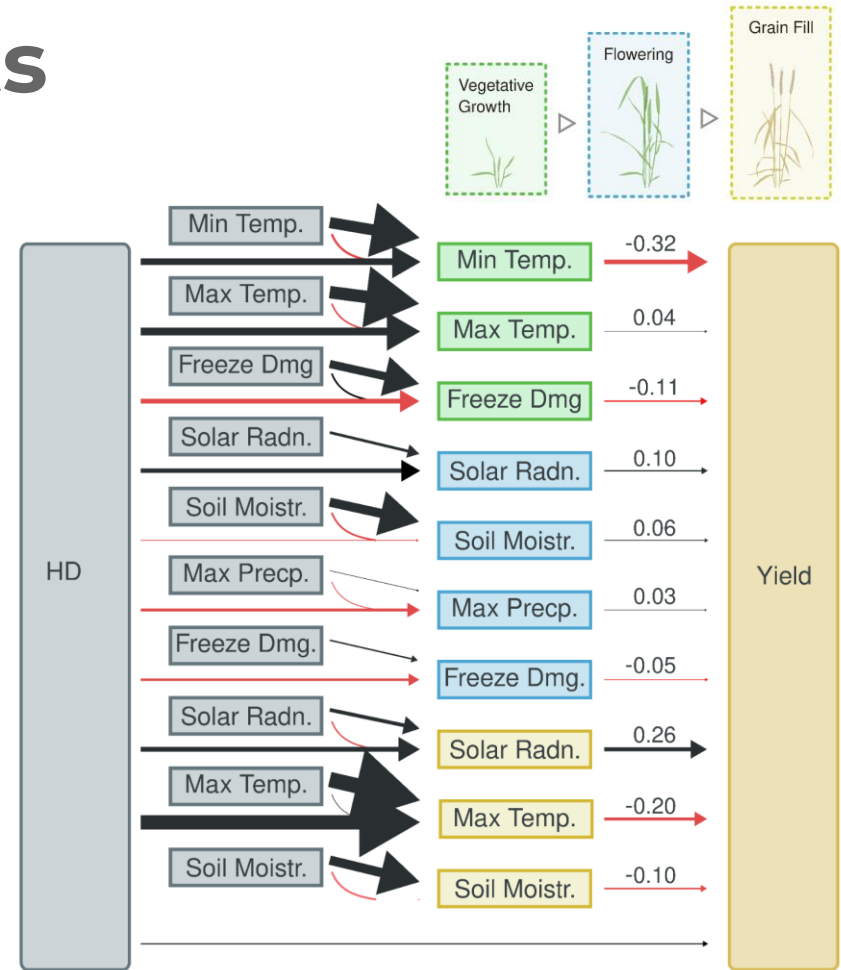
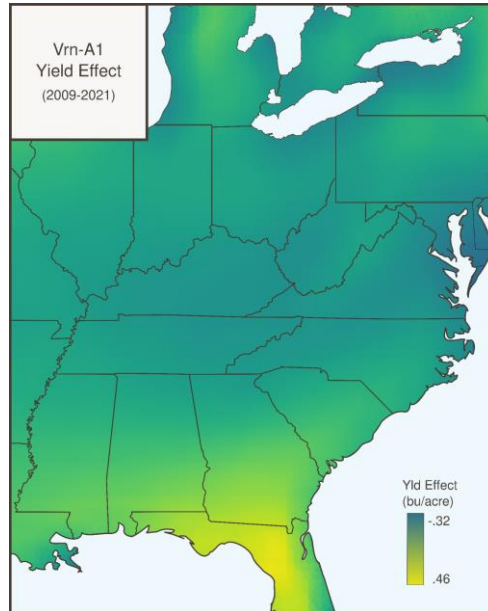


- Predict HD rank of all lines w/ markers
- Use HD x Weather interactions to help predict yield improves within-env accuracy
- HD x Weather interactions is primary driver of site-site predicted covariance
  - Improve prediction of HD, improve prediction of GxE
- Allele mine intermediate traits to improve GxE models



# Mediated Yield Effects

- SEM of HD effects on yield as mediated by specific stress variables
- Total mediated effect estimation of *Vrn-A1* earliness allele on yield across 10 years



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# Acknowledgements

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# LSU

## RECRUITING FOR FALL 2023!

