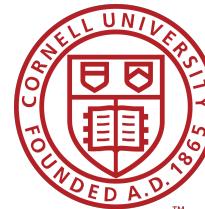


A meta-GWAS reanalysis of twenty years of quantitative traits in maize

AKA Elucidating the extent of pleiotropy in maize and its functional relevance towards trait prediction

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Phenotypic saturation will help uncover pleiotropic loci

USDA-ARS NCRPIS (Ames)



Fusarium Ear Rot



Sugary vs Starchy Kernels



Yellow vs. White Kernels

Nested Association Mapping



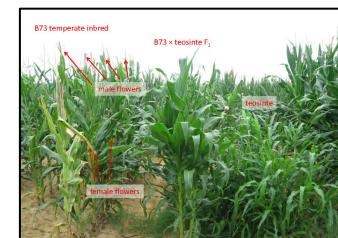
Flowering Time



Plant Height

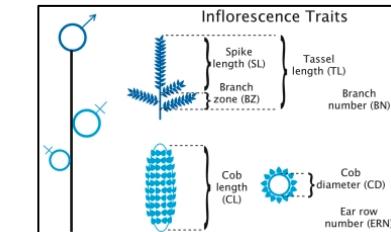


Northern Leaf Blight

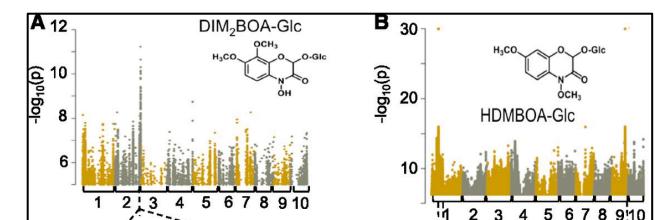


Day-length sensitivity

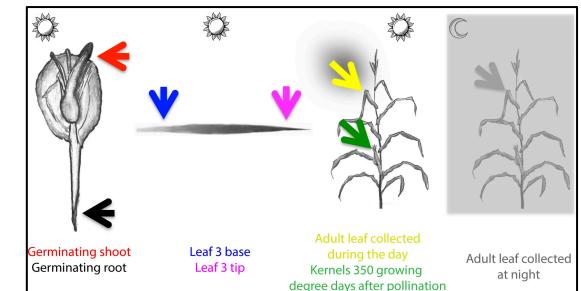
Goodman Association Panel



Inflorescence Architecture



Maize Metabolome

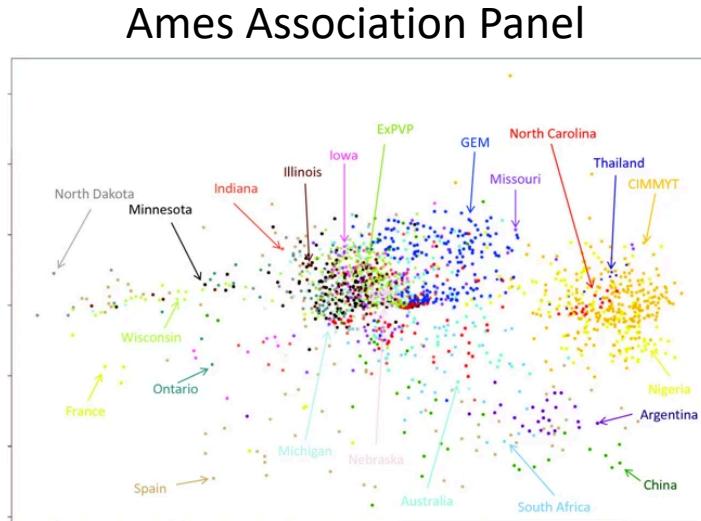


Expression Atlas

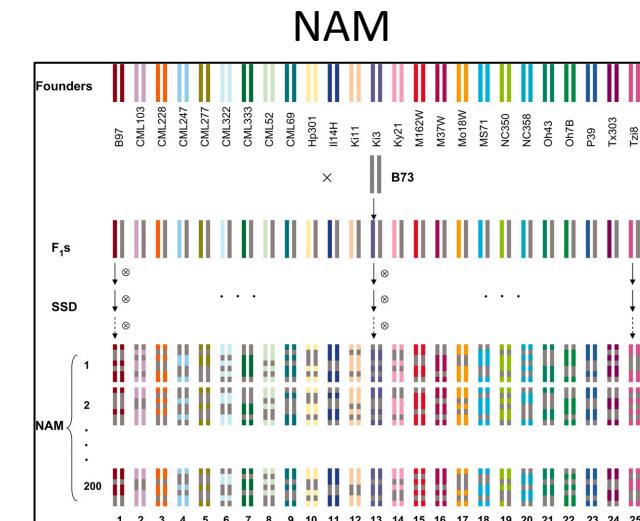
PCs calculated in diverse populations, transferred to inbred lines

$$y = X\beta_1 + 3 \text{ global PC} \pm \text{window PCs} + e$$

Collection of Diverse Lines

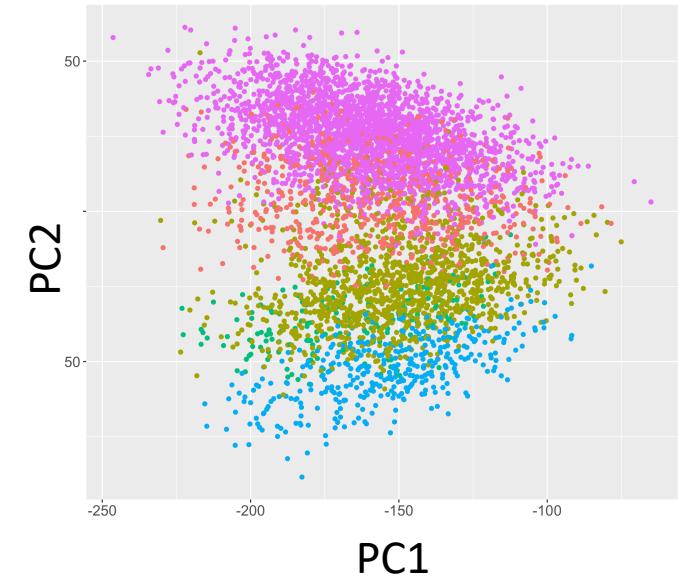
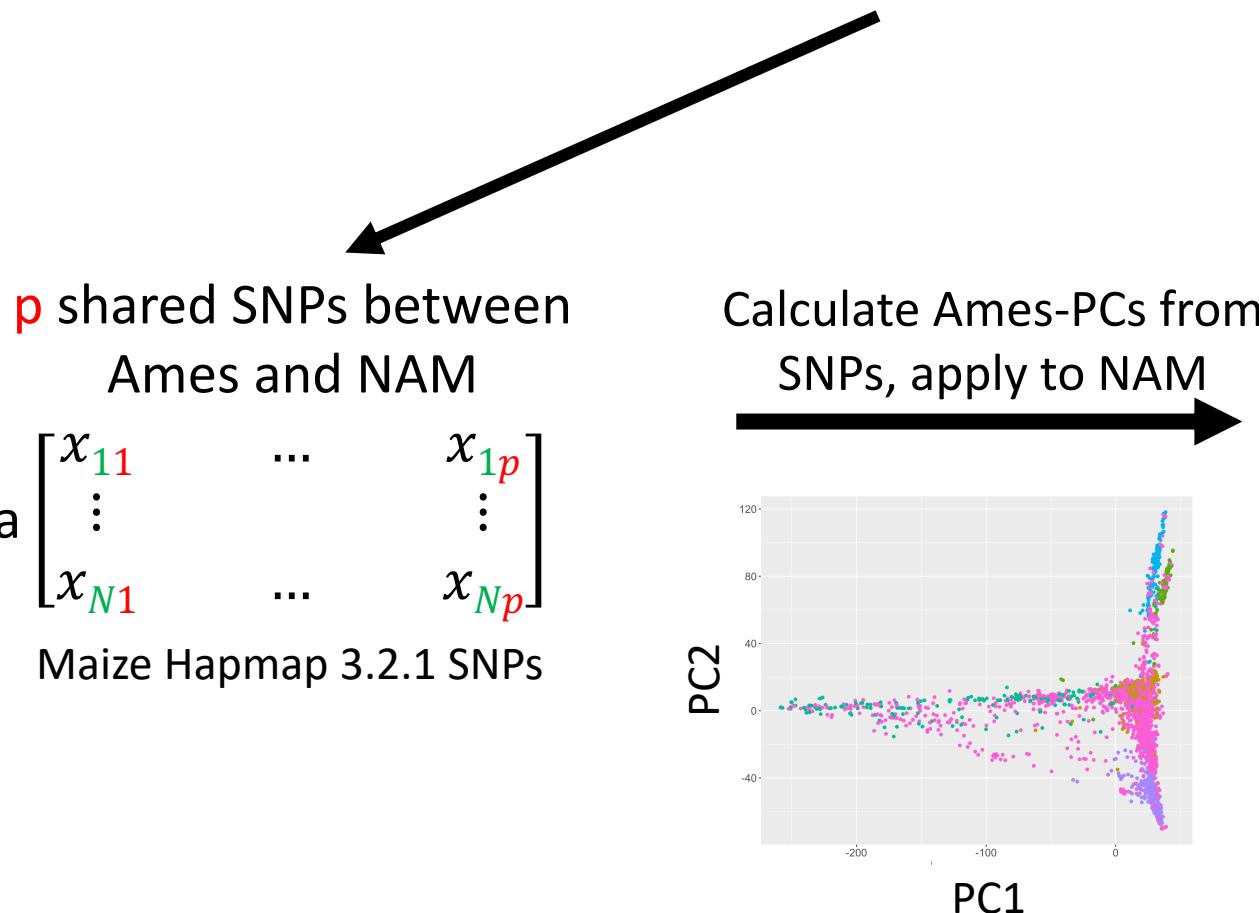


26 Inbred Lines



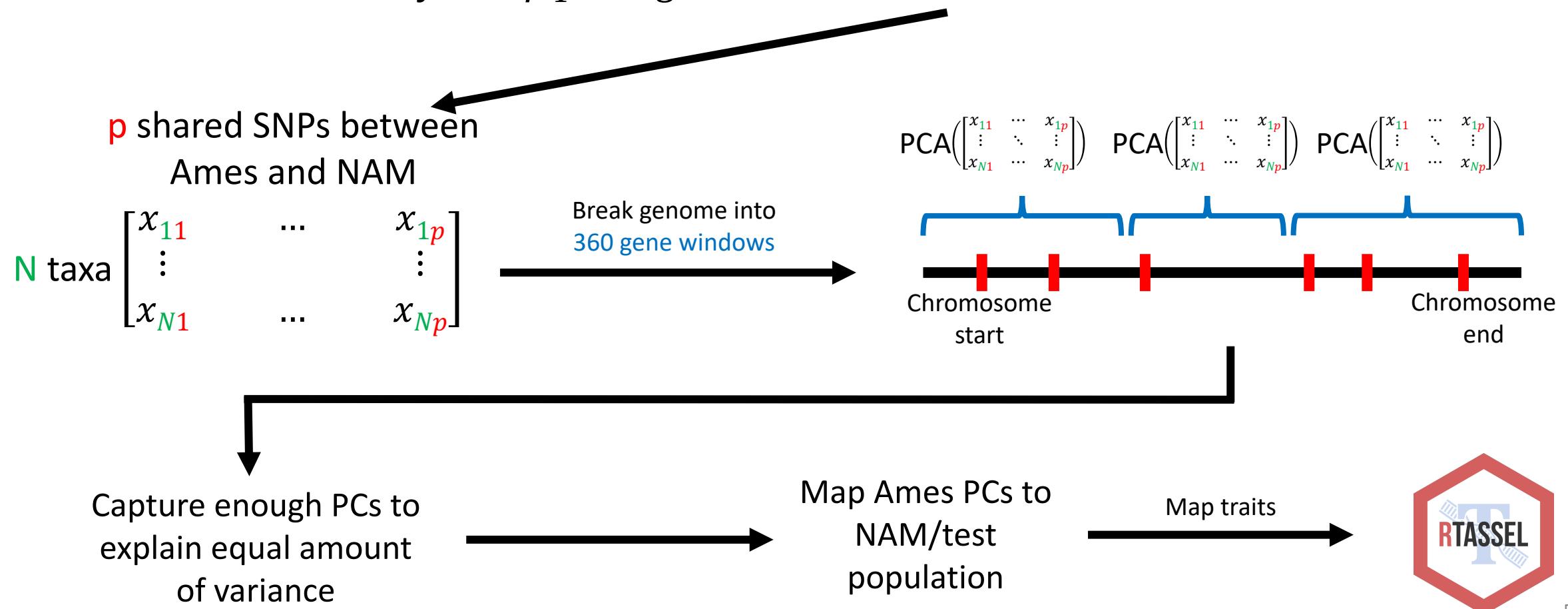
Global PCs account for chromosomal LD

$$y = X\beta_1 + 3 \text{ global PCs} \pm \text{window PCs} + e$$

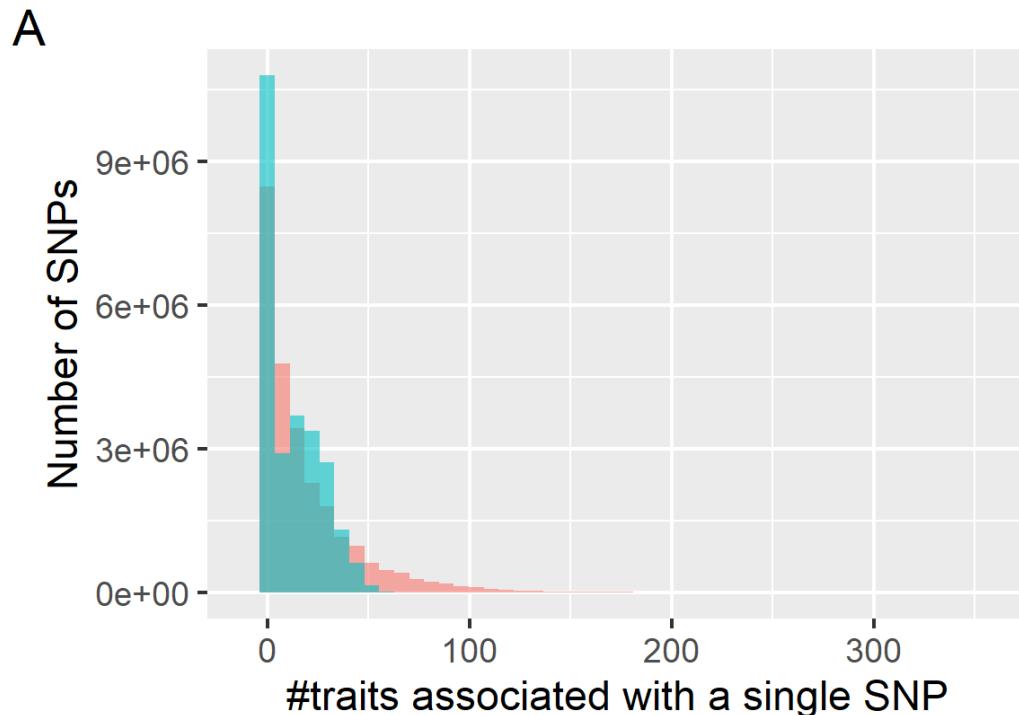


Window PCs account for inter-chromosomal LD

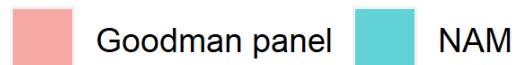
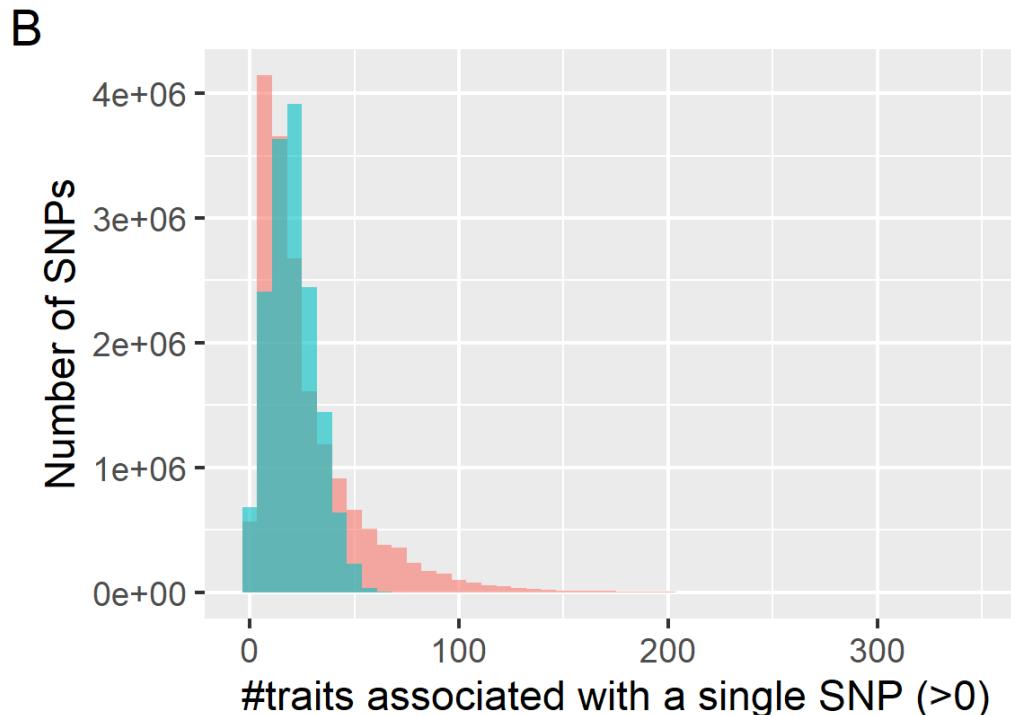
$$y = X\beta_1 + 3 \text{ global PC} \pm \text{window PCs} + e$$



30-40% SNPs have no trait associations



~19 traits associate with a single SNP



NAM + Goodman Panel Results ($p < 0.01$)

4035 physiological traits and metabolites

Thank You



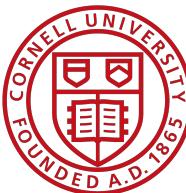
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