Characterization of a large, diverse population of maize near-isogenic lines

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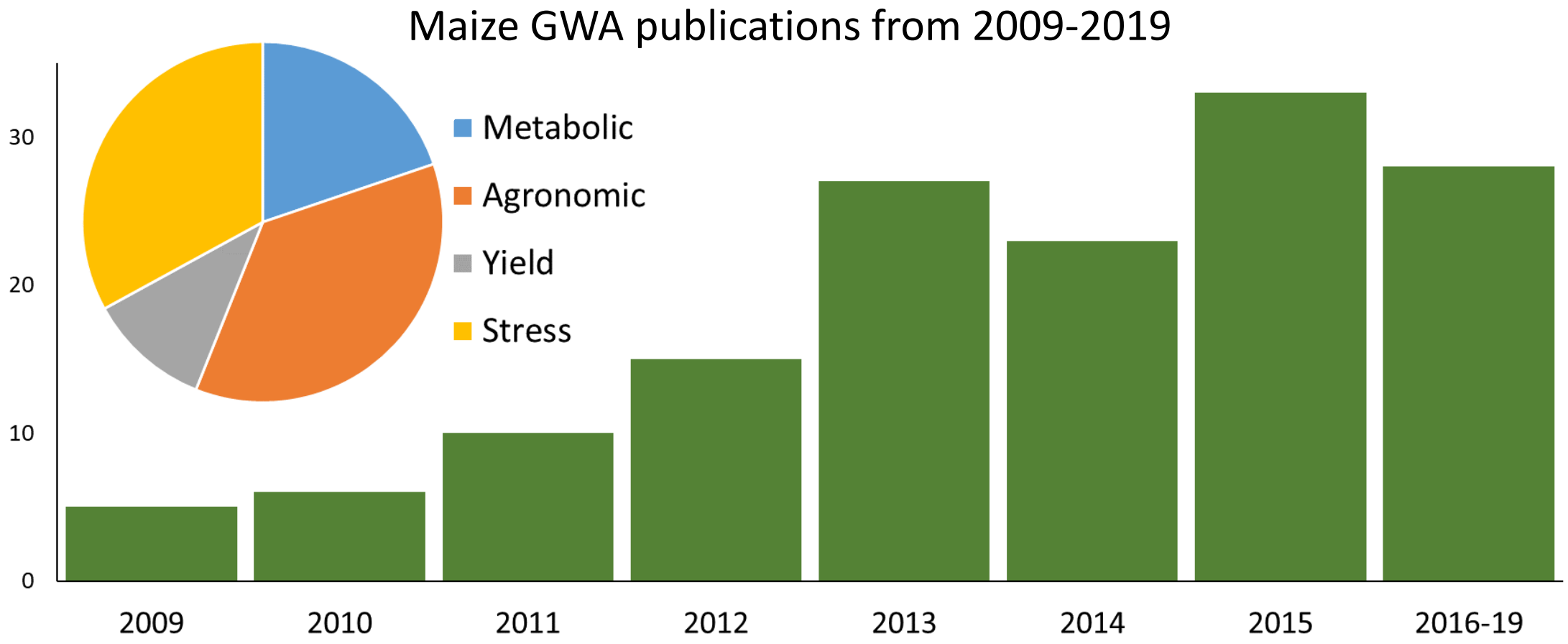
Explosion in genomic and phenotypic resources in maize

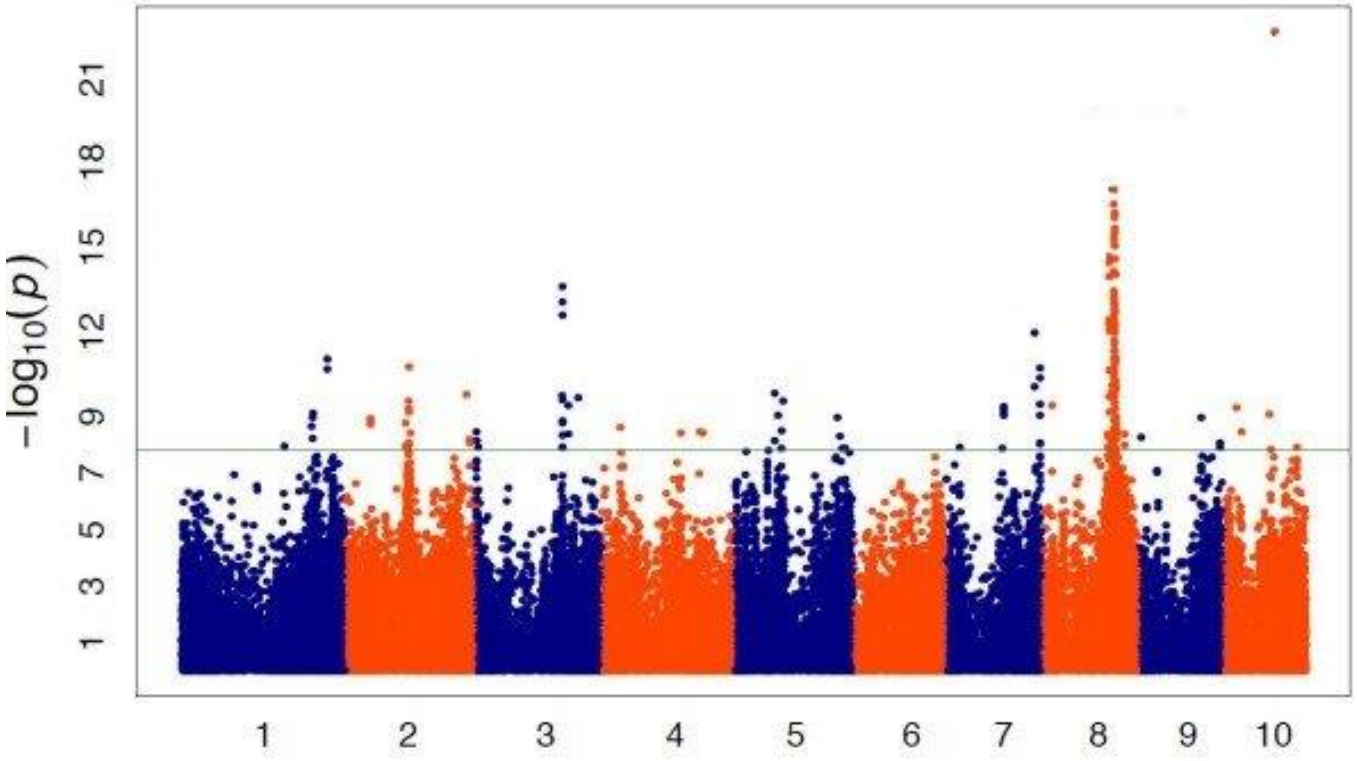


Adapted from Xiao et al. 2017. *Mol Plant*

Increased understanding of genetic architecture

- Quantitative inheritance of most agronomically important traits
- Many loci with small individual effects

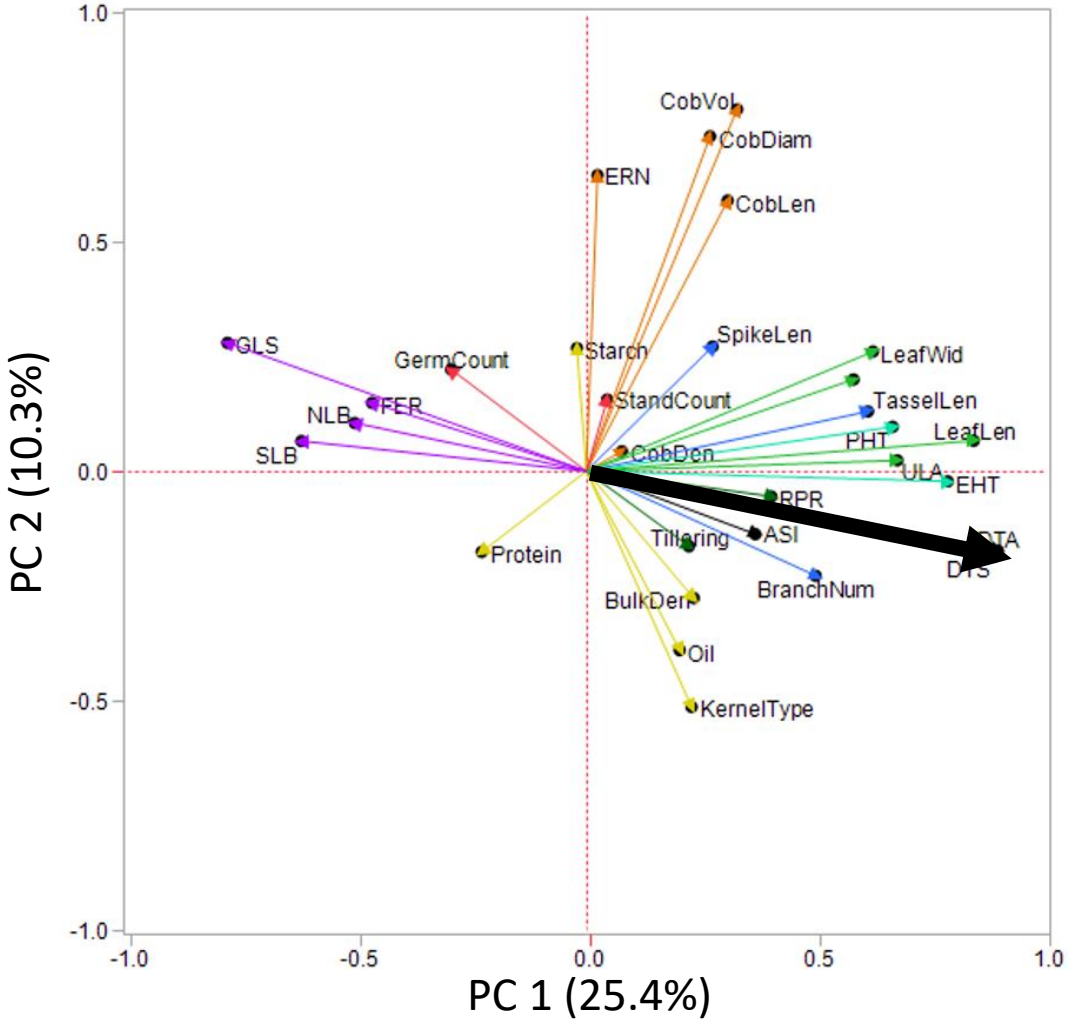
GWA of flowering time in USDA maize inbred seed bank



Romay et al. 2013. *Genome Biol*

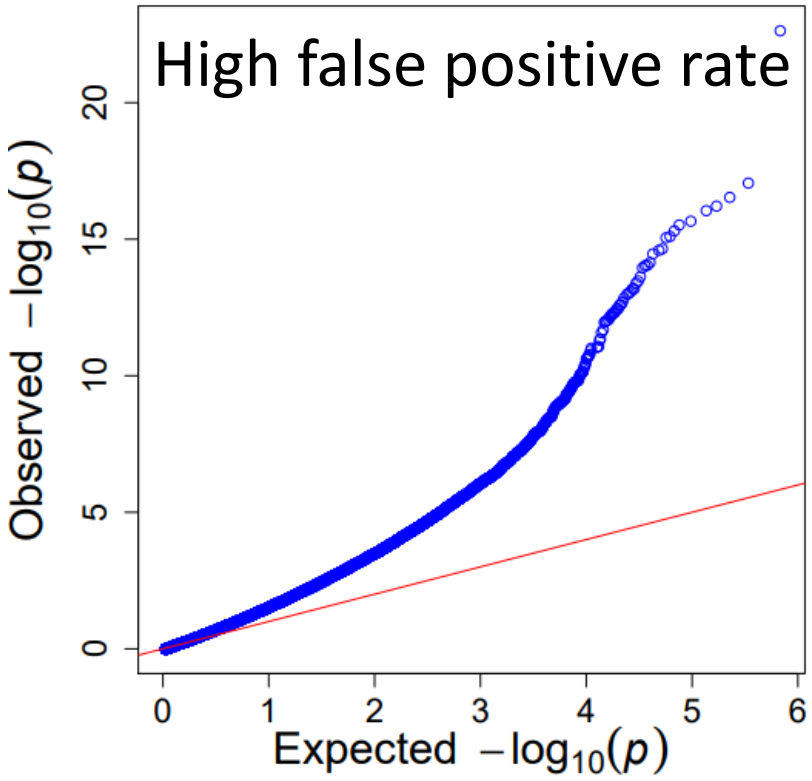
Trait dynamics across maize diversity

PCA of 33 traits in maize core diversity panel



- Flowering time
- Tassel
- Stalk
- Leaf
- Height
- Kernel
- Cob
- Vigor
- Disease

Flowering time correlated with population structure



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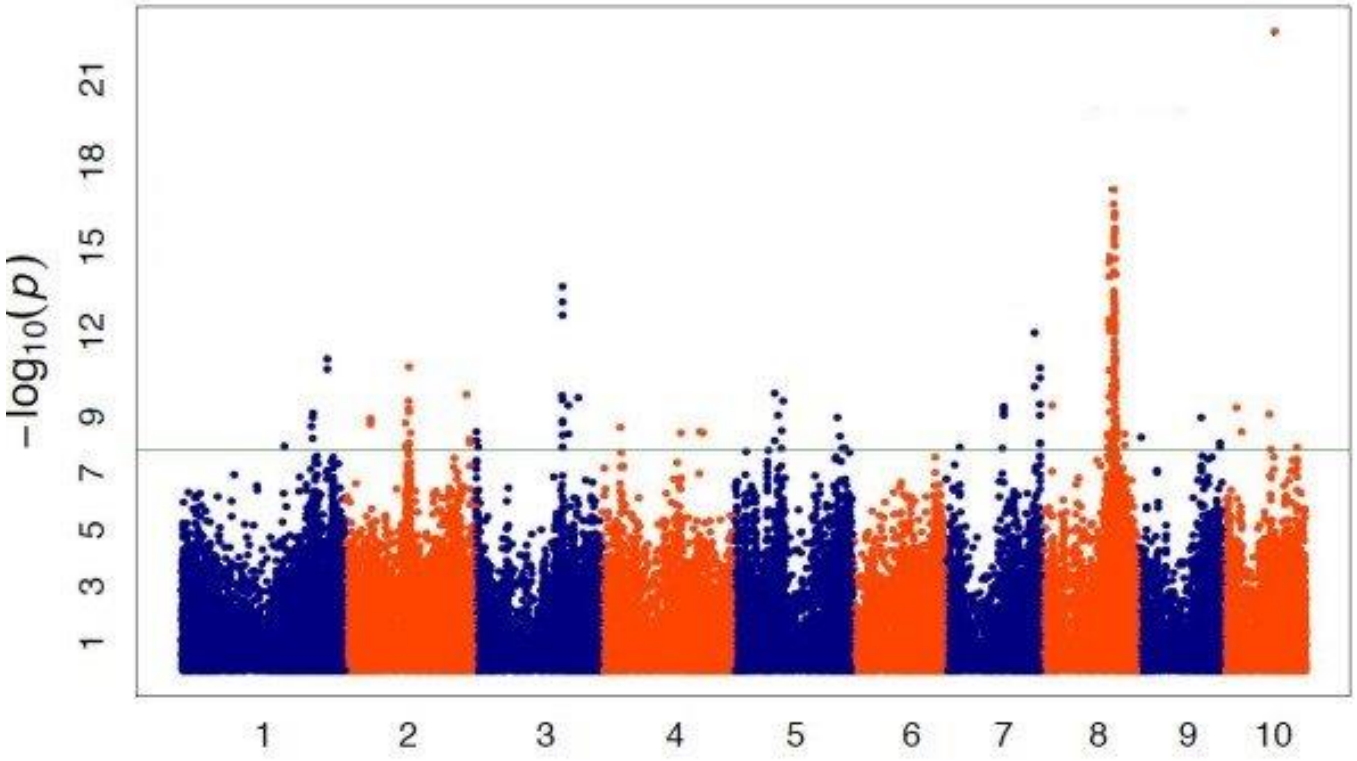
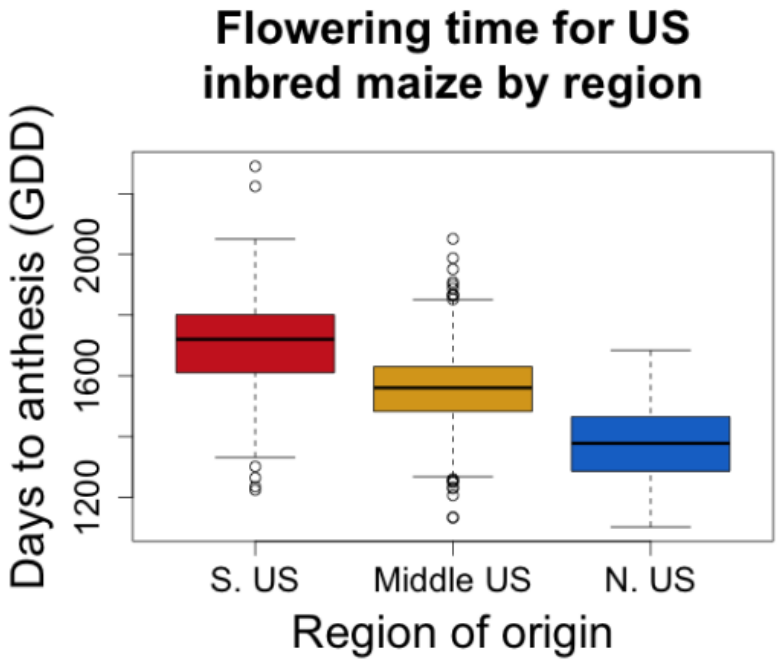


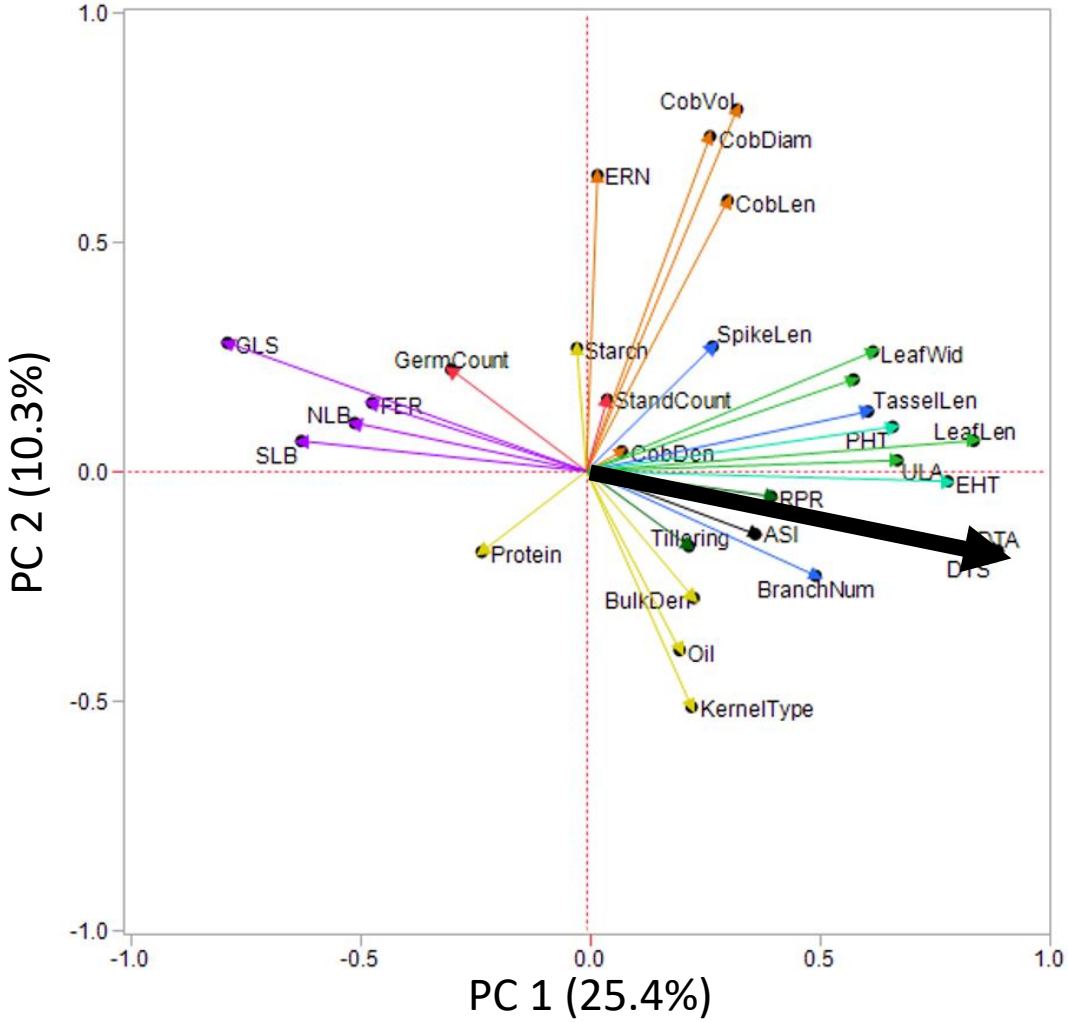
Romay et al. 2013. *Genome Biol*

Pleiotropy or population structure?



Swarts et al. 2017. *Science*

PCA of 33 traits in maize core diversity panel



- Flowering time
- Tassel
- Stalk
- Leaf
- Height
- Kernel
- Cob
- Vigor
- Disease

Breaking population structure with recombinant inbred lines

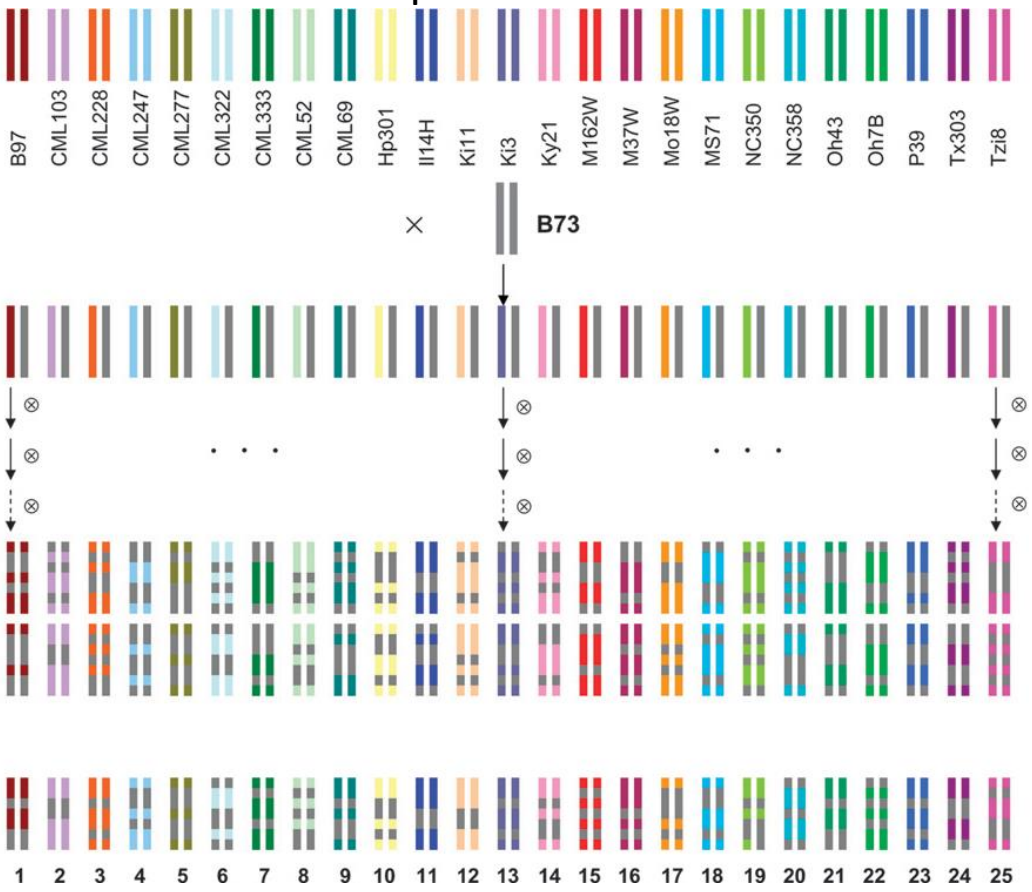
- Accurate allele effect estimation

Adapted from Li et al. 2013. *PLOS Genet*

NAM populations for dissecting trait architecture

- NAM: nested association mapping
- Common parent X diverse founders
- Linked RIL families

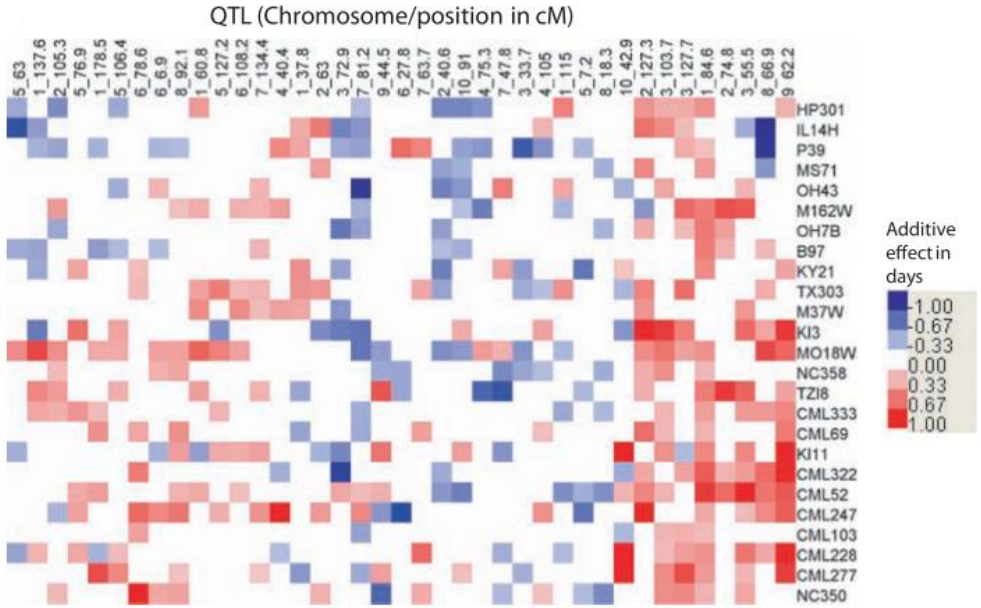
Development of USNAM



Yu et al. 2008. *Genetics*

Assessing allelic series and pleiotropy with NAM designs

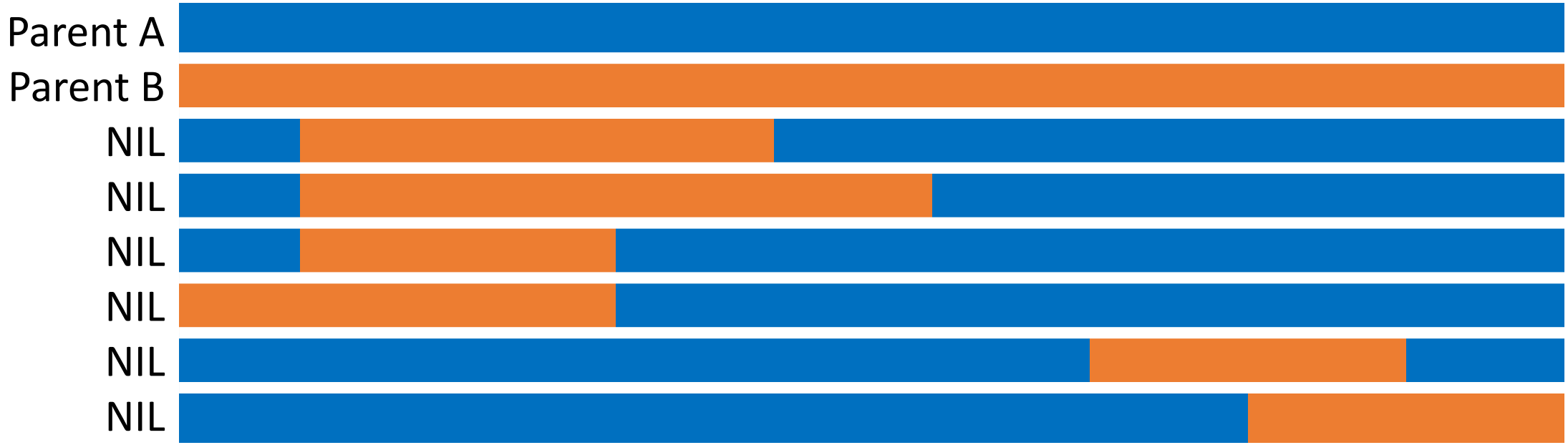
Pleiotropy:
common between related traits
rare between unrelated traits



Lots of QTL...now what?

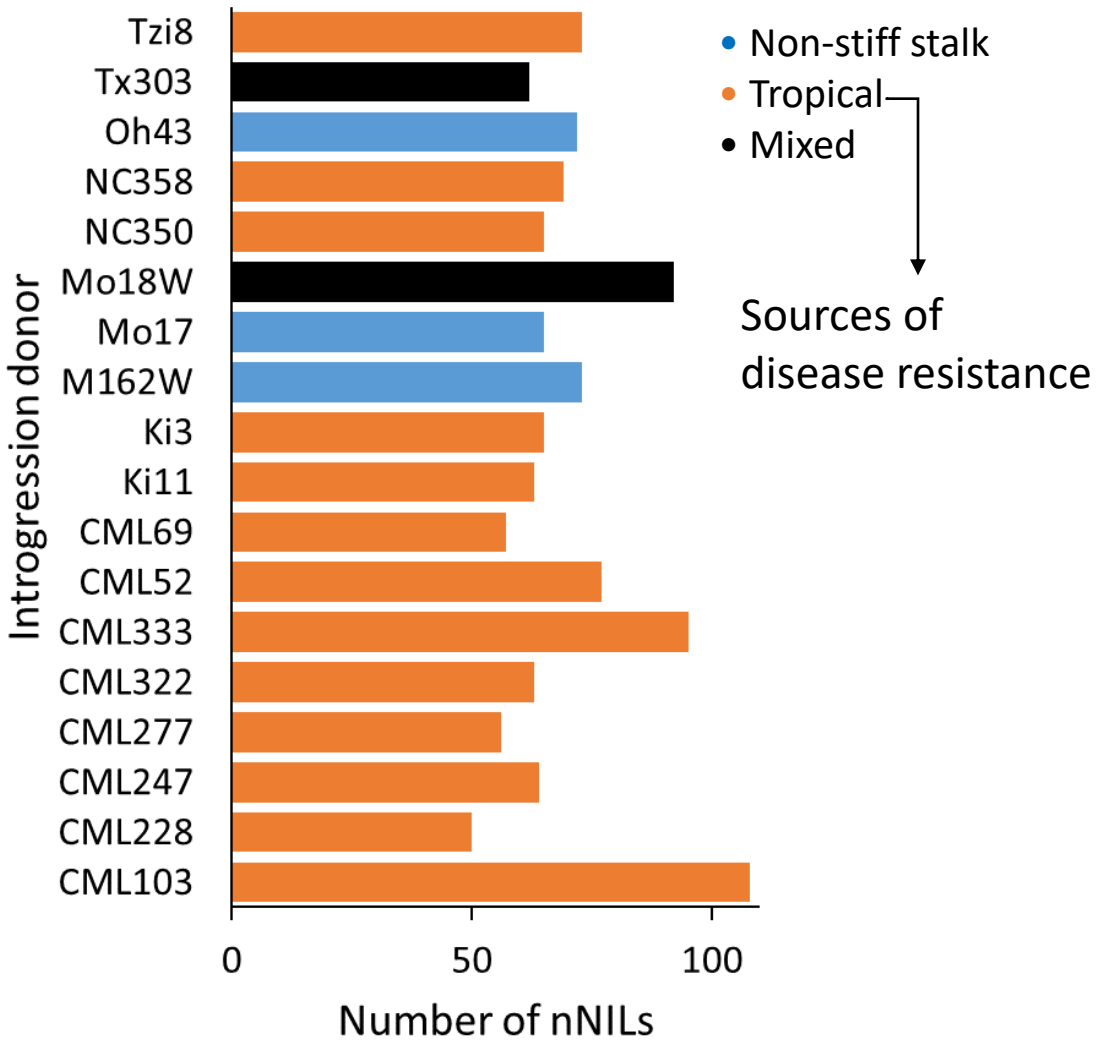
Validate QTL with NILs

- Near-isogenic lines (NILs) for fine-mapping QTL, functional studies
- NIL development costly and time-consuming
  - Extensive genotyping, many generations of back-crossing/selfing
  - Limited in size/diversity in public sector



Large, diverse panel of nested NILs (nNILs)

- 1270 “nested” NILs (nNILs)
  - B73 background
  - Introgressions from 17 founders of USNAM
- Developed by Syngenta AG
- Seed available via CIMMYT
- Genotyping-by-sequencing of ~900 nNILs

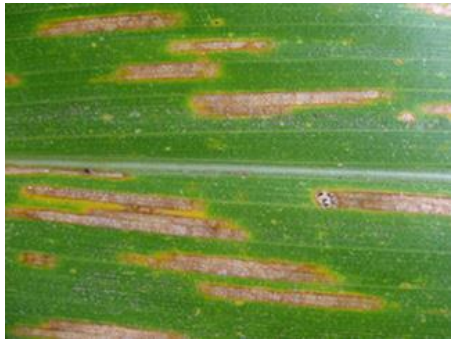


Morales et al. Submitted to *The Plant Journal*

Disease resistance and agronomic traits phenotyped in nNILs

- Important fungal foliar diseases in USA/Canada

Gray leaf spot (GLS)



Northern leaf blight (NLB)

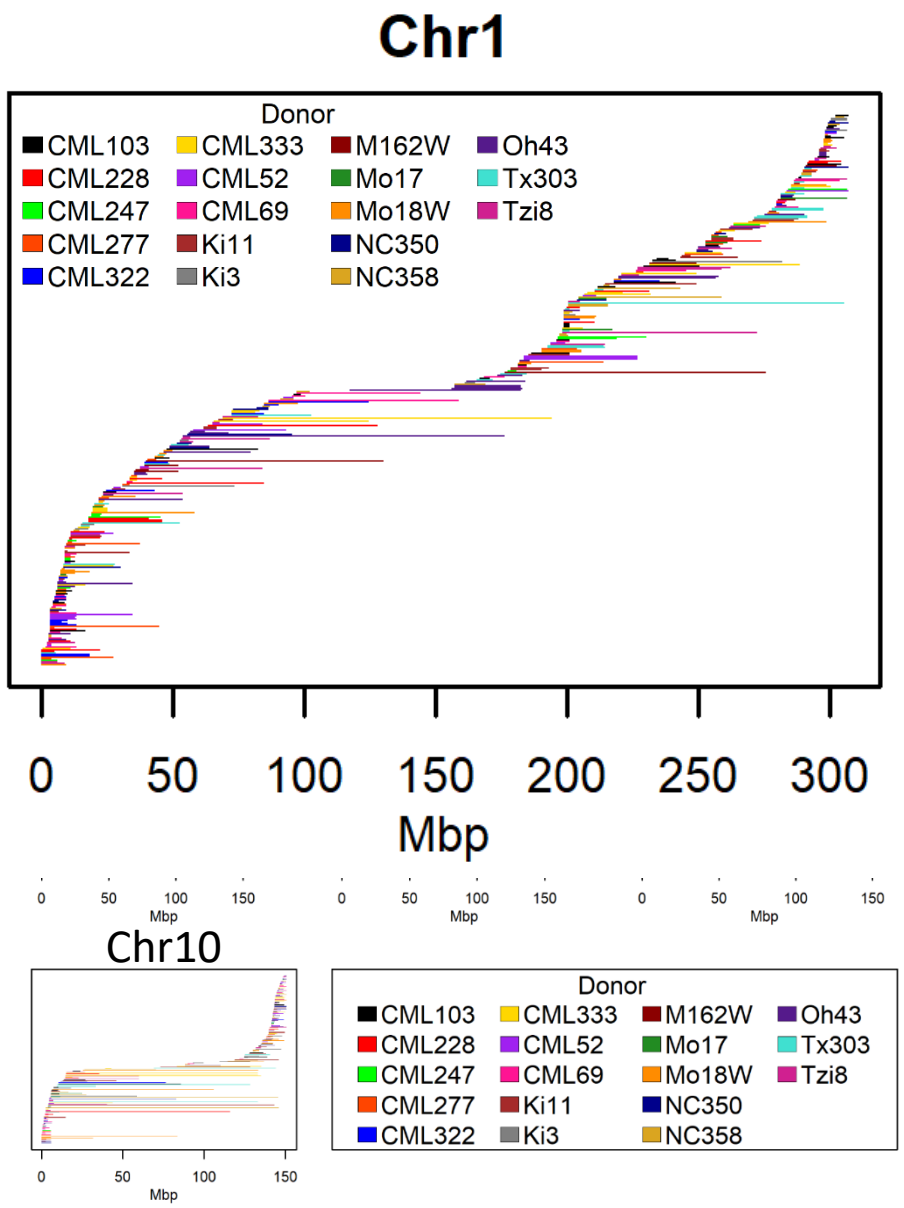
Southern leaf blight (SLB)

- Agronomic traits
  - Ear height (EHT), plant height (PHT)
  - Days to anthesis (DTA)

Morales et al. Submitted to *The Plant Journal*

NIL introgressions span genome with high allelic replication

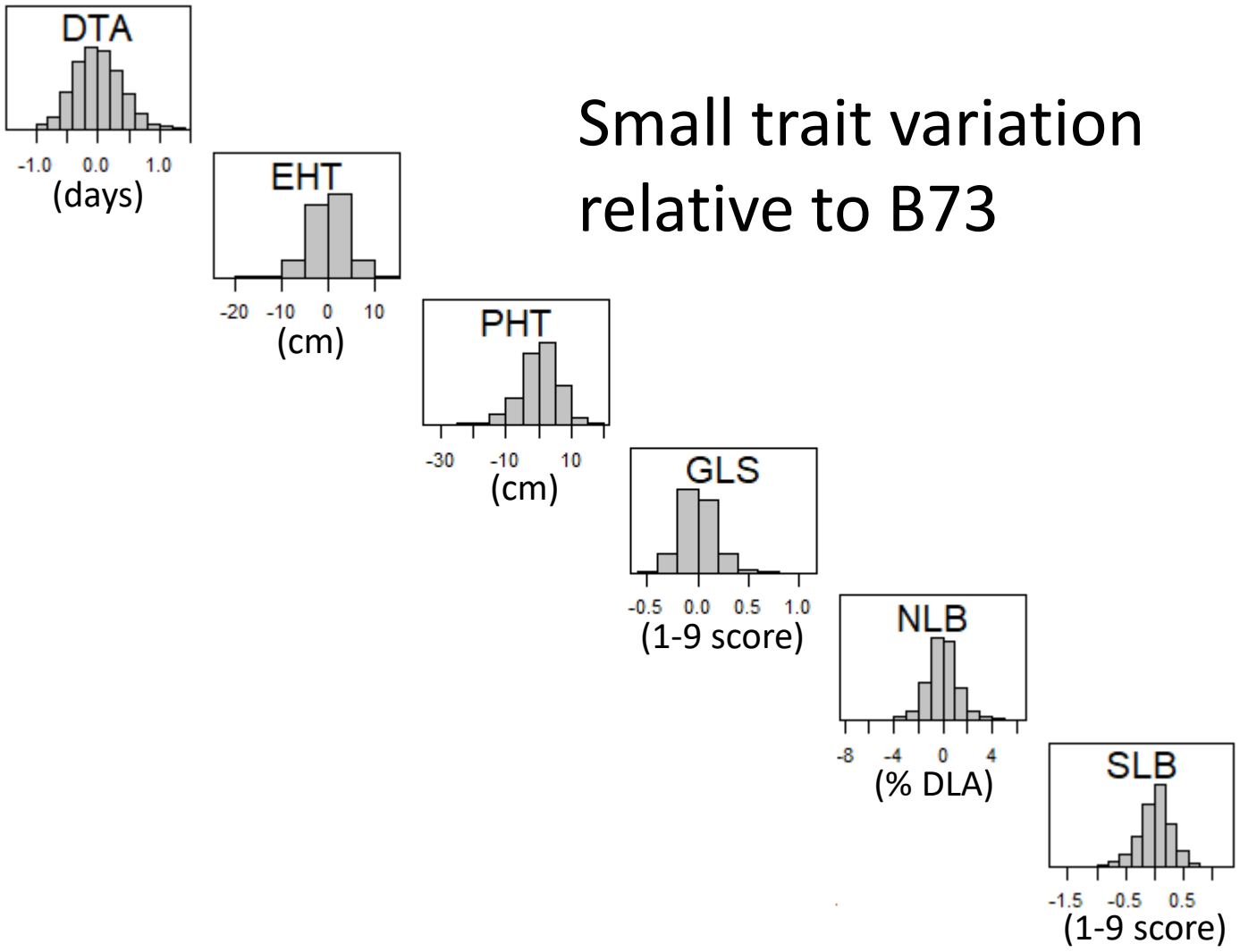
- Introgression length skewed
  - 13 ± 22 Mbp
  - Longer near centromere (low recomb.)
- Each introgression overlaps
  - 46 ± 24 introgressions from any donor
  - 3 ± 2 introgressions from same donor
  - ➢GWA feasible
- Each nNIL:
  - 3 ± 1 introgressions → fine-mapping
  - Introgressions comprised 2% of genome



Morales et al. Submitted to *The Plant Journal*

High heritability for disease resistance and height

Trait	H^2
DTA	0.4
EHT	0.7
PHT	0.7
GLS	0.6
NLB	0.6
SLB	0.8



Small trait variation relative to B73

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Disease resistance and height correlated in nNILs

Trait	H^2
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EHT	0.7
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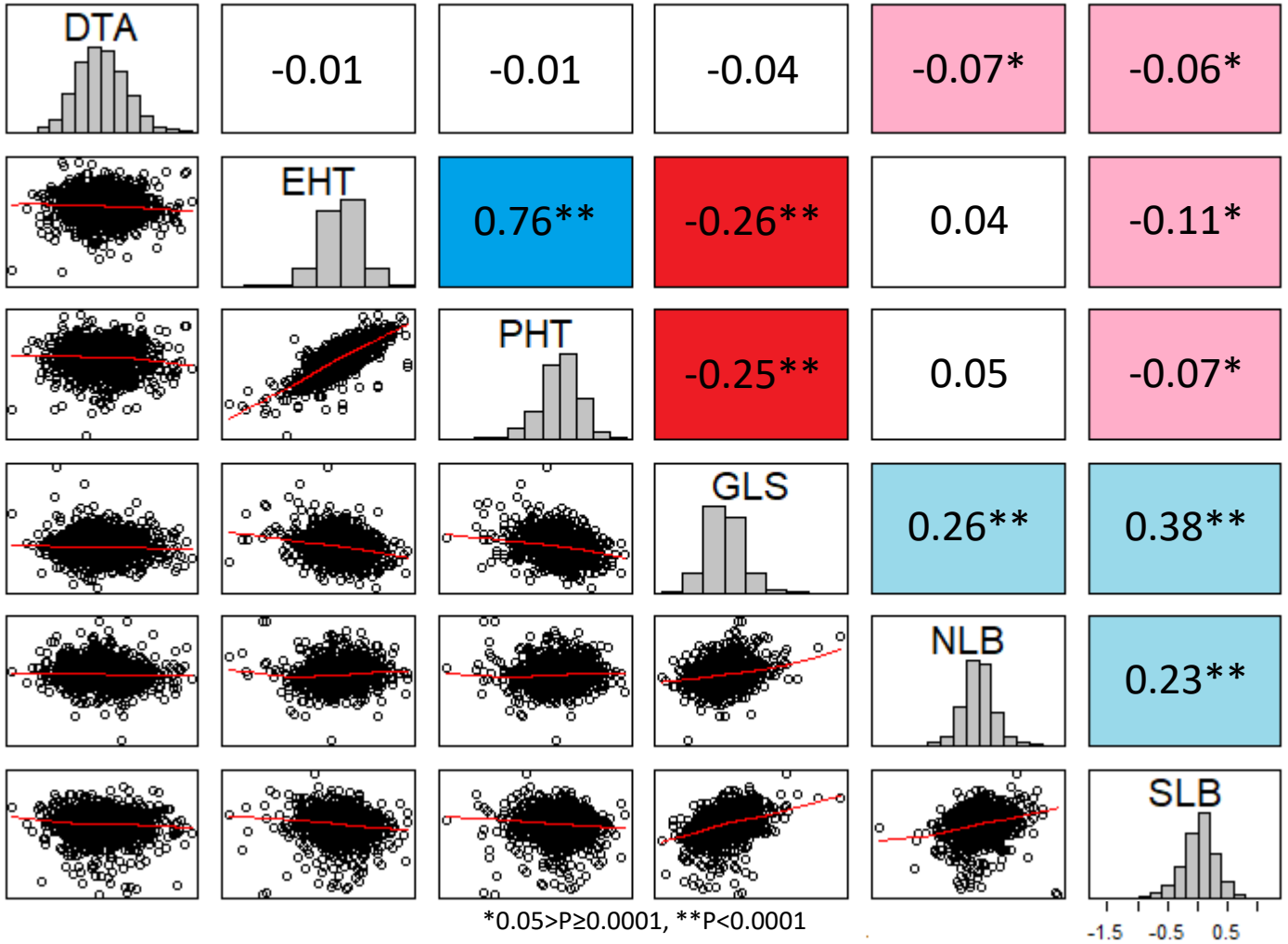
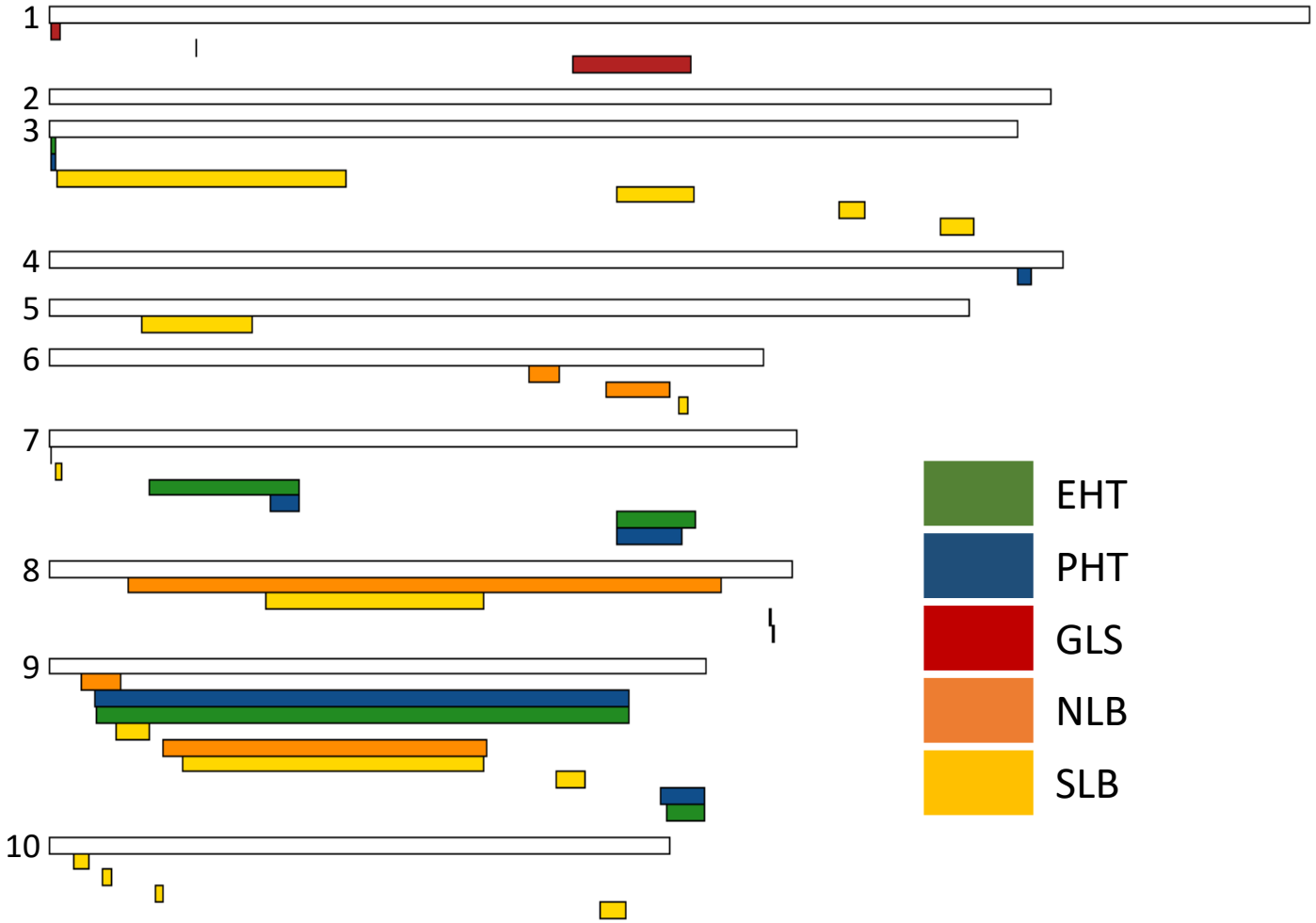


*0.05>P≥0.0001, **P<0.0001

Morales et al. Submitted to *The Plant Journal*

GWA identifies loci associated with height and disease resistance in nNILs

- 37 loci from GWA
  - 15 overlapped NAM QTL (Kump et al. 2011. *Nat Genet*; Poland et al. 2011. *PNAS*; Peiffer et al. 2014. *Genetics*)
  - 22 novel loci
  - No DTA loci



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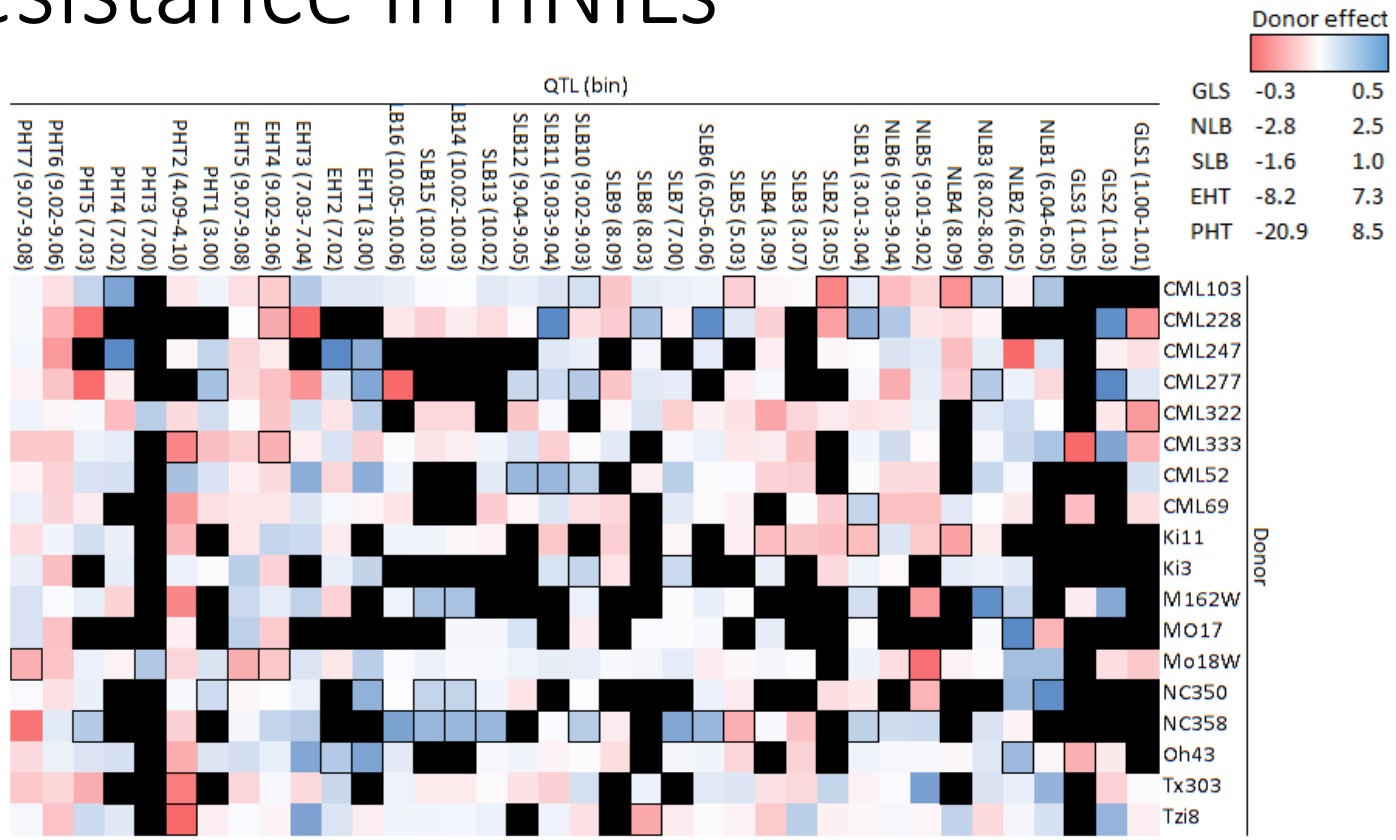
Allelic series at loci associated with height and disease resistance in nNILs

- Variation in donor allele effects on height and disease resistance

➢Assess pleiotropy



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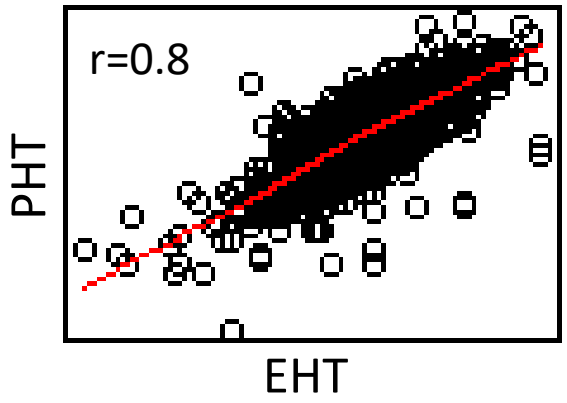
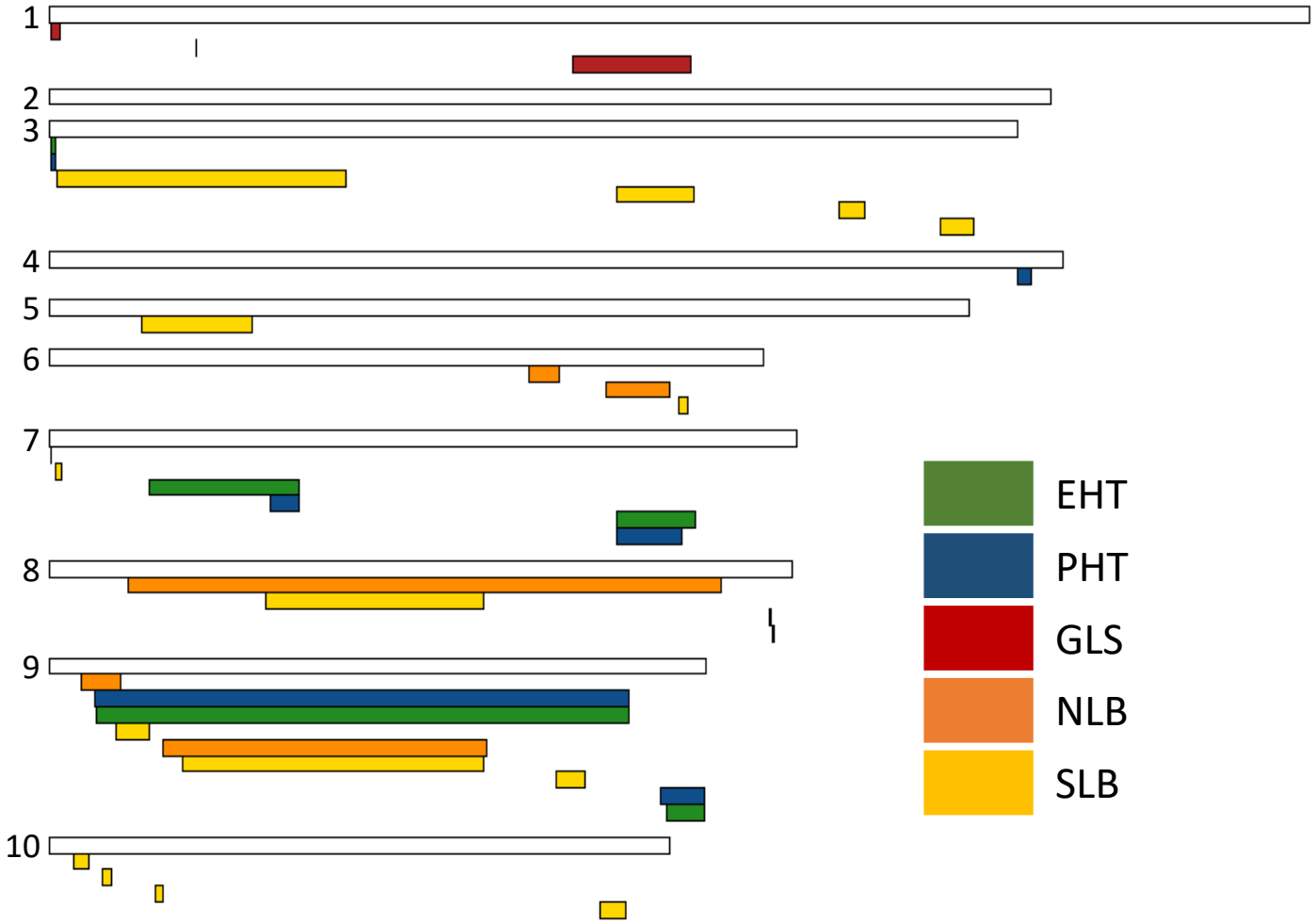
Pleiotropy for ear and plant height

- Colocalization of loci for EHT and PHT
- Correlated allelic effects at all EHT/PHT loci
  - r=0.5-0.9; p<0.05





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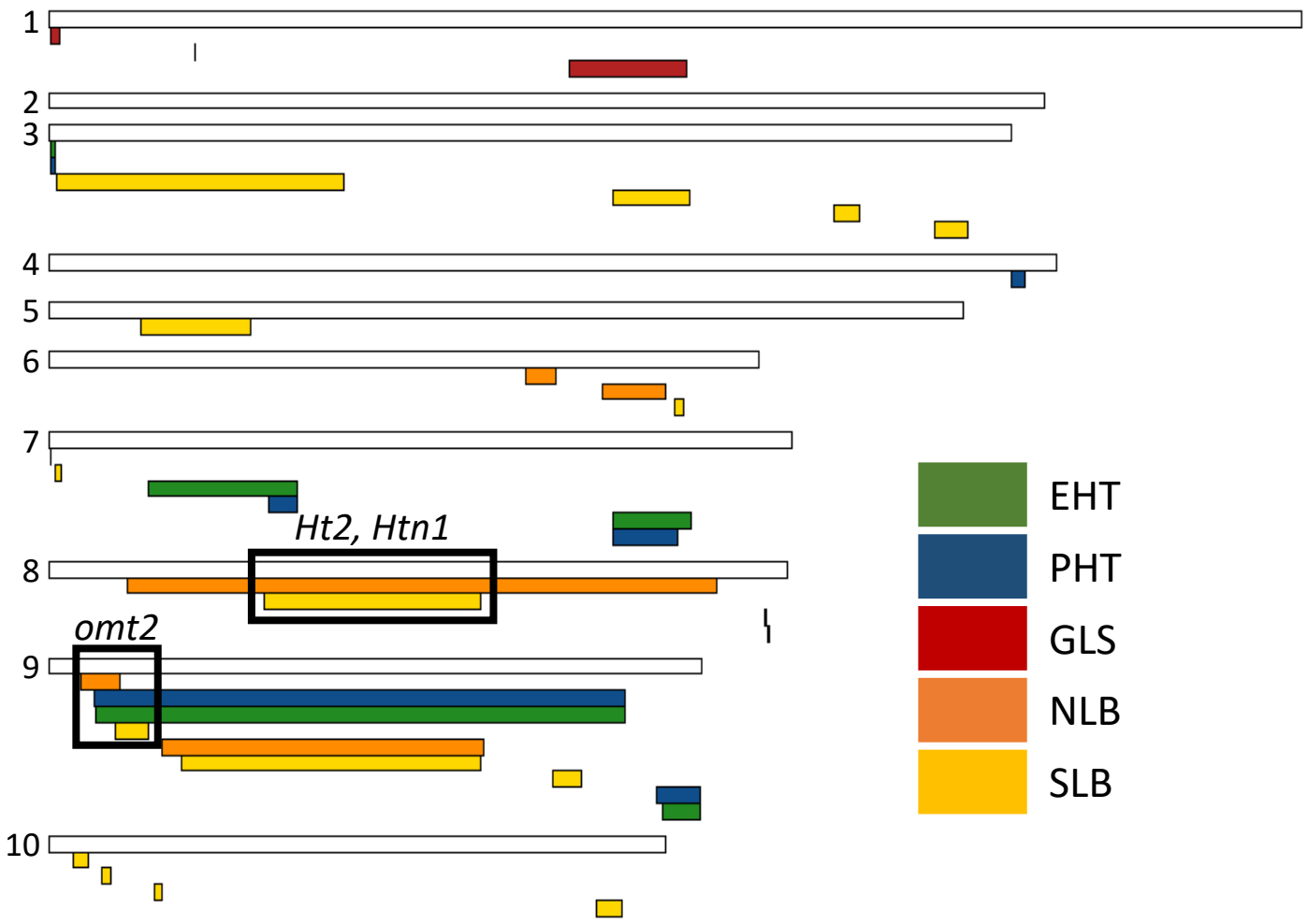
Colocalization of disease resistance loci

- NLB/SLB loci colocalize on chromosomes 8 and 9
  - Allelic effects positively correlated (r=0.2-0.3)
- Large chromosome 8 region: NLB R-genes *Ht2* and *Htn1* (Poland et al. 2011. *PNAS*)
- NLB/SLB colocalization with multiple disease resistance gene *omt2* (Yang et al. 2017. *Nat Genet*)



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The nNILs are a valuable resource for the maize genetics community

- QTL validation
- GWA + allelic analysis

Thanks!

Rebecca Nelson @
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