

Association Mapping in the S2MET Project

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Introduction

- Phenotypic stability may be useful for breeding widely adapted or locally adapted cultivars. It would be advantageous to explore the genetic architecture of this trait.
- There are three proposed gene models to explain stability:
 1. Pleiotropic / allele sensitivity (loci influence the mean differently in different environments)
 2. Epistatic / regulatory (differential regulation of loci influencing the mean)
 3. Overdominance (stability is a function of heterozygosity)
- Recent research has looked at mapping QTL for phenotypic stability and genotype mean:
 - In large populations [Kusmec et al., 2017]
 - In barley [Kraakman et al., 2004, Lacaze et al., 2009]

Objectives

- Discover loci associated with the trait mean per se and trait stability
- Examine genomic regions with highly stable or sensitive marker effects
- Look for overlap between the above regions/loci and summarize annotated genes or GO terms

Methods

Phenotype Data

- 3 traits in most environments
- Only include the 183 training population lines

trait	n_genotype	n_environment
GrainYield	183	29
HeadingDate	183	28
PlantHeight	183	29

- Spatial adjustment and BLUEs calculated per trial

Genotypic Data

9279 SNP markers from GBS genotyping and BOPA genotyping

chrom	BOPA	GBS	total
1	198	873	1071
2	263	1179	1442
3	291	1103	1394
4	198	617	815
5	339	1319	1658
6	215	970	1185
7	257	1457	1714

Stability

- Calculated the stability measures from Finlay and Wilkinson [1963] and Eberhart and Russell [1966]:
 $y_{ij} = \mu + g_i + (1 + b_i)h_j + \epsilon_{ij}$
- Linear stability: b_i
- Non-linear stability: $\delta_i^2 = \frac{1}{n} \sum (y_{ij} - \hat{y}_{ij})^2$

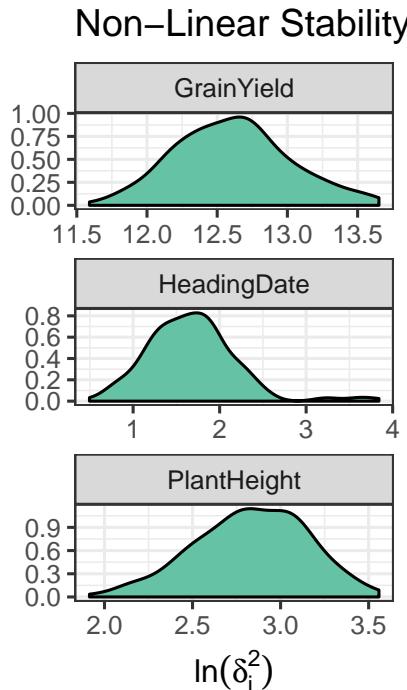
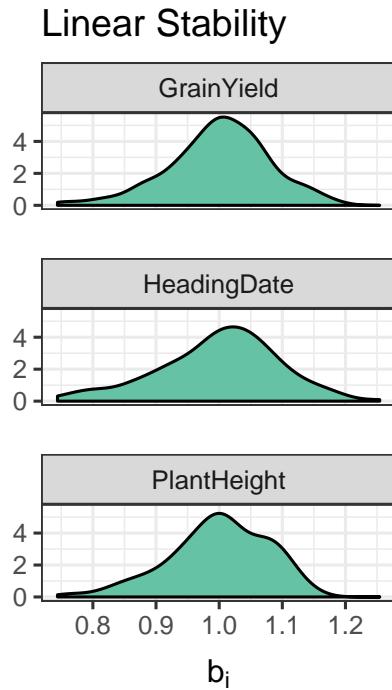


Figure 1: Distribution of stability measures

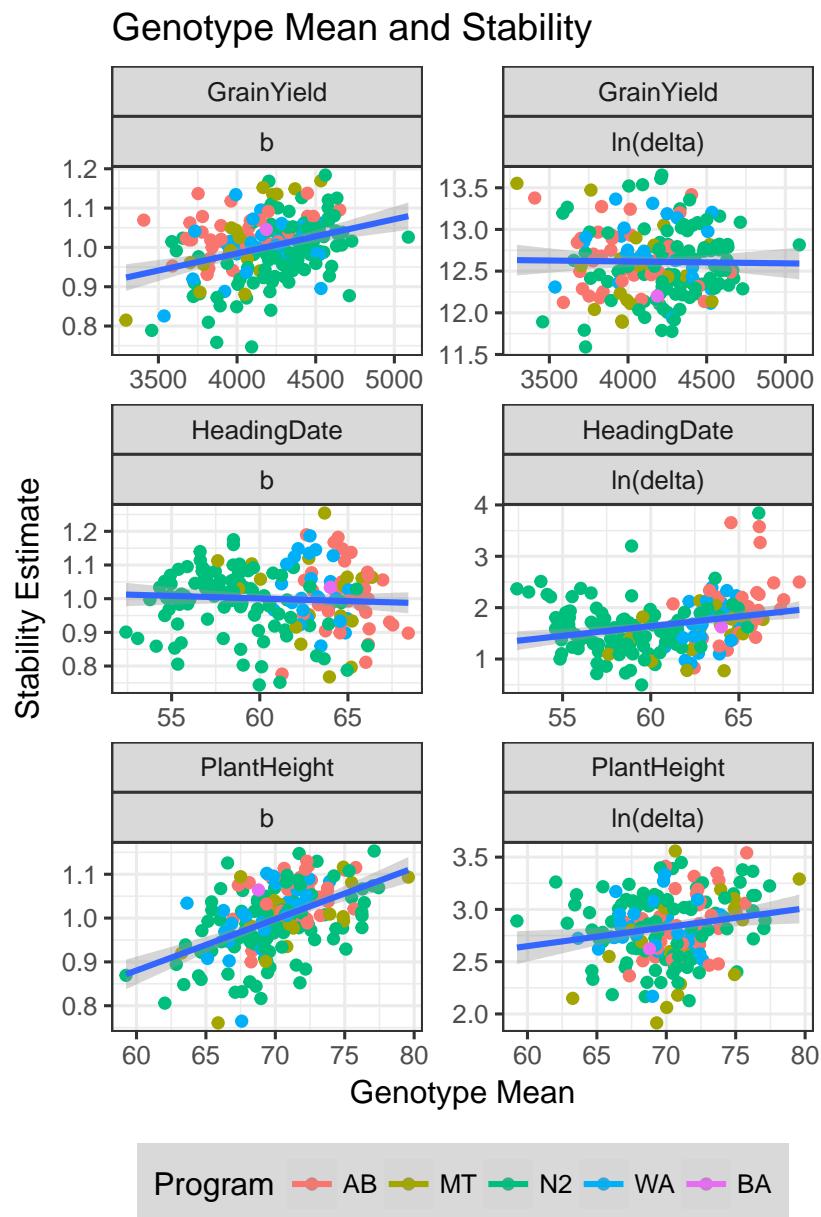


Figure 2: Relationship between genotype mean and stability

Association Mapping

- Used the G model from Bernardo [2013], Rincent et al. [2014], and Chen and Lipka [2016]

$$\mathbf{y} = \mathbf{X}\beta + \mathbf{S}\alpha + \mathbf{Z}\mathbf{u} + \mathbf{e}$$

- Association tested using Wald test
- p-values adjusted using the **qvalue** package
- How to read the following graphs:
 1. The $-\log_{10}(\text{q-value})$ points are plotted
 2. Chromosomes are represented by column-wise panels. Traits are represented by row-wise panels.
 3. The points for the genotype mean are always plotted in blue and are oriented upwards
 4. The points for the phenotypic stability (linear or non-linear) are plotted in orange and are oriented downwards.
 5. The dashed line refers to a cut-off that controls the genomewide FDR at 10%. Similarly, the solid line refers to FDR = 5%.

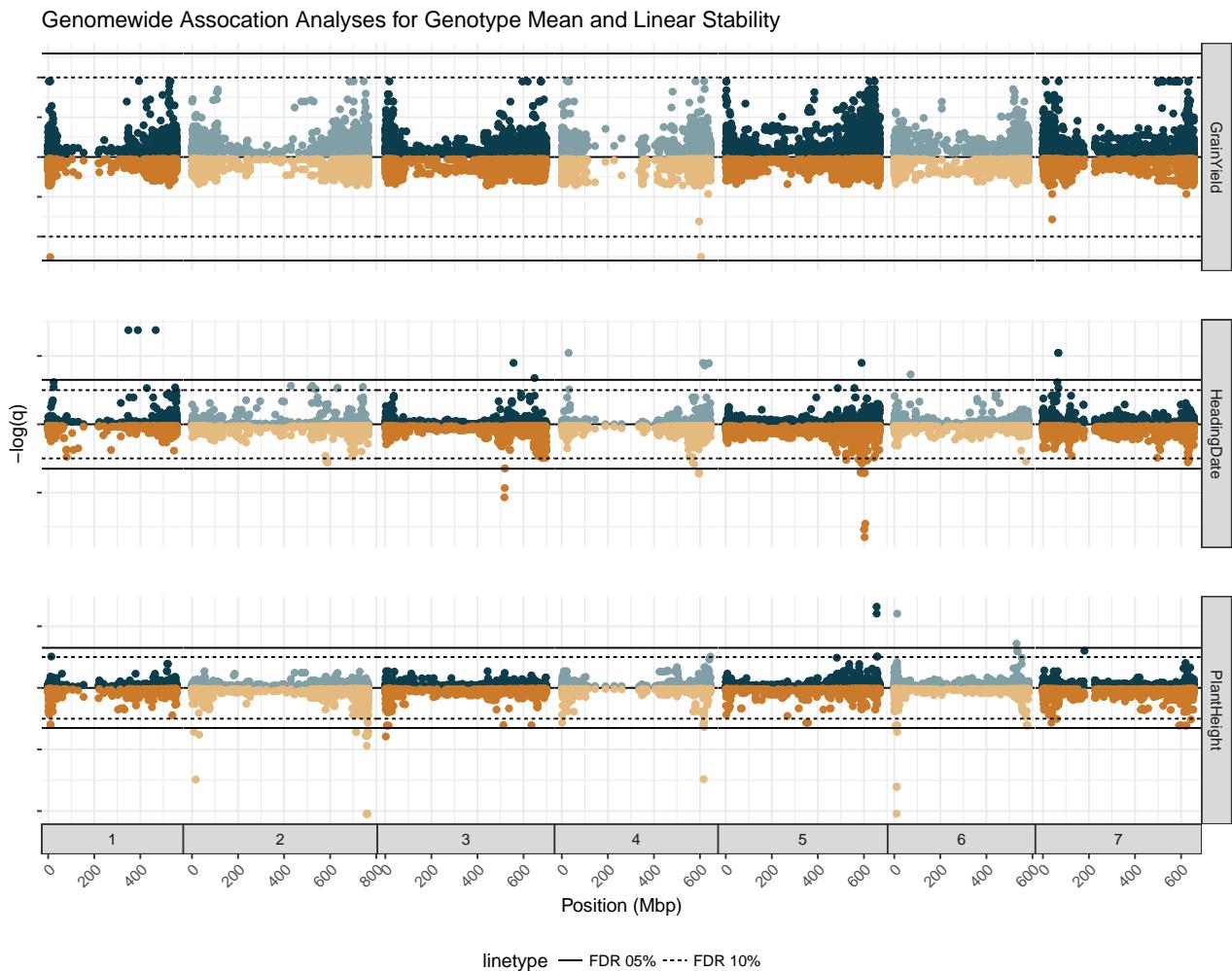


Figure 3: Association q-values for the genotype mean are shown in blue. Association q-values for phenotypic stability are in orange

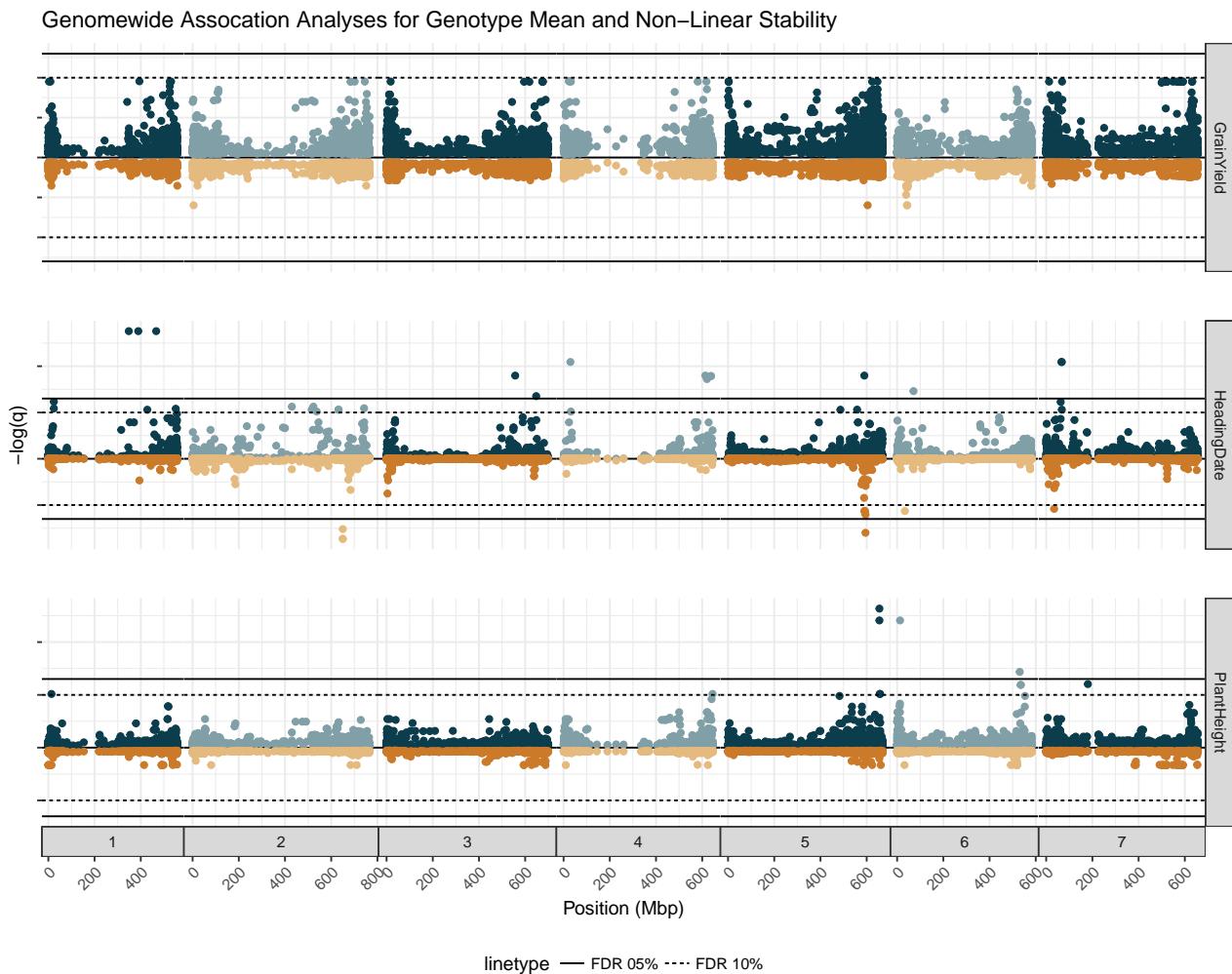


Figure 4: Association q-values for the genotype mean are shown in blue. Association q-values for phenotypic stability are in orange

Discussion

- Discussion points so far:
 1. Phenotypic data is sampled from an adequate range
 2. Lines are variable in genotypic means and linear and non-linear stability estimates
 3. For some traits, the genotype mean and stability are correlated (i.e. HeadingDate), and for others there is little to no correlation (i.e. GrainYield)
 4. We could detect significant associations for the genotype mean and for different estimates of stability for several traits
 - In some instances, significant loci for the mean overlapped with those for phenotypic stability (e.g. long arm of chromosome 5 for HeadingDate or the short arm of chromosome 6 for PlantHeight)
 - In other instances, significant loci for linear stability overlapped those for non-linear stability (e.g. long arm of chromosome 5 for HeadingDate)
 - More often, though, there was no overlap.
- Next steps:
 1. Calculate stability coefficients for marker effects across environments and find markers that are significantly plastic or stable
 2. Establish genomic regions of interest and look at gene annotation and GO terms

References

- Rex Bernardo. Genomewide markers as cofactors for precision mapping of quantitative trait loci. *Theoretical and Applied Genetics*, 126(4):999–1009, 2013. ISSN 00405752. DOI: 10.1007/s00122-012-2032-2.
- A H Chen and A E Lipka. The Use of Targeted Marker Subsets to Account for Population Structure and Relatedness in Genome-Wide Association Studies of Maize (*Zea mays L.*). *G3: Genes|Genomes|Genetics*, 6(August):2365–2374, 2016. ISSN 2160-1836. DOI: 10.1534/g3.116.029090. URL <http://www.ncbi.nlm.nih.gov/pubmed/27233668>.
- S A Eberhart and W A Russell. Stability Parameters for Comparing Varieties. *Crop Science*, 6(3), 1966.
- K.W. Finlay and G.N. Wilkinson. The analysis of adaptation in a plant-breeding programme. *Australian Journal of Agricultural Research*, 14(6):742, 1963. ISSN 0004-9409. DOI: 10.1071/AR9630742.
- Arnold T.W. Kraakman, Rients E. Niks, Petra M.M.M. Van Den Berg, Piet Stam, and Fred A. Van Eeuwijk. Linkage disequilibrium mapping of yield and yield stability in modern spring barley cultivars. *Genetics*, 168(1):435–446, 2004. ISSN 00166731. DOI: 10.1534/genetics.104.026831.
- Aaron Kusmec, Srikant Srinivasan, Dan Nettleton, and Patrick S. Schnable. Distinct genetic architectures for phenotype means and plasticities in *Zea mays*. *Nature Plants*, 3(9):715–723, 2017. ISSN 2055-0278. DOI: 10.1038/s41477-017-0007-7. URL <http://www.nature.com/articles/s41477-017-0007-7>.
- X Lacaze, P M Hayes, and A Korol. Genetics of phenotypic plasticity: QTL analysis in barley, *Hordeum vulgare*. *Heredity*, 102(2):163–173, 2009. ISSN 0018-067X. DOI: 10.1038/hdy.2008.76. URL <http://www.nature.com/doifinder/10.1038/hdy.2008.76>.
- Renaud Rincent, Laurence Moreau, Hervé Monod, Estelle Kuhn, Albrecht E. Melchinger, Rosa A. Malvar, Jesus Moreno-Gonzalez, Stéphane Nicolas, Delphine Madur, Valérie Combes, Fabrice Dumas, Thomas Altmann, Dominique Brunel, Milena Ouzunova, Pascal Flament, Pierre Dubreuil, Alain Charcosset, and Tristan Mary-Huard. Recovering power in association mapping panels with variable levels of linkage disequilibrium. *Genetics*, 197(1):375–387, 2014. ISSN 19432631. DOI: 10.1534/genetics.113.159731.