Identifying Genotype-by-Environment Interactions in the Metabolism of Germinating Arabidopsis Seeds Using Generalized Genetical Genomics

Joosen, Ronny Viktor Louis; Arends, Danny; Li, Yang; Willems, Leo A. J.; Keurentjes, Joost J. B.; Ligterink, Wilco; Jansen, Ritsert C.; Hilhorst, Henk W. M.

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Supplemental data files

Supplementary Table 1: Overview of QTLs shared between different models based on 95% confidence intervals.
Supplemental file 1: Metabolite centrotype data. Including peak numbers, retention time, hit quality, probability and mass used for quantification.
Supplemental file 2: ANOVA results from metabolic profiling of the parental lines Bay-0 and Sha.
Supplemental file 3: R-script with original data files allowing re-analysis of all data provided in this paper.
Supplemental file 4: Summary of all detected metabolic G QTLs.
Supplemental file 5: Summary of all detected metabolic G:E QTLs.

Supplemental figure 1: Allele distribution within the Bay-0 x Sha RIL population and the 4 selected sub-populations. Blue indicates the percentage of lines with a Bay-0 allele for a certain marker and red the number of lines with a Sha allele.
Supplemental figure 2: Principal component analysis plot showing the first two principal components of the metabolite analysis in the Bay-0 x Sha RIL population. Colors indicate the developmental stage (red = primary dormant (PD); blue = after-ripened (AR); green = 6 hours imbibed (6H); orange = seeds at radicle protrusion (RP), parental lines are indicated by triangles (Sha) or squares (Bay-0).
Supplemental figure 3: Transgression plot. Graph with scaled metabolite levels per RIL and parental levels.
Supplemental figure 4: Clustered heat map from the genetic (G) component showing the LOD profiles of all metabolites. Columns indicate marker positions along the five chromosomes; rows indicate individual-trait LOD profiles. A false-color scale is used to indicate the QTL significance. Positive values (yellow and red) represent a larger effect on the metabolite content for the Sha allele, and negative values (blue and green) represent a larger effect on the metabolite content for the Bay-0 allele. Clustering on the left shows correlation between QTL profiles.
Supplemental figure 5: Clustered heat map from the genetic x environmental (G:E) component showing the LOD profiles of all metabolites. Columns indicate marker

positions along the five chromosomes; rows indicate individual-trait LOD profiles. A false-color scale is used to indicate the QTL significance. Positive values (yellow and red) represent a larger effect of the treatment for the Sha allele, and negative values (blue and green) represent a larger effect of the treatment for the Bay-0 allele. Clustering on the left shows correlation between QTL profiles.

Supplemental figure 6: Flashcards of all identified metabolites. For full legend see figure 4.

Supplemental figure 7: KEGG metabolic pathway with flashcards overlay of the metabolites identified in this study.

Supplemental figure 8: Overview from HIF analysis with all metabolites with significant QTL confirmation.