

University of Groningen

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.

Published in:
 Plant Physiology

DOI:
[10.1104/pp.113.216176](https://doi.org/10.1104/pp.113.216176)

IMPORTANT NOTE: You are advised to consult the publisher's version (publisher's PDF) if you wish to cite from it. Please check the document version below.

Document Version
 Publisher's PDF, also known as Version of record

Publication date:
 2013

[Link to publication in University of Groningen/UMCG research database](#)

Citation for published version (APA):

Joosen, R. V. L., Arends, D., Li, Y., Willems, L. A. J., Keurentjes, J. J. B., Ligterink, W., Jansen, R. C., & Hilhorst, H. W. M. (2013). Identifying Genotype-by-Environment Interactions in the Metabolism of Germinating Arabidopsis Seeds Using Generalized Genetical Genomics. *Plant Physiology*, 162(2), 553-566. <https://doi.org/10.1104/pp.113.216176>

Copyright

Other than for strictly personal use, it is not permitted to download or to forward/distribute the text or part of it without the consent of the author(s) and/or copyright holder(s), unless the work is under an open content license (like Creative Commons).

The publication may also be distributed here under the terms of Article 25fa of the Dutch Copyright Act, indicated by the "Taverne" license. More information can be found on the University of Groningen website: <https://www.rug.nl/library/open-access/self-archiving-pure/taverne-amendment>.

Take-down policy

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

Downloaded from the University of Groningen/UMCG research database (Pure): <http://www.rug.nl/research/portal>. For technical reasons the number of authors shown on this cover page is limited to 10 maximum.

Supplemental data files

Supplementary Table 1: Overview of QTLs shared between different models based on 95% confidence intervals.

Supplemental file 1: Metabolite centrotpe 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.