



**UvA-DARE (Digital Academic Repository)**

**Genetic basis of allochronic differentiation in the fall armyworm**

Hänniger, S.; Dumas, P.; Schöfl, G.; Gebauer-Jung, S.; Vogel, H.; Unbehend, M.; Heckel, D.G.; Groot, A.T.

*Published in:*  
BMC Evolutionary Biology

*DOI:*  
[10.1186/s12862-017-0911-5](https://doi.org/10.1186/s12862-017-0911-5)

[Link to publication](#)

*Citation for published version (APA):*

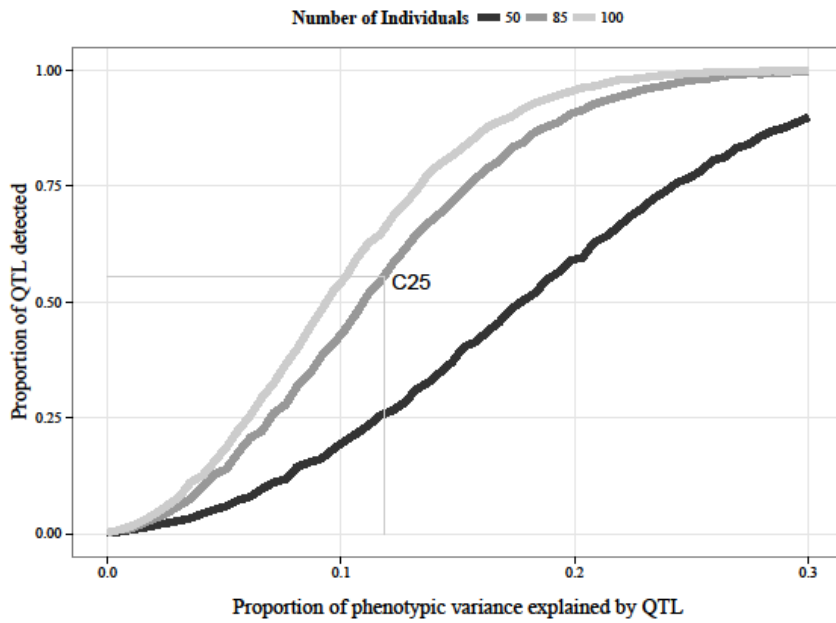
Hänniger, S., Dumas, P., Schöfl, G., Gebauer-Jung, S., Vogel, H., Unbehend, M., ... Groot, A. T. (2017). Genetic basis of allochronic differentiation in the fall armyworm. *BMC Evolutionary Biology*, 17, [68]. DOI: 10.1186/s12862-017-0911-5

**General rights**

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), other than for strictly personal, individual use, unless the work is under an open content license (like Creative Commons).

**Disclaimer/Complaints regulations**

If you believe that digital publication of certain material infringes any of your rights or (privacy) interests, please let the Library know, stating your reasons. In case of a legitimate complaint, the Library will make the material inaccessible and/or remove it from the website. Please Ask the Library: <http://uba.uva.nl/en/contact>, or a letter to: Library of the University of Amsterdam, Secretariat, Singel 425, 1012 WP Amsterdam, The Netherlands. You will be contacted as soon as possible.



### Additional file 12

Power analysis for backcross families with 50 (black line), 85 (corresponding to the QTL in this manuscript, dark grey line) and 100 (black line) progeny, respectively. The probability of detecting a QTL is plotted as a function of the fraction of phenotypic variance explained by the QTL.