

Association mapping for pre-harvest sprouting tolerance in European winter wheat (*Triticum aestivum* L.) germplasm

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Summary

Pre-harvest sprouting (PHS), the germination of mature grains in the spike before harvest, is an everpresent concern for many wheat-growing regions of the world. In Germany and Austria, wheat samples showing falling numbers (a measure for the effect of α -amylase on the rheological properties of starch) lower than 220 s are usually not marketable to the milling industry. The present study was undertaken with the objective of identifying markers linked to PHS tolerance quantitative trait loci in an elite association mapping panel of red-grained genotypes using Diversity Arrays Technology (DArT) markers. In 2009/2010 and 2010/2011 cropping seasons, 124 West European winter wheat genotypes were grown at eight locations in Germany and Austria, totalling 16 environments. The field trials included the genotypes with two replications. Four PHS data sets were collected: artificial wetting tests of intact spikes and germination tests of threshed seeds were applied to samples taken at physiological maturity from 13 and 12 environments, respectively, whereas falling number (14 environments) and percentage of sprout-damaged grains (4 environments) were determined from spikes that had experienced a period of natural/artificial weathering in the field (OBERFORSTER et al. 2012). Genotyping the sample population yielded 715 unique DArT marker signatures that were characterised by allele frequencies >5%

and missing genotype information <10%. The genotypic and phenotypic scores (of each single environment and across environments, respectively) were integrated in an association mapping framework consisting of generalized and mixed linear models with population and/or family structure as covariates. A total of 24 genomic regions/markers from 15 chromosomes were associated to at least one of the four PHS parameters of which 12 have already been described in previous studies. *Phs1*, a major locus for sprouting tolerance on chromosome 4AL repeatedly found in genetic analyses of PHS (MARES et al. 2005, TORADA et al. 2008), showed strong ($P < 0.01$) associations to intact-spike sprouting in 5 environments; weak association to the trait scores ($0.01 < P < 0.05$) was found for 3 environments. Concurrently, variation at *Phs1* was weakly associated to seed dormancy in 4 environments. Two marker loci on chromosomes 1DS and 5BL showed association with all parameters. In this study, several marker-trait associations were obtained that need to be confirmed with a larger sample population. For that, low running costs genotyping platforms are available that are ideal for the many thousands of samples of commercial breeding programmes.

Keywords

DArT, falling number, marker-trait association analysis, seed dormancy, sprout-damaged grains

Acknowledgments

We thank the following breeding companies for conducting the field trials and collaboration in the project: Lantmännen SW Seed GmbH (location Hadmersleben), Limagrain GmbH (location Rosenthal), Saatzucht Josef Breun GbR (location Herzogenaurach), Secobra Saatzucht GmbH (location Feldkirchen), Saatzucht Donau Ges.m.b.H & CoKG (location Reichersberg) and Saatzucht Edelhof (location Zwettl). Technical assistance provided by the working groups Wheat and Oat Breeding Research and Genome Analysis, and the department Quality Assurance and Analysis of the Bavarian State Research Center for Agriculture is gratefully acknowledged. CORNET project *Efficient phenotypic and molecular selection methods for enhancing preharvest sprouting tolerance of European wheat germplasm (Robust Wheat)* was supported by Bundesministerium für Wirtschaft und Technologie (BMWi), Allianz Industrie Forschung (AiF), Gemeinschaft zur Förderung der

privaten deutschen Pflanzenzüchtung (GFP) e.V., Österreichische Forschungsförderungsgesellschaft (FFG), Börse der landwirtschaftlichen Produkte in Wien and Vereinigung der Pflanzzüchter und Saatgutkaufleute Österreichs.

References

- MARES D, MRVAK, CHEONG J, WILLIAMS K, WATSON B, STORLIE E, SUTHERLAND M, ZOU Y, 2005: A QTL located on chromosome 4A associated with dormancy in white- and red-grained wheats of diverse origin. *Theor Appl Genet* 111, 1357-1364.
- OBERFORSTER M, RATZENBÖCK A, WERTEKER M, NEUMAYER A, ZECHNER E, HARTL L, 2012: Variabilität und Beziehungen von Samendormanz, Auswuchs und Fallzahl in einem Sortiment europäischer Winterweizen. Bericht 62. Tagung der Vereinigung der Pflanzzüchter und Saatgutkaufleute Österreichs 2011, 69-71.
- TORADAA, KOIKE M, IKEGUCHI S, TSUTSUI I, 2008: Mapping of a major locus controlling seed dormancy using backcrossed progenies in wheat (*Triticum aestivum* L.). *Genome* 51, 426-432.s

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