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**AB-QTL analysis for two populations of winter barley sharing the
donor of *Hordeum vulgare* ssp. *spontaneum***

**Inaugural-Dissertation
zur
Erlangung des Grades
Doktor der Agrarwissenschaften
(Dr. agr.)**

**der
Hohen Landwirtschaftlichen Fakultät
der Rheinischen Friedrich-Wilhelms-Universität Bonn**

vorgelegt am 22. April 2005

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Tag der mündlichen Prüfung: 17. Juni 2005

Schriftenreihe des Institutes für Pflanzenbau

Band 6/2005

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of winter barley sharing the donor of
*Hordeum vulgare ssp. spontaneum***

D 98 (Diss. Universität Bonn)

Shaker Verlag
Aachen 2005

Bibliographic information published by Die Deutsche Bibliothek

Die Deutsche Bibliothek lists this publication in the Deutsche Nationalbibliografie; detailed bibliographic data is available in the internet at <http://dnb.ddb.de>.

Zugl.: Bonn, Univ., Diss., 2005

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Printed in Germany.

ISBN 3-8322-4226-0

ISSN 1619-9456

Shaker Verlag GmbH • P.O. BOX 101818 • D-52018 Aachen

Phone: 0049/2407/9596-0 • Telefax: 0049/2407/9596-9

Internet: www.shaker.de • eMail: info@shaker.de

To my *memorable years* in Bonn
难忘Bonn岁月

Abstrakt (in Deutsch)

Die Ziel des vorliegenden Projekts war, vorteilhafte exotische QTL-Allele für die Verbesserung der agronomischen Leistung, der Krankheitsresistenz und der unspezifischen Blattflecken in zwei BC₂DH-Populationen zu ermitteln, die aus den Kreuzungen der beiden deutschen Wintergerstesorten Carola und Theresa (*Hordeum vulgare* ssp. *vulgare*, im folgenden mit *Hv* abgekürzt) mit der Wildgersten-Akzession ISR101-23 (*Hordeum vulgare* ssp. *spontaneum*, im folgenden mit *Hsp* abgekürzt) aus Israel abgeleitet wurden. Die zwei BC₂DH-Populationen (benannt C101 und T101) wurden mit 82 und 78 SSR-Markern genotypisiert. C101 und T101 bestanden aus 282 und 104 BC₂DH-Linien. Insgesamt 16 agronomische Merkmale, vier Krankheitsresistenzen sowie unspezifische Blattflecken wurden an bis zu sechs unterschiedlichen Umwelten und über zwei Jahre ausgewertet. Die QTL-Analyse wurde mit einer 3-faktoriellen ANOVA durchgeführt, mit dem Marker als fixen Effekt, der Linie geschachtelt in Markergenotyp, der Umwelt und den entsprechenden Interaktionen als zufällige Effekte. In C101 wurden 35 vorteilhafte exotische QTL-Effekte aus 183 putativen QTLs für 10 agronomische Merkmale, vier Krankheitsresistenzen und unspezifische Blattflecken ermittelt. Unter den vorteilhaften exotischen QTLs wurden 22 (19,1 %) vorteilhafte QTL-Effekte für agronomische Merkmale, und 13 (19,1 %) für Krankheitsresistenzen und unspezifische Blattflecken identifiziert. Ein crossover QTL-Effekt des *Hsp*-Alleles auf Ertrag, ermittelt auf Chromosom 6H in C101, war mit einer Ertragszunahme von 8,2 %, gemittelt über drei Umwelten, verbunden (Table 17). Allerdings war der *Hsp*-Effekt in den restlichen zwei Umwelten mit einer Ertragsabnahme von 4,6 % assoziiert. Die Symptome für Zwergrost, Netzflecken, Mehltau, *Rynchosporium* und unspezifische Blattflecken wurden in C101 durch exotische Allele an den QTLs *QlrC101-3H*, *QnbC101-6Hd*, *QpmC101-2H*, *QrhC101-7Ha* und *QnpbC101-5Ha* um 26,2 %, 20,8 %, 17,8 %, 4,9 % beziehungsweise 14,9 % reduziert. In T101 wurden 85 putative QTLs für elf agronomische Merkmale, Krankheitsresistenzen und unspezifische Blattflecken entdeckt. Der exotische Genotyp verbesserte die Leistung bei 13 (18,6 %) von 70 QTLs, die für agronomische Merkmale ermittelt wurden (Table 19). Insgesamt 39 putative QTLs, die in C101 ermittelt wurden, wurden durch 40 QTLs in T101 bestätigt. Von 268 putativen QTLs und 48 vorteilhaften exotischen Effekten, die in beiden Populationen gefunden wurden, konnten 65 (24,3 %) QTLs beziehungsweise 21 (43,6 %) vorteilhafte exotische Effekte in anderen QTL-Analysen der Gerste wiedergefunden werden. Ungefähr 64 % der vorteilhaften exotischen QTL-Allele, die in dieser Studie identifiziert wurden, konnten nicht in anderen Studien der Gerste ermittelt werden. Diese vorteilhaften *Hsp*-Allele könnten daher neue Allele sein.

Abstract (in English)

The objective of the present study was to detect favourable exotic QTL alleles for the improvement of agronomic traits, pathogen resistance and non-parasitic browning in two BC₂DH populations derived from the crosses of two German winter barley varieties, Carola and Theresa (*Hordeum vulgare* ssp. *vulgare*, in the following abbreviated *Hv*), with the wild barley accession ISR101-23 (*Hordeum vulgare* ssp. *spontaneum*, in the following abbreviated *Hsp*) from Israel. The two BC₂DH populations (termed C101 and T101) were genotyped with 82 and 78 SSR markers, respectively. C101 and T101 consisted of 282 and 104 BC₂DH lines, respectively. Sixteen agronomic traits, four pathogen resistances and the non-parasitic browning were evaluated at up to six different locations and in two consecutive years. QTL analysis was carried out with a three-factorial ANOVA including the marker as fixed effect and the environment and lines nested in the marker genotype as well as the respective interactions as random effects. In addition, cold damage (COD) and neighbouring plots of the seriously cold-damaged plots (N) were used as co-variables for those traits which were significantly affected by COD and N. In C101, 35 favorable exotic QTL effects out of 183 putative QTLs were detected for ten agronomic traits, four pathogen resistances and non-parasitic browning. Among these putative QTLs, 22 (19.1 %) of 115 QTLs detected for agronomic traits exhibited favorable effects and 13 (19.1 %) of 68 QTLs identified for disease resistances and non-parasitic browning were associated with improvements. A crossover interaction QTL effect of the *Hsp* allele on yield, detected on chromosome 6H in C101, was associated with a yield increase of 8.2 % averaged across three environments. However, in the remaining two environments the *Hsp* effect was associated with a yield reduction of 4.6 %. In addition, favourable effects of exotic alleles were detected for all pathogen resistances and non-parasitic browning in this study. For instance, the symptoms of leaf rust, net blotch, powdery mildew, scald and non-parasitic browning symptoms at *QlrC101-3H*, *QnbC101-6Hd*, *QpmC101-2H*, *QrhC101-7Ha* and *QnpbC101-5Ha* were reduced by 26.2 %, 20.8 %, 17.8 %, 4.9 % and 14.9 % in C101, respectively (Table 17). In T101, 85 putative QTLs were discovered for eleven agronomic traits, four pathogen resistances and non-parasitic browning. The exotic genotype improved the performance at 13 (19.4 %) of 67 QTLs detected for agronomic traits and no favorable QTL effect was identified for disease resistances and non-parasitic browning in T101 (Table 19). Thirty-nine putative QTLs detected in C101 were confirmed by 40 QTLs detected in T101. Altogether, 65 (24.3 %) QTL effects among 268 putative QTLs localized in both populations and 21 (43.8 %) favorable QTL effects among 48 favorable QTL effects identified in both populations were verified in other barley QTL and linkage analyses. About 56 % favorable exotic QTL alleles identified in this study were so far not detected in other barley QTL studies. These favorable *Hsp* alleles may be new alleles.

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