

**Comparative mapping of genes for plant disease resistance in
wheat 'advanced backcross' populations by means
of DNA markers**

Inaugural-Dissertation

zur

Erlangung des Grades

Doktor der Agrarwissenschaften

(Dr. agr.)

der

Hohen Landwirtschaftlicher Fakultät

der Rheinischen Friedrich-Wilhelms-Universität Bonn

vorgelegt am [13-09-2006]

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Tag der mündlichen Prüfung:	14-11-2006

Schriftenreihe des Instituts für
Nutzpflanzenwissenschaften und Ressourcenschutz

Band 11/2007

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**Comparative mapping of genes
for plant disease resistance in
wheat 'advanced backcross' populations
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D 98 (Diss. Universität zu Bonn)

Shaker Verlag
Aachen 2007

Bibliographic information published by the Deutsche Nationalbibliothek

The Deutsche Nationalbibliothek lists this publication in the Deutsche Nationalbibliografie; detailed bibliographic data are available in the Internet at <http://dnb.d-nb.de>.

Zugl.: Bonn, Univ., Diss., 2006

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Printed in Germany.

ISBN 978-3-8322-6183-2

ISSN 1864-1334

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

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

Internet: www.shaker.de • e-mail: info@shaker.de

Abstract

The present study was aimed to localise and detect the exotic QTL alleles for the improvement of pathogen resistance in advanced backcross (AB) populations derived from the crosses between elite wheat cultivars, Batis and Zentos, with the synthetic wheat accessions, Syn022L and Syn086L, respectively. The resulting populations containing 400 (BC_2F_3) lines of B22 and Z86 were investigated against *Fusarium* head blight (FHB), leaf rust (LR), powdery mildew (PM) and *Septoria* leaf blotch (SEP) to evaluate the adult plant resistance in the field. In addition, *in vitro* tests were conducted to analyse the seedling stage resistance against leaf and stripe rusts in B22 and Z86, respectively. Simultaneously, altogether 194 SSR markers were genotyped in B22 (85) and Z86 (109), which were distributed throughout the A, B and D genomes. Ultimately, phenotype and genotype data were subjected to QTL analysis with a GLM procedure in SAS programme (SAS Institute 2003) by applying a 3-factorial analysis of variance including marker as fixed effect, the environment, lines nested in marker genotypes and the marker*environment interactions as a random effect.

The QTL analysis revealed 71 putative QTLs derived from the exotic accessions for the adult plant resistance in both populations. Among the total, 39 (55%) putative QTLs were identified in B22, where at 20 (51%) loci the exotic alleles improved the resistance against the investigated traits. In Z86, 32 (45%) putative QTLs were identified, of which twelve (38%) loci resulted an improvement in disease resistances by the introgression of exotic alleles. In both populations, the exotic alleles demonstrated an increase in resistance against FHB (3 to 21%), LR (13 to 44%), PM (0.5 to 23%) and SEP (1 to 20%). For seedling stage resistance against leaf rust isolate 77XWR, six putative QTLs were detected in B22. All of them were associated with an increase in resistance (15 to 43%) by the transfer of exotic alleles from the donor parent, Syn022L. Likewise, the analysis yielded six putative QTLs for stripe rust seedling stage resistance in Z86, of which the exotic genotypes added resistance at four loci that range from 59% to 86%. Altogether, 83 putative QTLs were identified for the adult plant and seedling stage resistance across the A (27), B (26) and D (30) genomes. The present study has demonstrated that favourable effects of the exotic alleles can be transferred from the synthetic wheat accessions to elite cultivars for the improvement of resistance against a variety of pathogens. These favourable exotic QTL alleles will be tested in NILs (near-isogenic lines) and, if verified, individual genes might be isolated in the long run via map-based cloning procedure.

Abstract (in Deutsch)

Die Zielsetzung der Studie war exotische QTL-Allele zu bestimmen und zu lokalisieren um eine Verbesserung der pathogenen Resistenz in zwei AB- Populationen, die von Kreuzungen zwischen zwei Elite Kulturweizen (Batis und Zentos) und den Wildeltern (Syn 022L bzw Syn 086L) abgeleitet wurden, zu bekommen zu erreichen. Die daraus resultierenden Populationen bestehend aus 400 Linien (BC₂F₃) von B22 und Z86 wurden auf verschiedene Pathogene in verschiedenen Umwelten ausgewertet um bei Erwachsenenpflanzen Resistenz gegen Braunrost(FHB), Blattrost(LR), Mehltau(PM) und *Septoria* Blattfleckenkrankheit (SEP) zu untersuchen. Außerdem wurden in vitro Tests durchgeführt um die Resistenz im Keimstadium auf Blattrost und Gelbrost in B22 bzw Z86 zu analysieren. Gleichzeitig wurden beide Populationen mit 194 SSR- Markern, die über die Weizengenome A, B und D verteilt waren, genotypisiert. Schließlich wurden die phänotypischen und genotypischen Daten einer QTL-Analyse mit einer GLM Prozedur in SAS (SAS Institut 2003) unterzogen, unter Anwendung der 3-faktoriellen Varianzanalyse mit einem Marker als fixen Effekt, der Umwelt, Linien geschachtelt in Markergenotypen und den Umweltinteraktionen* als zufällige Effekte.

Die QTL-Analyse legt ergibt 71 putative QTLs, abgeleitet von der exotischen Zunahme der Resistenz bei Erwachsenenpflanzen in beiden Populationen, offen. In B22 wurden insgesamt 39 (55%) putative QTLs identifiziert, wobei in 20 (51%) Loci die exotischen Allele die Krankheitsresistenz verbessern im Vergleich zu den untersuchten Behandlungen. In Z86 wurden 32 (45%) putative QTLs identifiziert, wobei in 12 Loci sich die Resistenz durch die Introgression von exotischen Genotypen verbesserte. Das exotische Allel beweist eine Zunahme an Resistenz gegen Ährenfusarium (3 bis 21%) an 4Loci, Blattrost (13 bis 44%) an 4Loci, Mehltau (0,5 bis 23%) an 10 Loci bzw *Septoria* Blattfleckenkrankheit (1 bis 20%) an 4, 4, 10 bzw an 14 Loci in beiden Populationen. Für die Resistenz im Keimstadium gegen das Blattrost-Isolat 77XWR wurden 6 putative QTLs in B22 lokalisiert. Diese wurden alle mit einer Zunahme an Resistenz (15 bis 43%) durch den Transfer von exotischen Allelen vom Spender Syn 022L verknüpft. Ebenso ergab die Analyse 6 putative QTLs für Resistenz im Keimstadium von Gelbrost in Z86. Aus diesen ergab sich für die exotischen Genotypen eine Zunahme an Resistenz (59 bis 86%) an vier Loci. Überall wurden 27, 26, bzw 30 QTLs auf den Genomen A, B bzw D lokalisiert. Die vorliegende Studie hat bewiesen, dass günstige Effekte von den exotischen Allelen durch Übertragung vom synthetischen Weizen auf Eliteweizen zur Verbesserung der Resistenz gegen verschiedene Pathogene erreicht werden. Zukünftig sollen die günstigen exotischen QTL Allele in NILs (nahe isogene Linien) getestet werden und wenn sich dies Ergebnis bestätigt sollen individuelle langsame rusting Gene isoliert werden mit einem aufwendigen Verfahren, der kartierenden Klonierung.

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