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

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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.