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Mapping of QTLs for drought tolerance in barley at different developmental stages

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Abstract

In order to determine Quantitative Trait Loci (QTLs) involved in osmotic tolerance in barley, the Oregon-Wolfe-Barley (OWB) mapping population was examined at germination and seedling stages. The water stress was induced by adding poly-ethylene-glycol to the growing solution. The morphological responses for water stress were determined by reduction of shoot and root length at germination stage and by the shoots dry weight reduction at the seedling stage. Main QTLs could be localized on chromosomes 1(7H), 3(3H), 5(1H) and 7(5H). At germination and at seedling stages mainly different QTLs play a role with respect to osmotic tolerance. We found in two developmental phases only one common QTL, which supports the suggested developmentally regulated character of the genes affecting drought tolerance. The QTLs detected at germination stage may be not specific for drought, because the same QTLs were found for salt tolerance at germination stage, for pre-harvest sprouting and for dormancy in the OWB population; therefore, the screening for drought tolerance using a germination test seems to be not suitable for the selection at the adult stage.

Key words: drought tolerance, *Hordeum vulgare*, Oregon-Wolfe-Barley, QTL mapping

Introduction

Water deficit can occur during the whole life cycle of the plants and causes yield loss by the cultivated cereals. Determining major QTLs for drought tolerance could be helpful to identify favourable genotypes. However, their selection and breeding is complicated, because of the suggested developmentally regulated character of the genes affecting drought tolerance. For determining reliable QTLs the tolerance must be screened at several developmental stages. The aim of this study was to find common and stage specific QTLs involved in drought tolerance in barley.

Materials and Methods

Plant materials: 94 Double haploid (DH) lines and the parents (DOM, REC) of the Oregon-Wolfe-Barley (OWB) population were examined at two different developmental stages.

Germination stage: Tests were carried out on filter paper in plastic boxes moistened with 15 % (m/V %) poly-ethylene-glycol (PEG) resulting in an osmotic potential of –0.72 MPa, and with distilled water as control. The seeds were germinated and measured after 8 days. The shoot and root lengths were determined and its ratio under stress and non-stress conditions was used as a Tolerance Index for osmotic tolerance.

Seedling stage: Germinated seedlings were grown in half-strength Hoagland solution in the first week, and in complete Hoagland solution from the second week. The osmotic stress was induced by adding 15 % (m/V%) PEG to the solution from the second week. The Tolerance Index was calculated from the shoots dry weights at the end of the third week.

Statistical analysis and QTL mapping: The significance of differences between mean values was determined by one-way analysis of variance (ANOVA). The distribution of the phenotypic data was determined using the Statistica 6.0 software (STATASOFT INC. 2001), after which the linkage between individual marker alleles and a given phenotype was determined using the Kruskal-Wallis analysis. This was followed by simple interval mapping with maximum likelihood method (LANDER and BOTSTEIN 1989) using the program MapQTL 5 (VAN OOIJEN 2004).

Results

Mapping of QTLs influencing osmotic tolerance at germination stage

We found a great significant difference between the parents in respect of osmotic tolerance at germination stage: the parent REC was the tolerant, while the parent DOM the sensitive one. Based on the study of the OWB population, osmotic tolerance related QTLs were identified on chromosome 1(7H), 5(1H) and 7(5H) (Table 1).

Table 1: QTLs influencing osmotic tolerance at germination stage in the OWB population. Osmotic tolerance was calculated from the reduction of the root and shoot lengths under stress conditions.

Chromosome	**Marker**	**LOD**	**Phen. Var. %**
1 (7H)	*Nud*	2.68	14.4 %
5 (1H)	*Blp*	2.73	15.1 %
7 (5H)	*ABG496*	2.61	17.2 %
7 (5H)	*ABG610*	5.66	27.5 %

Mapping of QTLs influencing osmotic tolerance at seedling stage

We found a smaller, but also significant difference between the parents at seedling stage. REC was tolerant, while DOM was sensitive, similar to the germination stage. We found three QTLs affecting significantly the osmotic tolerance in barley. These QTLs were located on chromosomes 3(3H), 5(1H) and 7(1H) (Table 2).

Table 2. QTLs influencing osmotic tolerance at seedling stage in the OWB population. Osmotic tolerance was calculated from the reduction of the shoot dry weights under stress conditions.

Chromosome	Marker	LOD	Phen. Var. %
3 (3H)	*BCD907*	2.53	14.1 %
5 (1H)	*Bmag0211*	2.68	14.1 %
7 (5H)	*ABG496*	2.20	14.0 %

Discussion

At germination and seedling stages mainly different QTLs play a role with respect to the osmotic tolerance. We found in two developmental phases only one common QTL, it was located on the short arm of the chromosome 7(1H). QTLs affecting osmotic tolerance at germination stage on the chromosome 1(5H) and on the long arm of chromosome 7(1H) may be not specific for drought, because highly comparable QTLs were determined for salt-tolerance at the germination stage (WEIDNER et al. 2005), for pre-harvest sprouting and for dormancy (LOHWASSER et al. 2005) in the same population. The QTL identified on chromosome 1(7H) is linked to the morphological gene *Nud*, which is controlling the naked or hulled character of the grains. We supposed that this QTL could play a role in the germination ability of the seeds under stress conditions. Because of the non-specific character of the QTLs determined for osmotic tolerance at germination stage, the screening for drought tolerance using germination test seems to be not suitable for the selection at the adult stage.

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