QTL mapping for salt tolerance in barley at seedling growth stage

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Abstract

Barley (Hordeum vulgare L.), an important food and fodder crop, is potentially tolerant to salinity. To identify quantitative trait loci (QTLs) controlling salt tolerance, the population of 162 recombinant inbred lines (RILs) derived from F3 generation of Arigashar (an extremely salt tolerant Iranian six-rowed barley landrace) crossed with Igri (a salt semi-sensitive two-rowed cultivar) were evaluated. The growth of shoots, roots, and coleoptiles, and root numbers are four important growth characteristics severely affected by salt stress at seedling growth stages. A linkage map was constructed using 106 AFLP and SSR markers spanning six barley chromosomes including 2(2H), 3(3H), 4(4H), 7(5H), 6(6H), and 1(7H). Out of totally 26 detected QTLs, 17 QTLs were found effective for salt tolerance at 250 and 350 mM NaCl which localized on chromosomes 2H, 3H, 4H, 6H, 7H, and linkage group L1, whereas considering equivalent overlapped QTLs with a pleiotropic effect led to detection of totally 9 distinctive QTLs (QClgH2.1b, QSlgH2.1c, QNrgH2.1b, QTwgH2.2c, LSdg3Hb, QSlg4Hb1, QClg4Hb, and QSlg6Hc2) effective for salinity tolerance. 2(2H), 4(4H), and 6(6H) were major chromosomes harboring QTLs which effectively controlled salt tolerance in the Igri×Arigashar population. An interesting QTL, QTwg4Hc, was localized on chromosome 4H in the XE41-M61 marker distance that controls several traits including shoot and coleoptile lengths and shoot fresh mass under salt stress. A dense marker cluster around a resistance gene could offer a starting point for positional cloning.

Additional key words: AFLP, Hordeum vulgare, RILs, SSR.

Introduction

Soil salinity is one of the major environmental constraints limiting crop production in many parts of the world (Munns et al. 2006). Salt tolerance is a multigenic trait including salt partitioning within the plant, osmotic adjustment, and morphological changes (Munns 2005). Development and utilization of stress-resistant genotypes is an efficient approach to reduce a yield loss. Current strategies used to create more stress-tolerant crops include genetic engineering, QTLs mapping, and conventional breeding (Zhang et al. 1999a,b). Barley is an important crop species and it is an ideal material for genetic studies because of its relatively simple genetic background (Costa et al. 2001).

In barley, as in other cereals, the genome consists of a complex mixture of unique and repeated nucleotide sequences (Flavell 1980). Approximately 10 - 20 % of the barley genome is randomly arranged by repeated sequences, whereas 50 - 60 % of repeated sequences is interspersed among one another or among unique nucleotide sequences (Rimpau et al. 1980). The total genetic length of the barley maps ranges from 970 to 1873 cM, whereas the length of the most comprehensive


Abbreviations: AFLP - amplified fragment length polymorphism; LOD - logarithm of the odds value; QTL - quantitative trait locus; PAGE - polyacrylamide gel electrophoresis; RIL – recombinant inbred line; SSR - simple sequence repeat.

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