

Abstract

Cultivated barley (*Hordeum vulgare* ssp. *vulgare*) is a close relative of wheat and the fourth most important cereal crop worldwide, used for animal feed, malting and human consumption. Domestication from its wild progenitor (*H. vulgare* ssp. *spontaneum*) started around 10,000 years before present in the Fertile Crescent. Like in other crop species, barley domestication and trait selection reduced genetic variation in domesticated barley compared to wild barley populations. We utilised a mapping population derived from a cross between cultivated barley and wild barley lines from different parts of the Fertile Crescent and China to map QTLs for tiller number and awn length as two agronomically relevant traits. We identified and confirmed two QTLs for tiller number on chromosome 2H (chapter II) and one QTL for awn length on chromosome 7H (chapter IV).

One of the QTLs for tiller number was located close to the flowering time locus *Eam6*. In addition to the differences in tiller number, near-isogenic lines (NILs) differing at this locus consistently showed differences in flowering time and plant height. The other QTL co-located with the row type gene *Vrs1*. NILs differing at *Vrs1* or another row type locus (*Int-c*) exhibited differences in tiller number. To investigate whether row type genes affect tiller number directly, we studied tiller number over plant development for allelic series of mutants at nine independent row type loci (chapter III). With one exception, all row type mutations reduced total tiller number and all mutations reduced average grain size and weight. For several mutant loci (including *vrs1*), the effect on tiller number appeared to be indirect, while other loci (including *int-c*) affected tiller number directly.

The awn length QTL was confirmed with NILs differing at this locus. Using plants from two independent recombinant inbred lines (RILs) segregating for the genomic region containing the QTL, the locus was fine mapped to an interval of less than 0.5 cM. Sequencing of mRNA derived from developing apices was used as an approach for candidate gene identification. A FYVE-type zinc finger protein was identified as a candidate due to a SNP in the longer awned NIL causing an amino acid substitution disrupting an important motif of the FYVE domain.

Understanding the genetic bases of correlations between agronomic traits is important for the genetic manipulation of individual yield components. This work introduces a novel mapping population including wild and cultivated barley useful for QTL analyses. It emphasizes the relevance of pleiotropic effects among seemingly unrelated traits such as row type and tiller number and describes an approach for fine mapping and candidate gene identification.

