

# Identification of QTL associated with drought tolerance in barley (*Hordeum vulgare* L.)

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## Abstract:

One hundred fifty eight recombinant inbred lines (RILs) derived from a cross between the cultivars Tadmor (drought tolerant) and Er/Apm (drought susceptible) were grown at Ghwair agricultural research station in order to identify quantitative trait loci (QTL) for grain yield and its components. A linkage map including 87 AFLP markers assigned to 14 linkage groups was constructed with genome distance coverage of 1321.7cM. This covered 94.4 % of barley genome. Single-marker analysis, and interval marker analysis, including interval mapping (IM) and composite interval mapping (CIM), were used for QTL identification. Thirty-one QTL were identified for the measured characters, using a significant threshold of 2.5 LOD, in both IM and CIM. The phenotypic variation explained by individual QTL ranged from 2% to 82.1%. In total, 32 and 47 different QTL were detected by IM and CIM respectively. Several major QTL were shown to be linked to two or more traits, this was evident at linkage group 1, where one QTL affected grain yield and tiller number; spike width, harvest index and biological yield; awn length, spike width and harvest index; fertile tiller number and harvest index. For linkage group 2, where four QTL affected harvest index, days to heading, and peduncle length For linkage group 3, where one QTL affected node number and leaf width. These QTL might be utilized as a beginning basis for cloning specific genes in barley improvement.