TOWARDS THE FINE MAPPING OF Fr-H2 – A MAJOR QTL CONTROLLING FROST RESISTANCE IN BARLEY


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Barley (Hordeum vulgare) is an economically important diploid model for the Triticeae. We developed a new resource for genetic analysis of winterhardiness-related traits, the Nure (winter) x Tremois (spring) barley mapping population. Two low temperature QTLs were found to segregate on the long arm of chromosome 5H. A first distal QTL for low-temperature tolerance was identified at the VrnH1/Fr1 region (Fr-H1). A second proximal QTL for low-temperature tolerance was identified (Fr-H2) and it was coincident with the QTLs regulating the accumulation of two different and well characterized COR proteins (COR14b and TMC-Ap3). A population of 1,849 recombinant plants was constructed and the resulting F3 families harboring none, both and only one QTL were phenotypically tested for validation of the two QT loci Fr-H1 and Fr-H2.

The frost tolerance of F3 selected recombinants was evaluated under controlled conditions (growth chamber) on cold acclimated plants in the first leaf stage. The frost-induced damage was measured in the leaves as a decrease in the photochemical capacity of photosystem II (PSII), using the chlorophyll fluorescence parameter Fv/Fm. Our results provide a useful advance for the isolation of the genetic determinants of Fr-H2 and Fr-H1, the two major loci of low-temperature tolerance in cultivated barley. Having validated the presence of these two QTLs in the Nure x Tremois cross, we are concentrating our efforts towards the positional cloning of Fr-H2. In this view, reciprocal QTL-NILs at Fr-H2 are being developed, and a high-resolution genetic map of the HvCBF gene cluster is being constructed in order to find informative recombinants amongst the HvCBF candidates.