

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

E. FRANCIA*,****, D. BARABASCHI*,****, A. TONDELLI*, G. LAIDÒ*, F. RIZZA*,
A.M. STANCA*, M. BUSCONI**, C. FOGHER**, E.J. STOCKINGER***, N. PECCHIONI****

*) CRA Istituto Sperimentale per la Cerealicoltura, Sezione di Fiorenzuola d'Arda (PC), I-29017, Italy

***) Università Cattolica del Sacro Cuore, Facoltà di Agraria, Piacenza, I-29100, Italy

****) Department of Horticulture and Crop Science, The Ohio State University/OARDC, Wooster, OH-44691, USA

*****) Università di Modena e Reggio, Facoltà di Agraria, Reggio Emilia, I-42100, Italy

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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 winterhardness-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.