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# Mapping candidate genes for drought tolerance in barley

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Barley is an important diploid model for the *Triticeae* (Hayes *et al*., 2003). In order to study in an unique genetic system drought and cold stresses a new genetic map based on the Nure x Tremois (NT) doubled-haploid population has been developed (Francia *et al*., 2004). The winter parent Nure – Italian two-rowed feed-barley cultivar– has a wide range of adaptability, including South European environments. The spring parent Tremois –French two-rowed malting variety– is adapted to fertile environments.

Besides the NT population, two other well characterized barley segregating populations (i.e. Steptoe x Morex, and Proctor x Nudinka) have been used to map candidate genes (CGs) involved in the response to abiotic stresses (Table 1).

Table 1. Candidate genes for abiotic stress tolerance mapped in this work by linkage analysis

| Gene name | Accession No. | Mapping population† | Gene name | Accession No. | Mapping population† |
|---|---|---|---|---|---|
| HvZFP1 | BQ761311 | NxT | HvCBF2B | AF442489 | NxT |
| HvMYB2 | X70880 | NxT | HvCBF3A | AF298231 | NxT |
| HvPRR (Ppd-H1) | AY970701 | SxM | HvCBF4 | AF298230 | NxT |
| HvBM8 | AJ249146 | NxT | HvCBF6 | AY785860 | NxT |
| HvMYB4 | X99973 | PxN | HvCBF10B | AY785885 | NxT |
| HvCDPK7 | TC146711 | SxM | HvCBF12 | DQ095157 | NxT |
| HvMYB-like1 | TC140881 | SxM | HvMYB1 | X0879 | NxT |
| HvGAMyb | AY008692 | SxM | HvBM5a (Vrn-H1) | AJ249144 | NxT |
| HvWCK-1 | AF79318 | SxM | HvWRKY38 | AY541586 | NxT |
| HvBM1 | AJ249142 | PxN | HvSAD | AJ312297 | NxT |
| HvZCCT-H (Vrn-H2) | AY485978 | NxT | HvKGM | AY167561 | SxM |
| HvLOS2 | TC138581 | NxT | HvFRY1 | TC147474 | NxT |
| HvBPBF | AJ000991 | NxT | HvFT-like | TC237313 | SxM |
| HvABI5 | AY156992 | NxT | HvICE1 | TC104574 | PxN |
| HvCBF8 | AY85868 | NxT | HVP1 | AB032839 | NxT |

†NxT: Nure x Tremois; PxN: Proctor x Nudinka; SxM: Steptoe x Moex.

Linkage analysis in the individual mapping populations was performed with the software MAPMAKER 3.0 by adding the markers to the available 'NxT', 'PxN' and 'SxM' (http://wheat.pw.usda.gov) linkage maps. The consensus map including mostly transcription factors was then constructed by using the software JoinMap 2.0 (Fig. 1; Tondelli *et al*., 2006). The final marker order was compared with the order of each constituent map, and as main reference, with the barley BIN map (Kleinhofs and Graner, 2001).

The candidate gene strategy shows promise to bridge quantitative and molecular genetics to study complex traits such as barley adaptation to drought.

Co-location of QTLs along with CGs putatively related to plant response to adverse environmental conditions has been found in our preliminary analyses. Complementary validation experiments should be conducted to confirm the actual involvement of a co-segregating CG in the trait variation, including association mapping and expression studies (Pflieger *et al*. 2001), but above all genetic transformation. A validated CG could then represent a very efficient molecular marker for MAS applications. In the case of regulatory CGs the integration of favourable alleles into a genotype should have the consequence of activating a cascade of molecular responses, resulting in a major effect on the phenotype. This MAS strategy would lead to improvement of barley as well as of other *Triticeae* species in abiotic stress tolerance and, consequently in grain yield in limiting conditions.

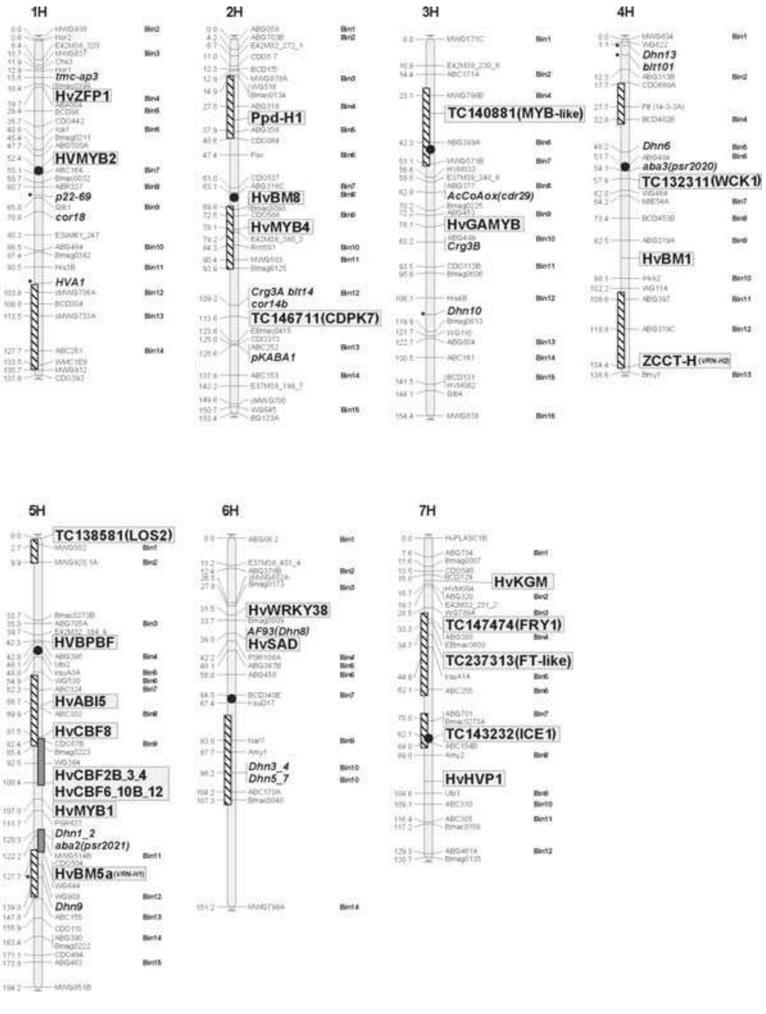

Fig. 1. The barley consensus function map. Candidate genes either collected from GenBank accessions (Hv-) or obtained by homology searches (TC-) mapped in this study are boxed. *COR* and other abiotic stress-induced effector genes are in bold italic. *Solid* and *hatched* boxes inside chromosomes represent cold and drought tolerance QTLs currently available in the barley literature (Francia *et al*., 2004; Diab *et al*., 2004).

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