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Poster Abstract - C.11

A NEW BARLEY CONSENSUS FUNCTION MAP OF ABIOTIC-STRESS RELATED GENES

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The integration in an ideal genotype of favourable alleles at candidate genes having major effect on observed variability for tolerance to abiotic stresses will lead to improvement of barley productivity in stressful conditions. In order to study in an unique genetic system drought and cold stresses, a new barley consensus function map has been developed, based on three well characterized mapping populations: 'Nure' x 'Tremois' (NxT), 'Steptoe' x 'Morex' (SxM) and 'Proctor' x 'Nudinka' (PxN).

The candidate-gene (CG) strategy was here applied to find putative candidates for barley abiotic-stress tolerance: barley CGs were selected from literature and GenBank database screening on the basis of their involvement in abiotic-stress response. Greater importance was here given to transcription factors and regulatory genes rather than to structural genes, because a transcription factor usually can regulate the expression of several downstream stress-responsive genes.

Candidates were screened on the six parental genotypes using Single Strand Conformation Polymorphism (SSCP) technique, to search for Single Nucleotide Polymorphisms (SNPs) and short INsertion/DELetions (INDELs). Depending on the polymorphism type, new CAPS, ARMS-PCR and SSCP markers were developed to map CGs on the NxT, PxN and SxM populations. Based on the presence of markers in common to the three linkage maps, segregation data were analyzed with anappropriate software to create the initial barley consensus function map.

The inferred position on the molecular consensus map of previously reported QTLs for barley frost- and drought-tolerance revealed, among the functional candidate genes mapped, some interesting positional candidates. These results represent a good example of the application of the candidate-gene approach for the dissection of a complex phenotypes such as the tolerance to abiotic stresses. Complementary validation experiments are being conducted to confirm the actual involvement of co-segregating CGs in the traits variation.