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Stress tolerance in cereals: From genomics to tolerant varieties

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The molecular dissection of the abiotic stress response has revealed a complex situation, where the co-ordinated expression of many stress-related genes is associated with resistance. The lecture will present data obtained from several genomics studies focussed on the understanding of the genetic/molecular bases of cold and drought resistance in barley and wheat. A QTL approach has led to the identification of few major QTLs controlling stress resistance. The comparison of mapping data and expression studies has allowed the identification of several candidate genes (*Cbf* and others) whose analysis is presently in progress. Affymetrix chips and Real Time Q-PCR have been used for analysis of gene expression in response to cold in barley chloroplast mutants showing a complete susceptibility to frost and in response to drought in wheat cultivars with contrasting level of stress resistance. We have shown that barley plants carrying a mutation preventing chloroplast development, beside the expected *albino* phenotype, are completely frost susceptible as well as impaired in the expression of several *cor* (cold-regulated) genes. Functional genomic studies are in progress to define the function of genes related to cold acclimation or dehydration through the identification and the analyses of *A. thaliana* homozygous T-DNA knock-out lines carrying an insertion in sequences homologous to the genes isolated in response to stress in barley. A physiological characterization of the insertional lines will be presented.