

## Abstract

The aim of this dissertation was to study the mechanism of cold acclimation via the dynamics of cold regulated proteins (such as WCS120 or DHN5) in different frost-tolerant wheat and barley cultivars. Mass spectrometry analysis of a total sample of proteins, soluble upon boiling, showed qualitative differences between cold-acclimated (e.g., 7 COR proteins) and non-acclimated (e.g., only 3 COR proteins) samples of the winter wheat Mironovskaya 808. Furthermore, by 2-DE or W-blot analysis, there were found quantitative differences in the accumulation of WCS120 proteins between cultivars, grown under different time, photoperiod, and/or temperature conditions. The higher levels of WCS120 proteins are associated with higher frost tolerance of cultivars, grown under constant and low temperature. However, the dynamics of WCS120 proteins during long-term cold-acclimation, with periods of de-acclimation and re-acclimation, demonstrated that plants with the same level of frost tolerance could be distinguished by the level of accumulation of the WCS120 proteins. These results indicated that developmental genes influence the ability to re-accumulate WCS120 proteins by the partial vernalization of plants, while the ability to induce high frost tolerance was only influenced by the saturation of vernalization. Using five wheat and two barley cultivars with different abilities to resist frost, it was also shown that dry weight content, frost tolerance and accumulation of dehydrins (WCS120 in wheat, or DHN5 in barley) in the leaves is both tolerance- and temperature-dependent.

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