

PROJECT TITLE

Evaluation of physiological and biochemical characteristics changes of winter wheat Sucrose synthase1 (SS1) nonsense mutants during cold acclimation

CONSORTIUM

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SUMMARY OF THE REPORT

Freezing tolerance of winter wheat develops during cold acclimation, which is triggered by the induction of cold-responsive genes at low temperatures. Sucrose synthase (E.C. 2.4.1.13) is one of the main enzymes of carbohydrate metabolism and it shows increased expression and activity during cold acclimation in winter wheat. The main aim of this project was to verify if premature stop codon mutation (W374*) of Sucrose synthase 1 (SS1) gene identified in M631 from winter wheat TILLING population affects physiological and biochemical changes of SS1 mutants compared with WT plants during cold acclimation and additionally at the later stages of plant development. Four sinter lines (SL01, SL02, SL03 and SL14) of SS1 mutant were chosen for experiments. Specific primers were constructed to subgenomes A, B and D of wheat SS1 gene to aiming to identify in which subgenome mutation is localized. Results showed that mutation (W374*) is localized in D subgenome of SS1 gene in all sister lines. The freezing test showed that all mutant M631 sister lines are less freezing tolerant compared with WT plants. Project phenotyping experiments were carried out at the Finnish National Plant Phenotyping Infrastructure (NaPPI) located at the University of Helsinki. Small NAPPI unit was employed to identify if this mutation affects plants during cold acclimation. Four sinter lines of SS1 mutant and WT plants were grown under cold acclimation conditions at plant growth chamber for 9 weeks. RGB, Thermal and Chlorophyll fluorescence cameras were used to take images of plants once per week. Results revealed that SS1 mutant sister lines grew faster and higher compared with WT, so was decided to carry out phenotyping of mutant plants from tillering to the flowering stage at large NAPPI unit. Same genotypes were sown and vernalized for 8 weeks and later transferred to large NAPPI unit. Total 15 biological replications per genotype were phenotyped each two to days using RGB side cameras (0°, 120° and 240° angle) for four and a half month. Results showed that morphological parameters such green leaf area, perimeter, width and height of SS1 mutant sister lines were significantly higher comparing WT plants starting from booting stage (GS45). After this experiment was done plants were kept until the seeds were ripened and multiplied seeds will be used for further research. Valuable results obtained from phenotyping will contribute to the validation of SS1 gene role in the cold acclimation process and it is the first step to use it as a marker for selection of freezing tolerance genotypes of winter wheat.