

## Leaf Proteome and Metabolome Analysis of Wheat-rye Translocation Lines

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### [Introduction]

Wheat (*Triticum aestivum* L.,  $2n=6x=42$ , AABBDD) grain is the principal cereal as the second most produced food among the whole cereal crop. Cultivated rye (*Secale cereal* L.,  $2n=2x=14$ , RR) is one of the major cereal crops for both grain and forage. Several molecular breeding has been attempted through the introgression of rye chromosome arms to wheat chromosome for the consistently resistant wheat-rye translocation lines. Recently the yield potential of wheat grain has been increased by acquiring traits for the biotic and abiotic tolerance. The present study was focused on the proteomic profiles of leaf, stem and root from 2BS.2RL wheat-rye translocation line.

### [Materials and Methods]

The three lines (Coker797, Hamlet and Near Isogenic Line) were used. For proteomic analysis, the leaves were cut and quickly frozen in deep freezer prior to use. The wheat proteins solubilized in Rehydration Buffer were quantified by a modified Bradford method. 2-DE electrophoresis was performed to confirm the protein separation and MALDI-TOF/TOF MS was applied to identify the proteins.

### [Results and Discussion]

Wheat-rye translocation lines were developed to produce a main crop resistant to biological and physical stress. “Chaupon” rye contains 2RL chromatin to harbor resistance genes for powdery mildew and leaf rust. In order to identify chromosome 2RL-derived rye proteins and 2RL-perturbed proteins in wheat-rye translocation lines, the gel-based proteomics was employed with “Coker797” (non-2RL), “Hamlet” (2RL) and “near-isogenic line” (stabilized 2RL). The leaf proteome was resolved on 2D-gel, resulting in 216 spots in a final selection. A total of 90 proteins were identified with the identification success rate of 42%. The identified proteins were classified by functional annotation: metabolism (64%), cellular process (5%), translation (2%), regulatory function (1%) and hypothetical (28%). The proteins belonged to metabolism were subdivided into carbohydrate metabolism (36%), energy metabolism (35%), metabolism of lipid, amino acid, other amino acid and biosynthesis of secondary metabolites (each 6%) and others (5%). A total of 53 proteins were differentially expressed, in which  $\beta$ -glucosidase, in particular, originated from the chromosome 2RL of rye, was exclusively appeared in NIL. In addition, small Ras-related GTP binding-protein assigned to wheat was predominantly found in 2RL rye chromatin-possessing NIL. These results suggest that the acquired genetic traits obtained from rye 2RL enhance the resistance to biotic and abiotic stress in wheat-rye translocation lines by altered the proteome expression. In leaf metabolome analysis, 11 predominant metabolites containing trans-aconitate, glutamate, and betaine were identified by 1H-NMR-based metabolite fingerprinting. The overall metabolites pattern of NIH appears to be closer to Coker797 rather than Hamlet. Thus, the metabolic phenotype of NIL was not so much lineated from Hamlet contrast to proteomic phenotyping.

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