

## **D-D2-33**

### **Optimization of protein extraction and preparation from wheat-rye translocation lines for 2D gel-based proteomic analysis**

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The wheat-rye translocation lines have been agriculturally developed for the resistance to the biotypes of Hessian fly as a major insect pest of wheat. In order to compare the proteomic profiles between 'Coker797' (non-2RL), 'Hamlet' (2RL), and near-isogenic line (NIL) carrying 2RL, we evaluated the protein extraction and preparation methods for two-dimensional gel electrophoresis approach. The tissues such as leaves, stems, and roots from three wheat-rye lines were extracted by following trichloroacetic acid (TCA)/acetone precipitation. In a preliminary proteome analysis, a commonly expressed protein in Hamlet and NIL strain was identified as methionine synthase annotated in *Hordeum vulgare* subsp. The present study will provide the experimental guideline for the proteomic study of other useful crop plant tissues.

## **D-D2-34**

### **Characterization of the epistatic effects and QTL×environment interactions on the chemical constituents of rice**

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The objective of this study was to characterize the epistatic QTLs and QTL-by-environment interactions (QE), which are involved in the control of amylose, protein and lipid content. A population of doubled haploid (DH) lines derived from a cross between 'Samgangbyeon', a Tongil type rice variety, and 'Nagdongbyeon', a japonica rice variety, was used, and data were collected from a field experiment conducted in three years. A genetic linkage map consisting of 172 marker (SSR and STS) loci was constructed, and QTLMAPPER version 1.6 was used for the detection of epistasis and QE interactions. Digenic epistatic effects for three physico-chemical traits were detected in fifteen pairs of loci, five of which for lipid and protein content involved three main effect QTLs. On the whole, the additive-by-additive effects totally accounted for 12.99%, 26.67% and 40.80% of phenotype variations for amylose, lipid and protein content, while the interactions between environment and additive effect of single locus, or digenic epistatic effect totally accounted for 2.97%, 2.71% and 2.26% or 2.08%, 1.26% and 1.75% of phenotype variations for three traits, respectively.

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