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Protein profiling in disomic addition lines of wheat carrying *Leymus racemosus* chromosomes

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Abstract

Wheat wild relatives that have never been domesticated contained useful genetic resources such as the resistance to abiotic and biotic stresses. *Leymus racemosus* is one of the wild species. It can grow in a harsh environment like seaside and distribute by healthy rhizomes. Also, it has a useful genetic resource such as salt tolerance and different diseases resistance. Wheat (*Triticum aestivum* L. cv. Chinese Spring; CS) was crossed with *L. racemosus*. Wheat-*L. racemosus* disomic addition lines were produced. The purpose of this study is to identify protein expression in each disomic addition line compared to CS. We performed two-dimensional electrophoresis. Two-dimensional gels stained with coomassie brilliant blue (CBB), a total of 1566 differentially expressed proteins were identified by Progenesis Same Spots software from the cultivars. However, a total of 90 protein spots were identified to be either present or absent or showing significantly differential expression when the difference threshold was set to more than 1.5 fold. However, out of the 90 differentially protein spots, a total of 74 spots were sorted for mass spectrometry analysis. The identified proteins may provide important clues for better understanding the molecular changes in the chromosomes carrying *Leymus racemosus*.

Keywords: wheat, *Leymus racemosus*, protein expression

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