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Comparative proteome analysis of seeds of proso millet (*Panicum miliaceum*) cultivars

Swapan Kumar Roy¹⁾, Soo Jeong Kwon¹⁾, Hyeong-Jun Park¹⁾, Je-Hyeok Yu¹⁾, Kabita Sarker¹⁾, Seong-Woo Cho²⁾, Tae-Wook Jung³⁾, Cheol-Ho Park⁴⁾, and Sun-Hee Woo^{1*)}

¹⁾ Dept. of Crop Science, Chungbuk National University, Cheong-ju 28644, Korea

²⁾ Department of Crop Science and Biotechnology, Chonbuk National University, Jeon-ju 54896, Korea

³⁾ Rural Development Administration, Jeon-ju 54875, Korea

⁴⁾ College of Biomedical Science, Kangwon National University, Chuncheon 24341, Korea

Abstract

Since the composition of proteins from the Korean cultivars of Proso millet is unknown; thereby, the present study was conducted to obtain a reference map of millet seed proteins and identify the functional characteristics of the identified proteins. Proteins extracted from the millet seeds of various cultivars, were investigated using proteomic techniques as 2D electrophoresis coupled with mass fingerprinting. The 1152 (differentially expressed) proteins were detected on 2-D gel. Among them, 26 reproducible protein spots were analyzed by MALDI-TOF-TOF mass spectrometry. Out of 26 proteins, 2 proteins were up-regulated towards all cultivars of millet, while 7 proteins were up-regulated and 13 proteins were down-regulated against only one cultivar. However, abundance in most identified protein species, associated with metabolism, transcription and transcription was significantly enhanced, while that of another protein species involved in polysaccharide metabolism, stress response and pathogenesis were severely reduced. Taken together, the results observed from the study suggest that the differential expression of proteins from the four cultivars of millet may be cultivar-specific. Taken together, a proteomic investigation of millet seeds from different cultivars, we sought to better understand the genetic variation of millet cultivars representing the future millet research, and the functional categorization of individual proteins on the basis of their molecular function.

Keywords: seed protein; protein profiling; proso millet; 2-DE

Corresponding author*

Sun-Hee Woo

Address: Chungbuk National University, 1, Chungdae-ro, Seowon-gu, Cheongju-si, Chungbuk 28644

Korea (Republic of)

Fax: +82-43-273-2242

Tel: +82-43-261-2515

E-mail: shwoo@chungbuk.ac.kr