

Uncovering the Proteome Characterization of Tartary Buckwheat (*Fagopyrum tataricum*) using Domestic and Overseas Cultivars

Ju-Young Choi¹, Seong-Woo Cho², Swapan Kumar Roy¹, Soo-Jeong Kwon¹, Sun-Hee Woo^{1*}

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

²Dept. of Crop Science and Biotechnology, Chonbuk National University, Jeon–ju 54896, Korea

[Introduction]

Unlike common buckwheat, tartary buckwheat remains in the wild as an autogamous. The buckwheat belongs to a wide range of proteins. However, Buckwheat proteins are demonstrated to be rich in lysine, arginine and asparagine acids compared to other plants and crops, and the composition of amino acids is superior in nutrition. In addition, it is also rich in minerals such as zinc, magnesium, manganese, copper and iron, and has high levels of vitamins B1, B2, and E. Furthermore, this type of tartary buckwheat is rich in various nutrients, and its protein content is high (12%) and fat content (3.9%).

[Materials and Methods]

We used a tartary buckwheat collection gene. Seven of the 100 collectors were selected. The selected genetic sources are Kochang County (CBU263), Nepal Khairenitar (CBU280), Slovenia Sevnica (CBU287), China Batang Sichuan (CBU301), China Zhongza sichuan (CBU302), China Xinning (CBU305), China Yunnan (CBU307). SDS-PAGE (sodium dodecyl sulfate polyacrylamide gel electrophoresis) was used in the electric dynamic system (Company EIDO NA-1013).

[Results and Discussion]

In this study, as part of the analysis of proteomics in each country, we compared the expression patterns of the protein in the seed, discovered the unique expression protein, and characterized with it to obtain basic data. Using SDS-PAGE, the seeds storage protein development patterns of the buckwheat gene sources were compared for each country. The first SDS-PAGE electro-motivation resulted in the generation of Band's expression for each species being 32, 35, 47, and 49 kDa common parts. In particular, the protein content of Slovenia Sevnica (CBU287) was found to be high compared than Slovenia Sevnica (CBU287), China Yunnan (CBU307), China Xining (CBU305), and Nepal Khaireenit. The second SDS-PAGE electro-motivation resulted in China's Batang Sichuan (CBU302) oil field being unique in 45–49 kDa areas. According to the analysis of China Batang Sichuan (CBU301), which is a source of electricity collected in the same country, the comparison group showed similar expression to that of Koh Chang-gun (CBU263). Also, the China Batang Sichuan (CBU302) gene has high protein content at 23 kDa unlike other genetic sources. The comprehensive seed proteome was performed to examine the molecular characterization in Buckwheat. Extracted seed proteins were separated using 2-DE and the spot patterns were compared. The protein spots from the different cultivars showed pronounced differential expression between domestic and overseas cultivars.

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*Corresponding author: E–mail, shwoo@chungbuk.ac.kr