

The mitochondrial proteome analysis in wheat roots

Da-Eun Kim¹⁾, Swapan Kumar Roy¹⁾, Abu Hena Mostafa Kamal¹⁾, Soo Jeong Kwon¹⁾, Kun Cho²⁾,
Seong-Woo Cho³⁾, Chul-Soo Park⁴⁾, and Sun-Hee Woo^{1*)}

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

²⁾ Mass Spectrometry Research Center, Korea Basic Science Institute, Chungbuk 28119, Korea

³⁾ Lab. of Molecular Breeding, Arid land Research Center, Tottori University, Japan

⁴⁾ Dept. of Crop, Agriculture and Life Science, Chonbuk National University, Jeonju 54896, Korea

Abstract

Mitochondria are important in wheat, as in all crops, as the main source of ATP for cell maintenance and growth including vitamin synthesis, amino acid metabolism and photorespiration. To investigate the mitochondrial proteome of the roots of wheat seedlings, a systematic and targeted analysis were carried out on the mitochondrial proteome from 15 day-old wheat seedling root material. Mitochondria were isolated by Percoll gradient centrifugation; and extracted proteins were separated and analyzed by Tricine SDS-PAGE along with LTQ-FTICR mass spectrometry. From the isolated the sample, 184 proteins were identified which is composed of 140 proteins as mitochondria and 44 proteins as other subcellular proteins that are predicted by the freeware subcellular predictor. The identified proteins in mitochondria were functionally classified into 12 classes using the ProtFun 2.2 server based on biological processes. Proteins were shown to be involved in amino acid biosynthesis (17.1%), biosynthesis of cofactors (6.4%), cell envelope (11.4%), central intermediary metabolism (10%), energy metabolism (20%), fatty acid metabolism (0.7%), purines and pyrimidines (5.7%), regulatory functions (0.7%), replication and transcription (1.4%), translation (22.1%), transport and binding (1.4%), and unknown (2.8%). These results indicate that many of the protein components present and functions of identifying proteins are common to other profiles of mitochondrial proteins performed to date. This dataset provides the first extensive picture, to our knowledge, of mitochondrial proteins from wheat roots. Future research is required on quantitative analysis of the wheat mitochondrial proteomes at the spatial and developmental level.

Key words: mitochondrial proteins, wheat Roots, SDS-PAGE, LTQ-FTICR, proteomics

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