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Aluminum toxicity-induced alterations of root proteome in wheat seedlings

Myeong Won Oh¹⁾, Swapan Kumar Roy¹⁾, Kun Cho²⁾, Seong-Woo Cho³⁾, Chul-Soo Park⁴⁾,
Keun-Yook Chung⁶⁾, Jong-Soon Choi⁵⁾, 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

⁵⁾ Division of Life Science, Korea Basic Science Institute, Daejeon 34133, Korea

⁶⁾ Department of Environmental & Biological Chemistry, Chungbuk National University, Cheong-ju 28644, Korea

Abstract

Aluminum is the most abundant metallic element in the Earth's crust and considered as the most limiting factor for plant productivity in acidic soils. The inhibition of root growth is recognized as the primary effect of Al toxicity. Seeds of wheat cv. Keumkang (Korean cultivar) were germinated on petridish for 5 days and then transferred hydroponic apparatus which was treated with 0 μM AlCl_3 (control), 100 μM AlCl_3 and 150 μM AlCl_3 for 5 days. The length of roots, shoots and fresh weight of wheat seedlings were decreased under aluminum stress. The concentrations of K^+ , Mg^{2+} and Ca^{2+} were decreased whereas Al^{3+} and P_2O_5^- concentration was increased under aluminum stress. Using confocal microscopy, the fluorescence intensity of aluminum was increased with morin staining. In this study, a proteome analysis was performed to identify proteins, which is responsible to aluminum stress in wheat roots. In 10-day-old seedlings, proteins were extracted from roots and separated by 2-DE, stained by CBB. Using image analysis, a total of 47 differentially expressed protein spots were selected, whereas 19 protein spots were significantly up-regulated such as s-adenosylmethionine, oxalate oxidase, malate dehydrogenase, cysteine synthase, ascorbate peroxidase and 28 protein spots were significantly down-regulated such as heat shock protein 70, o-methyltransferase 4, enolase, amylogenin by aluminum stress following protein spots analyzed by LTQ-FTICR mass spectrometry. The results provide the global picture of Al toxicity-induced alterations of protein profiles in wheat roots, and identify the Al toxicity-responsive proteins related to various biological processes that may provide some novel clues about plant Al tolerance.

Keywords: aluminum stress, LTQ-FTICR-MS, proteomics, wheat root, 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