# [O12] Concepts, Prospects, and Potentiality of Crop Production in East Asia

*Sponsored by the Korean Society of Crop Science
Chair: Sang-In Shim (Gyeongsang National University, Korea)
Chair: Takeo Sakaigaichi (Kyushu Okinawa Agricultural Research Center, National Agriculture and Food Research Organization, Japan)
Chair: Hiroshi Ehara (Nagoya University, Japan)
2021年9月9日(木) 14:30 ～ 16:30 Room 1 (Oral) (Field Crop Production)

15:55 ～ 16:10

## [O12-06]Physiological and Proteome Analysis in *Brassica napus* L. of Leaves in Response to Copper Stress and Citric-Acid Application

*Nominated for Presentation Awards

○Yong-Hwan Ju[1], Ju Young Choi[1], Swapan Kumar Roy[1], Soo Jeong Kwon[1], Kwang Soo Kim[2], Sun Hee Woo[1]
(1.Dept of Crop Science, Chungbuk National University, Korea, 2.Bio-Energy Plant Research Center, National Institute of Crop Science, Korea)

Copper (Cu) is one of the essential nutrients but excess Cu induces phytotoxicity, leading to inhibit plant growth characteristics. This study aimed to invest the proteome changes of *Brassica napus* L. under Cu stress and Citric-acid (CA) application over 7 days. The 21-days-old seedlings were exposed to different concentrations of Cu (25 and 50μ M $CuSO_4$) and CA (1.0 mM). Results showed that the fresh and dry weights of Cu + CA treated seedlings were higher than those of the Cu treated seedlings. The application of CA further enhanced the activities of antioxidant enzymes as compared with their respective Cu-only treatment. Using the gel-free proteome approach, a total of 1473 proteins were successfully identified in *B. napus* seedlings. Of these, 67 proteins were identified only in Brassica species, whereas 36 proteins identified from *B. napus* that were classified as differentially abundant proteins (DAPs). Among the 36 proteins, a total of 21 proteins were upregulated and 15 proteins were downregulated Cu stress and CA application treated. To understand molecular functions and biological processes involved in *B. napus* response to Cu stress, Gene Ontology analysis was performed whereas the most of the DAPs were annotated to protein metabolism, fatty acid biosynthetic process, TCA cycle, carbon fixation, photorespiration, fructose catabolic process and glyoxylate cycle. Taken together, this study may provide new insights into the molecular mechanisms of plant response to Cu stress, and CA application may alleviate the stress symptoms.