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## Physiological and Proteomic Changes of *Brassica napus* L. Under Copper Stress

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### [Introduction]

Recently, contaminants, including heavy metals have been increased by mining waste, garbage reclamation, and industrial effluents. It is difficult to remediate by itself and it could affect to people, so remediation is essential. *Brassica napus* L. has higher copper tolerance than other plants and can remediate metals from contaminated soils. Copper (Cu) is one of the essential nutrients for plant growth and development, but excess Cu in the soils may interrupt normal plant growth and development. However, exogenous citric acid (CA) could enhance the uptake of heavy metals in *B. napus* and tolerance to toxicity of heavy metals, when its small amount is applied. In this study, we investigate physiological, biochemical and proteome changes under Cu stress.

### [Materials and Methods]

The seeds (*B. napus* cv. Jungmo 7001) were collected from Mokpo in Korea. The seeds were germinated in growth chamber at 25~23°C for 3 days. After 3 days, uniformed seedlings were selected and germinated 4 days more. After germinating uniformed seedlings were transferred into a box containing Hoagland's solution. The solution was changed every 3 days and maintained continuous aeration. After two weeks, the various concentration of Cu and CA were treated on plants for 5-days. The plants were exposed to various treatments of CuSO<sub>4</sub> and CA as Cu (25 µM), Cu (50 µM), CA (1.0 mM), CA (1.0 mM) + Cu (25 µM), and CA (1.0 mM) + Cu (50 µM) whereas control was treated by nothing. After treatment, the plants were harvested and measured physiological, biochemical and proteome analysis.

### [Results and Discussion]

The morpho-physiological parameters were decreased by Cu stress. The fresh weight, dry weight, SPAD values, and chlorophyll contents were decreased, however when brassica was exposed to Cu with CA, these parameters were slightly increased. Proline contents were increased by Cu whereas slightly decreased by CA. Accumulation of Cu was increased when *B. napus* seedlings were exposed to Cu but when rapes exposed to Cu with CA, Cu accumulation was more increased. Using the label-free proteomics, a total 937 proteins were identified in rape exposed to Cu stress. Of these, a total of 213 differentially abundant proteins (DAPs) were identified in response to Cu stress. For investigating these proteins, proteins were categorized using Gene ontology (GO) analysis based on biological process, cellular component, and molecular functions. In biological process, 14 proteins were identified about response to cadmium ion and 3 proteins were identified about response to copper ion. In cellular component, 36 proteins were categorized about apoplast. In molecular function, each 14 proteins were identified about ATP binding and protein binding. Taken together, this study may provide new insights into the molecular mechanisms of plant response to Cu stress.

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