

## [P3] Abiotic Stress for Crop Production

2021年9月9日(木) 12:15 ~ 14:00 Room 3 (Poster) (Abiotic Stress for Crop Production)

12:15 ~ 13:00

### [P3-47] Integrated Transcriptome and Proteome Analysis Reveals Complex Regulatory Mechanism of Maize (*Zea mays* L.) in Response to Zinc Deficiency Stress

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Zinc (Zn) is one of the essential micronutrients for plant growth and development. To investigate the molecular mechanism of maize response to Zn-deficiency stress, maize variety ZD958 was used to perform transcriptome and proteome integrated analysis. Through transcriptome analysis in maize roots under Zn-deficiency stress for 10 days (10DAT) and 15 days (15DAT), we identified 271 and 519 differentially expressed genes (DEGs) at 10 and 15 DAT, while 2048 and 2380 DEGs were identified in leaves at 10 and 15 DAT, respectively. A total of 1258 and 1099 differentially abundant proteins (DAPs) were found from roots and leaves at 10 DAT in proteome data, while 627 and 1553 DAPs at 15 DAT, respectively. DEGs or DEPs involved in ROS, carbohydrate metabolic process, signal transduction, phenylpropanoid biosynthesis and nitrogen metabolism were enriched in roots, while photosynthesis including chlorophyll synthesis, metabolic process of carbohydrate, reactive oxygen species (ROS), cellular amino acid and gene expression were changed among the identified DEGs or DEPs in maize leaves. Detail analysis of the DEGs or DEPs revealed that complex metabolism, such as photosynthesis, mitogen-activated protein kinase (MAPK) signaling cascade, activation of antioxidant and nitrogen metabolism, were participated in regulating Zn deficiency response in maize. Information provided in this omics research advanced our understanding of the molecular response mechanisms to Zn-deficiency, and further research is needed to cognize the new response genes.