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Metabolomics and proteomics analysis of stripe rust resistant wheat near-isogenic line Taichung 29*6/Yr10

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Metabolomics and proteomics analysis of stripe rust resistant wheat is helpful for understanding the mechanism of resistance. Wheat near-isogenic line Taichung 29*6/Yr10 is breeded and it contains a stripe rust resistant gene Yr10. Based on GC-MS method performed on a GC-MS QP 2010 Plus (Shimadzu), metabolomics analysis of near-isogenic line Taichung 29*6/Yr10 and its backcross parent showed that 136 and 143 peaks were detected, respectively and a total of 121 metabolites were identified. Among all identified metabolites, eight of them had high levels in Taichung 29*6/Yr10 and most of them were organic acids, while 13 of them had low levels and most of them were alkanes. Meanwhile, based on label-free quantitative method performed on an Orbitrap Ms, Q Exactive Plus (Thermo Fisher), proteomics analysis of Taichung 29*6/Yr10 and its backcross parent showed that a total of 2,257 proteins were identified in the two samples, including 1549 proteins with accurate quantitative information and 102 differentially expressed proteins whose content changed more than twice. Functional enrichment analysis showed that most of them were located in organelles such as cell matrix and ribosome, which had functions of binding and catalysis. They mainly participated in biological processes such as metabolism, cell process and stress, including superoxide dismutase, methionyl aminopeptidase, lysosome-beta-glucosidase and ferritin.

Biography

Yinghong Pan has worked for the Institute of Medicinal Plant Development, Chinese Academy of Medical Sciences. He had his researches on medicinal plants and bioactive proteins in 1982-1999. He has worked since 1999 for the State Key Laboratory for Biology of Plant Diseases and Insect Pests, Institute of Plant Protection and the National Key Facility for Crop Gene Resources and Genetic Improvement, Institute of Crop Science, Chinese Academy of Agricultural Sciences and he is engaged in research on plant proteomics. He has published more than 20 papers related to medicinal plants and more than 55 related to proteins and proteomics.

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