JOINT EVENT

9th International Conference and Expo on

Proteomics and Molecular Medicine

&

9th International Conference on

Bioinformatics

November 13-15, 2017   Paris, France

A proteomics strategy to analyze complex traits and gene functions

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Proteomics analysis of complex trait is useful to understand gene functions and trait mechanisms. But the reliability of proteomics analysis is affected by many factors, such as genetic background influences, sampling variations and experimental conditions. In this strategy, four near isogenic lines (NILs) of Dwarf male-Sterile (DS) wheat with different genetic backgrounds were analyzed and a large Mass Spectrometry (MS) data from multiple batches were used to study the DS traits in wheat. At first, another and immature spike proteins from four NILs of DS wheat were prepared in different ways and detected with different mass spectrometry and a total of 58170 protein groups were detected from sixteen independent experiments. Secondly the abundance distributions of proteins that detected at different frequencies and expressed types were analyzed. By using several simple formulae which were introduced to evaluate the reliability of protein expression, a database contained expression levels of 58170 protein groups and comprehensive evaluation values of 17187 proteins without duplications was established. As focusing on nuclear male sterile trait mechanism and the function of Taigu Genie Male-Sterile Wheat (TGMSW) gene ms2 in those NILs, proteomes of immature spike from three DS wheat NILs were analyzed under same conditions and 160 differentially expressed proteins and 43 highly expressed proteins detected in this experiment were compared with database. Finally, it is determined that 28 proteins were closely related to male-sterile trait. The result show that large MS data from multiple batches is helpful for studying the complex traits and gene functions.

Biography

Yinghong Pan worked for the Institute of Medicinal Plant Development (IMPLAD), Chinese Academy of Medical Sciences and is engaged in research on medicinal plants and bioactive proteins during 1982-1999. Since 1999, he worked for the State Key Laboratory for Biology of Plant Diseases and Insect Pests (SKLBPI), Institute of Plant Protection and the National Key Facility for Crop Gene Resources and Genetic Improvement (NFCRI), 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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Notes:

J Proteomics Bioinform, an open access journal
ISSN: 0974-276X

Proteomics & Bioinformatics Congress 2017
November 13-15, 2017

Volume 10, Issue 11(Suppl)

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