

March 12-13, 2018  
London, UK

Zhaohua Peng, Int J Drug Dev & Res 2018, Volume 10

## PROTEIN LYSINE MALONYLATION, CROTONYLATION, SUCCINYLATION, AND 2-HYDROXYISOBUTYRYLATION IN DEVELOPING RICE SEED AND THEIR ROLES IN SEED METABOLIC REGULATION AND NUTRIENT RESERVOIR DEVELOPMENT

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**P**rotein lysine malonylation, succinylation, crotonylation, and 2-hydroxyisobutyrylation have been recognized as new post-translational modifications (PTMs) in recent years. It is plausible that these modifications may have a greater functional impact than lysine acetylation due to bulkier structural changes and larger charge differences introduced on the modified lysine residues. However, the identity of proteins harboring these modifications and their corresponding functions in cereal plants remain largely unknown. Using antibody-based affinity enrichment of modified peptides followed by nano-HPLC/MS/MS analyses, we identified from a few hundreds to over nine thousands modification sites for these modifications in developing rice (*Oryza sativa*) seeds, respectively. Distinct sequence motifs at the modification sites were identified for each of the modification. Proteins with different sequence motifs were shown to be favorably associated with unique metabolic pathways or protein function domains. Many of the modified proteins and the corresponding modification sites were conserved from *E. coli*, human, to plants. Remarkably, heavy modifications were detected on major seed storage proteins together with the key enzymes participating in central

carbon metabolism and storage starch biosynthetic pathways, which are essential for rice seed nutrition reservoir development. Rice proteins with co-modifications of succinylation, malonylation, crotonylation, 2-hydroxyisobutyrylation, acetylation, ubiquitination, and phosphorylation were studied through a comprehensive comparison analysis. In addition, the impact of lysine modification on lysine bioavailability in rice proteins is also analyzed. Our study delivers a platform for expansive investigation of the molecular networks administrating cereal seed development via PTMs.

### Biography

Zhaohua Peng is a Professor in the Department of Biochemistry, Molecular Biology, Entomology, and Plant Pathology at Mississippi State University. He received his BS and MS degrees in Biophysics at China Agriculture University and his PhD degree in Plant Molecular Biology at Ohio State University. From 1997 to 2001, he received training at Yale University as Postdoctoral Fellow. He joined Mississippi State University Faculty as an Assistant Professor in 2002. He was promoted to Associate Professor in 2008 and Full Professor in 2013. His research focuses on the regulation of rice seed development and seed storage nutrient production with emphasis on proteomics and epigenetic studies.

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