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## Global analysis of lysine acetylation suggests the involvement of protein acetylation in diverse biological processes in rice (*Oryza sativa*)

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Lysine acetylation is a reversible, dynamic protein modification regulated by lysine acetyltransferases and deacetylases. Recent Ladvances in high-throughput proteomics have greatly contributed to the success of global analysis of lysine acetylation. A large number of proteins of diverse biological functions have been shown to be acetylated in several reports in human cells, *E.coli*, and *Arabidopsis*. However, the extent of lysine acetylation in non-histone proteins remains largely unknown in monocots, particularly in the cereal crops. Here we report a large scale enrichment and mass spectrometry examination of lysine acetylation in rice (*Oryza sativa*). Many lysine acetylated sites on proteins of diverse biological functions were identified. Immunoblot studies further validated the presence of a large number of acetylated non-histone proteins. Examination of the amino acid composition revealed substantial amino acid bias around the acetylation sites and the amino acid preference is conserved among different organisms. Gene ontology analysis demonstrates that lysine acetylation occurs in diverse cytoplasmic, chloroplast and mitochondrial proteins in addition to the histone modifications. Our results suggest that lysine acetylation constitutes an important regulatory mechanism for a large number of proteins, including both histones and non-histone proteins of diverse biological functions.

## **Biography**

Zhaohua Peng completed his Ph.D. studies at The Ohio State University in 1997 and postdoctoral training at Yale University in 2001. He is a distinguished fellow in the Institute of Genomics, Biocomputing, and Biotechnology and associate professor in the Dept. of Biochemistry and Molecular Biology at Mississippi State University.

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