

Plant Genomics

July 14-15, 2016 Brisbane, Australia

New insights into genome-wide change of DNA methylation and its association with gene expression in cadmium-exposed rice (*Oryza sativa*)

Zhi Min Yang¹, Sheng Jun Feng¹, Xue Song Liu¹, Shang Kun Tan¹, Shan Shan Chu¹, Hua Tao¹, Tao Liu¹ and Youko Oono²¹Nanjing Agricultural University, China²National Institute of Agrobiological Sciences, Japan

Plant exposure to cadmium (Cd) affects transcriptional responses. Whether Cd modified DNA methylation marks are associated with transcription and functional consequences in plants remain unknown. We present the genome-wide single base resolution maps of methylated cytosines in Cd exposed rice, along with global transcriptional change in mRNA. Widespread differences were identified in the composition and patterning of CG and non-CG methylation marks between Cd exposed and control rice genomes. There are 2393 non-redundant differentially methylated regions (DMRs). RNA sequencing revealed that most of DNA methyltransferases, histone methyltransferases and DNA demethylases differentially changed in transcription under Cd exposure. By profiling global DNA methylation and gene transcription, we found more genes hypermethylated than those hypomethylated in CG, CHH and CHG (where H is A, C or T) contexts in the regions of upstream, gene body and downstream under Cd stress. Seventy-nine genes ($p < 0.05$, two-fold change) with a strong preference of differential expression in Cd exposed rice plants was identified. Many of them were involved in stress response, metal transport and transcription factors. A subset of loss of function mutants defective in DNA methylation/demethylation and histone modification activities were used to identify transcript abundance of selected genes. In most cases, genes in the mutants were repressed by Cd treatment. Provision of azacitidine (a global DNA methylation inhibitor) attenuated root growth inhibition but promoted biomass and Cd accumulation under Cd exposure. Finally, we identified 108 transposons and 254 retrotransposons that were modified by methylation, where transcriptional expressions of 30 neighboring genes were changed under Cd exposure.

Biography

Zhi Min Yang is a Professor of Plant Physiology and Molecular Biology in Nanjing Agricultural University (NAU). He has earned his PhD degree at NAU in 1999 and received his Postdoctoral training at the University of Kagawa, Japan and Justus-Liebig University, Germany. He is working on physiological and molecular mechanisms for plant abiotic stress responses (salt, drought or heavy metals). His major interest is in epigenetic regulation of stress tolerance, toxic metal uptake and accumulation in plants through small/long non-coding RNAs (e.g. microRNAs) and DNA methylation. He has published 80 peer-reviewed papers and serves as Associate/Academic Editor of *Gene*, *Plant Gene* and *PloS One*.

zmyang@njau.edu.cn

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