**Reversible RNA Adenosine Methylation in Plant Biological Regulation**

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m6A is the most prevalent internal modification in eukaryotic mRNA and preferentially occurs at the consensus sequence [G/A/U][G>A]m6AC[U>A>C] with a non-stoichiometric ratio. Although it was first found in the 1970s, relative to DNA modifications, the research on m6A lagged behind due to the lack of detection techniques for RNA modification. Until 2011, the discovery of FTO as an m6A-demethylase demonstrates m6A is a reversible and dynamic RNA modification and reignites investigation of m6A. In 2012, two research group developed an m6A antibody immunoprecipitation-based sequencing method (termed m6A-seq or MeRIP) and reported the whole-transcriptomic m6A maps. m6A is installed by a methyltransferase complex (writer) with key subunits identified as METTL3 (Methyltransferase-like 3), METTL14 and WTAP (Wilms tumour 1-associating protein). So far, only two m6A demethylases (eraser), FTO and ALKBH5 (AlkB homolog 5), have been characterized. m6A is recognized by reader proteins (such as YTH family proteins) to regulate RNA fate, including mRNA stability, splicing, nuclear export, translation, primary microRNA processing, and RNA-protein interactions. These processes affect circadian rhythms, stem cell pluripotency, cancer stem cell proliferation, RNA virus infection, sex determination in *Drosophila*, and so on, revealing that m6A plays critical roles in various biological processes. However, the study of m6A methylation in *Arabidopsis thaliana* has been limited to the m6A methyltransferase. Here we will discuss our discovery and characterization of reversible m6A methylation mediated by demethylase and read by m6A-binding protein in *A. thaliana*, and noticeable regulatory roles of these RNA demethylase in reader in plant development, especially floral transition. Our findings reveal potential broad functions of reversible mRNA methylation in plants.

**Keywords:** Epitranscriptome; RNA modification; *N*6-methyladenosine (m6A); m6A demethylase; m6A-binding protein (m6A reader)

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**Biography**

Guifang Jia is currently an Associate Professor at Department of Chemical Biology, College of Chemistry and Molecular Engineering of Peking University since 2012. She received her B.S. in Chemistry from China Agricultural University in 2002 and her Ph.D. in Pesticide Residue Analysis from China Agricultural University in 2008. She became a visiting student at the University of Chicago to study chemical biology under the supervision of Prof. Chuan He in 2007, and continued her postdoctoral research in the laboratory of Prof. Chuan He at the University of Chicago. Her current research interests include the biological functions of epitranscriptomics/RNA modifications in human health and plant developments, and the development of small molecule tuning of epitranscriptomic regulation.