

# 6<sup>th</sup> Global Summit on Plant Science

October 29-30, 2018 | Valencia, Spain

## DNA methylation and its analysis on *Gossypium* under the salt and drought stress

Wuwei Ye

Institute of Cotton Research-CAAS, China

DNA methylation, an important component of epigenetics induced usually by adversity, plays a vital role in the response to various stresses including drought and salt. A methylation-sensitive amplification polymorphism method based on capillary electrophoresis was used to explore the epigenetic mechanisms of salt tolerance and heterosis in upland cotton (*Gossypium hirsutum* L.), and the results indicated that hyper methylation and demethylation could be an important mechanism to resist the stresses. And the demethylation could be the mechanism to explain heterosis in cotton hybrid. The results of whole genome methylation sequencing showed high DNA methylation density usually occurs in promoter regions and transposons areas. Methylated cytosines in different sequence contexts (CG, CHG and CHH) have different functions and methylation levels. And the results also showed methylated cytosines in asymmetric CHH sequence context are dynamic, being mostly related to stresses. Combined with transcriptome data, we found long non-coding RNAs (lncRNAs) may involve in the regulation of DNA methylation in response to drought stress. All these results could provide theoretical reference value for the mechanism research of tolerance in cotton.

### Recent Publications

1. Kunbo Wang, Zhiwen Wang, Fuguang Li, Wuwei Ye, Junyi Wang, Guoli Song, et al., (2012) The draft genome of a diploid cotton *Gossypium raimondii*. *Nature Genetics* 44(10):1098-1103.
2. Min Mu, Xu-Ke Lu, Jun-Juan Wang, De-Long Wang, Zu-Jun Yin, Shuai Wang, Wei-Li Fan and Wu-Wei Ye (2016) Genome-wide identification and analysis of the stress-resistance function of the TPS (Trehalose-6-Phosphate Synthase) gene family in cotton. *BMC Genetics* 17:54.
3. Xiugui Chen Xuke Lu, Na Shu, Shuai Wang, Junjuan Wang, Delong Wang, Lixue Guo and Wuwei Ye (2017) Targeted mutagenesis in cotton (*Gossypium hirsutum* L.) using the CRISPR/Cas9 system. *Scientific Report* 7:44304.
4. Baohua Wang, Mi Zhang, Rong Fu, Xiaowei Qian, Ping Rong, Yan Zhang, Peng Jiang, Junjuan Wang, Xuke Lu, Delong Wang, Wuwei Ye and Xinyu Zhu (2016) Epigenetic mechanisms of salt tolerance and heterosis in upland cotton (*Gossypium hirsutum* L.) revealed by methylation-sensitive amplified polymorphism analysis. *Euphytica* 208(3):477-491.
5. Xuke Lu, Xiugui Chen, Min Mu, Junjuan Wang, Xiaoge Wang, Delong Wang, Zujun Yin, Weili Fan, Shuai Wang, Lixue Guo and Wuwei Ye. Genome-wide analysis of long noncoding RNAs and their responses to drought stress in cotton (*Gossypium hirsutum* L.). *PLOS One* 11(6):e0156723.

### Biography

Wuwei Ye is a Professor and Deputy Director in Cotton Germplasm Research Department of Institute of Cotton Research at CAAS, China. He has been involved in studies related to cotton germplasm identification, innovation and biodiversity research for 30 years, focusing on resistant on cotton germplasm, such as salinity and drought-resistance. He is responsible for the coordination of identification and implementation of cotton germplasm identification center in China.

Yew158@163.com.cn