

Plant Science 2018- DNA methylation and its analysis on *Gossypium* under the salt and drought stress- Wuwei Ye- China

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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.

As plants are sessile, they are more vulnerable to harm than creatures under biotic and abiotic stress. abiotic stresses, including high saltiness, high or low temperatures, and dry season, cause genuine misfortunes in agrarian efficiency every year. Lately, a developing number of studies have demonstrated that methylation status changes as often as possible (particularly in stress-related qualities) in creating plants under abiotic stress. Saltiness is one of the most genuine natural constraining variables for crop efficiency. Unfavorable impacts of high salt fixation incorporate diminished plant cell movement, and diminished profitability, germination rate and plant stature. The methylation status of various species and assortments differs under salt pressure. For instance, the DNA methylation levels of rice assortment 'IR29' and rapeseed assortment 'Exagone' both abatement under salt pressure. Strikingly, when Exagone plants were developed under states of salt worry for about fourteen days, the quantity of completely methylated groups expanded in the plants permitted to recoup from salt worry for 1-2 days contrasted and plants developed in high saltiness for the whole time frame. During the salt worry, there are away from in the methylation of qualities engaged with physiological procedures in Exagone; for instance, the polymorphic piece Bn_05 is homologous to the quality encoding Plasma Membrane Intrinsic Protein 2, which is associated with salt resilience, and the polymorphic section Bn_09 is homologous to an *Arabidopsis thaliana* quality that encodes a Trehalose Phosphatase/Synthase 4 (TPS4) protein,

which is engaged with trehalose biosynthesis. Trehalose, which is a nonreducing disaccharide of glucose, can expand plants pressure resistance through creation of sugar changes.

Dry season is the most genuine condition pressure that cutoff points plant advancement and creation in most downpour took care of frameworks around the world. In ongoing decades, dry spell pressure related plant mortality has expanded. Plant tallness, blossoming, proportion of spikelet sterility, and leaf shape and shading are additionally influenced by dry season pressure. Plants under dry spell pressure show dynamic methylation levels. In *Populus trichocarpa*, dry season pressure builds methylation; utilizing bisulfite sequencing (BS-seq) to recognize methylation levels, the extent of methylated cytosines is 10.04% under dry spell pressure, while it is just 7.75% in the very much watered treatment. A positive connection was found between quality articulation and methylation levels under dry spell pressure, showed by 7329 upregulated qualities with expanded methylation levels, and 10 322 downregulated qualities with diminished methylation levels.

There are additionally various changes in methylation status in different species or genotypes under dry season pressure. For instance, utilizing MSAP (Methylation-Sensitive Amplification Polymorphism), the methylation level of lasting ryegrass diminished from 57.67% in the control to 47.39% under dry spell pressure; the degree of completely methylated DNA is remarkably down-directed by 12.58% in the dry season condition. One piece in which the methylation level abatements under dry spell pressure is seen as homologous to LOC100833067, which encodes respiratory burst oxidase homolog (Rboh) protein. Rboh-NADPH oxidases produce oxygen intermediates that manage abiotic stress reactions. In the dry season lenient rice assortments 'PMK3' and 'PL', methylation levels additionally diminished under dry spell pressure contrasted and the control condition. Curiously, the methylation designs in rice (*Oryza sativa* L.) are influenced by multi-generational dry spell pressure treatment. So as to adjust to a drawn out dry season pressure, rice play out a high extent of dry spell initiated epimutations through changed DNA methylation status.

References

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.