

SDG102, a H3K36-methyltransferase-encoding gene, regulates flowering time and other processes in maize (*Zea mays* L.)

Yongjian Li¹, Weifeng Sun¹, Chang Wan¹, Jun Zhang¹, Xin Qi¹, Zhenhui Wang¹, and Jian Zhang¹

¹Jilin Agricultural University Library

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Abstract

Studies on histone lysine methylation in *Arabidopsis thaliana* and rice (*Oryza sativa*) have notably progressed in recent years. Despite these advances in knowledge, the function of histone lysine methylation in maize (*Zea mays* L .) remains poorly characterized. To better understand the function of histone lysine methylation in maize, *SDG102*, a maize H3 lysine 36 (H3K36) methylation gene, was chosen to study functional characterization using overexpressed and knockout transgenic plants. SDG102-deficiency in maize caused multiple phenotypes, including yellow leaves in seedling, late-flowering, and increased adult plant height, while overexpression of *SDG102* led to reduced adult plant height. The key flowering genes, *ZCN8/ZCN7* and *MADS4/MADA67*, were downregulated in SDG102-deficient plants. Chromatin immunoprecipitation (ChIP) experiments showed that H3 lysine 36 trimethylation (H3K36me3) levels were reduced at these loci. Perturbation of *SDG102* expression caused misexpression of multiple genes. Interestingly, overexpression or knockout of *SDG102* also led to genome-wide decreases or increases in H3K36me3 levels respectively. Together, our results suggest that SDG102 is a methyltransferase in maize that catalyzes trimethylation of H3K36 of many genes across the genome, which are involved in multiple biological processes including those controlling flowering time.

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