

Transcriptome dynamic landscape underlying the improvement of maize lodging resistance under coronatine treatment

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Abstract

Lodging is a threat for maize production worldwide. Coronatine (COR) is a jasmonic acid analog hopeful to be a new plant growth regulator in agriculture. In this study, we demonstrated that the plant height of ZD958 and XY335, two cultivated maize hybrids, was significantly decreased under COR treatment via reducing internode length and thus improve lodging resistance. To explore gene expression changes driving the responses of internode to COR, spatio-temporal transcriptomic data of inbred B73 internode were generated under normal condition and COR treatment, including the fixed, meristem and elongation regions. The transcriptional features of the three regions at normal condition were characterized and then compared with that upon COR treatment. A total of 8605 COR-responsive genes (COR-RGs) were identified, including 802 internode specific genes. Both the number and function categories were greatly changed for COR-RGs identified in fixed, meristem and elongation regions, indicating different groups of genes were regulated at the three regions. Besides, we found the expressions of more than 80% of gibberellin and jasmonic acid related genes were changed under COR treatment. The characterization of gene expression response in internode under COR treatment here is useful for further unraveling the mechanism of plant height decrease by COR.

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