

**Research on the molecular mechanism of boron-induced resistance to cucumber green mottled mosaic virus (CGMMV) in watermelon**

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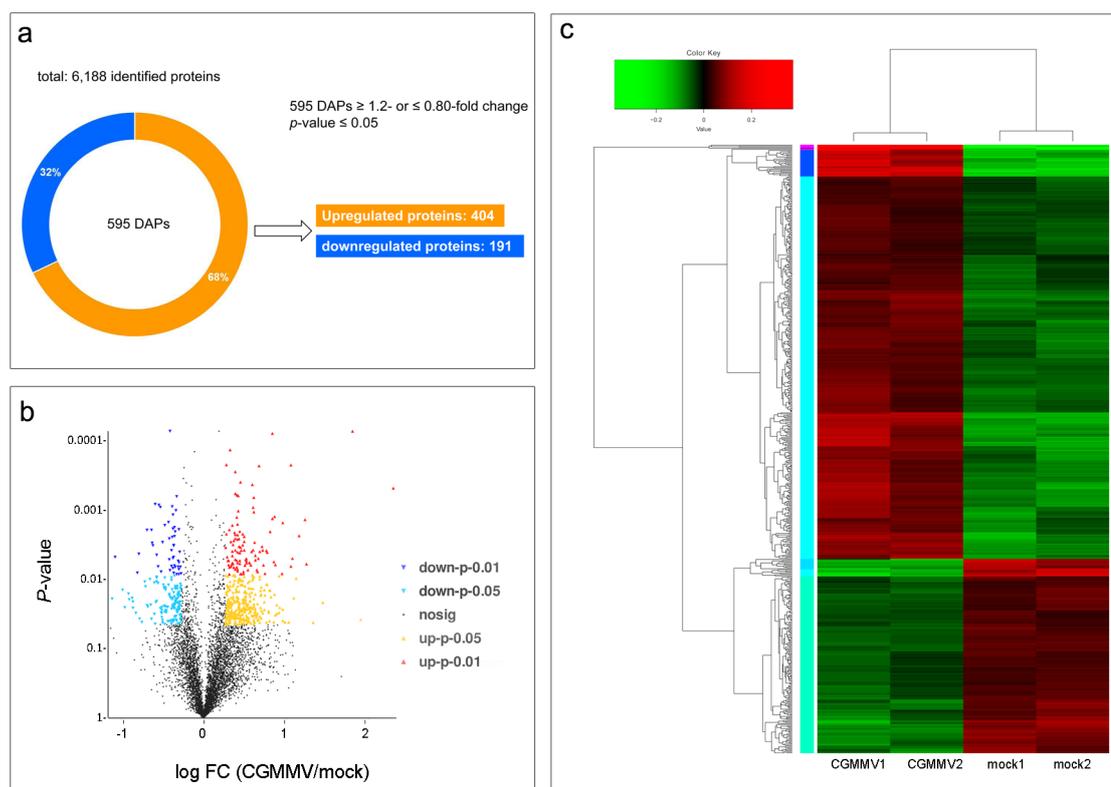
Watermelon (*Citrullus lanatus* Thunb.) is considered one of the most popular nutritious fruit crops and is widely cultivated throughout the world, however the yield is seriously threatened by pathogen, pests and abiotic stress. Cucumber green mottle mosaic virus (CGMMV) is a member of the genus *Tobamovirus*, and is an important global quarantine pest in cucurbitaceae crops. CGMMV infection usually results in severe disease symptoms in watermelon, especially causing fruit decay, which is also called "watermelon blood flesh". In order to study the CGMMV infection mechanism and molecular mechanism of boron (B) regulation, transcriptome and proteome sequencing analyses were conducted on treated watermelon fruit samples. DAPs of watermelon responding to CGMMV infection mainly involved the biological processes (including metabolic process, cellular process and single-organism process), the cellular component (including cell part organelle and biological membrane), the molecular functions (including catalytic activity and binding) in GO database. KEGG analysis showed that DAPs mainly involved in the metabolic pathways of plant hormone signal transduction, starch and sucrose metabolism, carbon metabolism, photosynthesis, and photosynthesis-antenna proteins, etc. In response to boron inhibiting CGMMV infection, DAPs of watermelon also participated in the metabolic pathway, such as phenylalanine metabolism, phenylpropanoid biosynthesis, amino sugar and nucleotide sugar metabolism, biosynthesis of amino acids, and plant-pathogen interaction, besides signal transduction of plant hormones, metabolism of starch and sucrose, and carbon metabolism. These pathways were closely related to cell wall synthesis and homeostasis, carbohydrate transport and metabolism, and maintenance of cell membrane homeostasis and function in watermelon fruits, which showed that boron increased watermelon resistance to CGMMV infection. In this study, through transcriptome and proteome sequencing analyses of watermelon fruits responding to CGMMV infection and spraying boron to regulate CGMMV infection, we found ATP synthase, RCCR, Psy, NCED3, PEPCKPK, HKs, CS, and UGE, etc were significantly changed. This work was initially revealed the molecular mechanism of CGMMV infection causing watermelon flesh blood, and the relationship between boron element and the formation of flesh blood symptom. This study provides the theoretical basis for the green prevention of CGMMV and control and the use of gene regulation to create watermelon with long-lasting resistance to disease.

**References**

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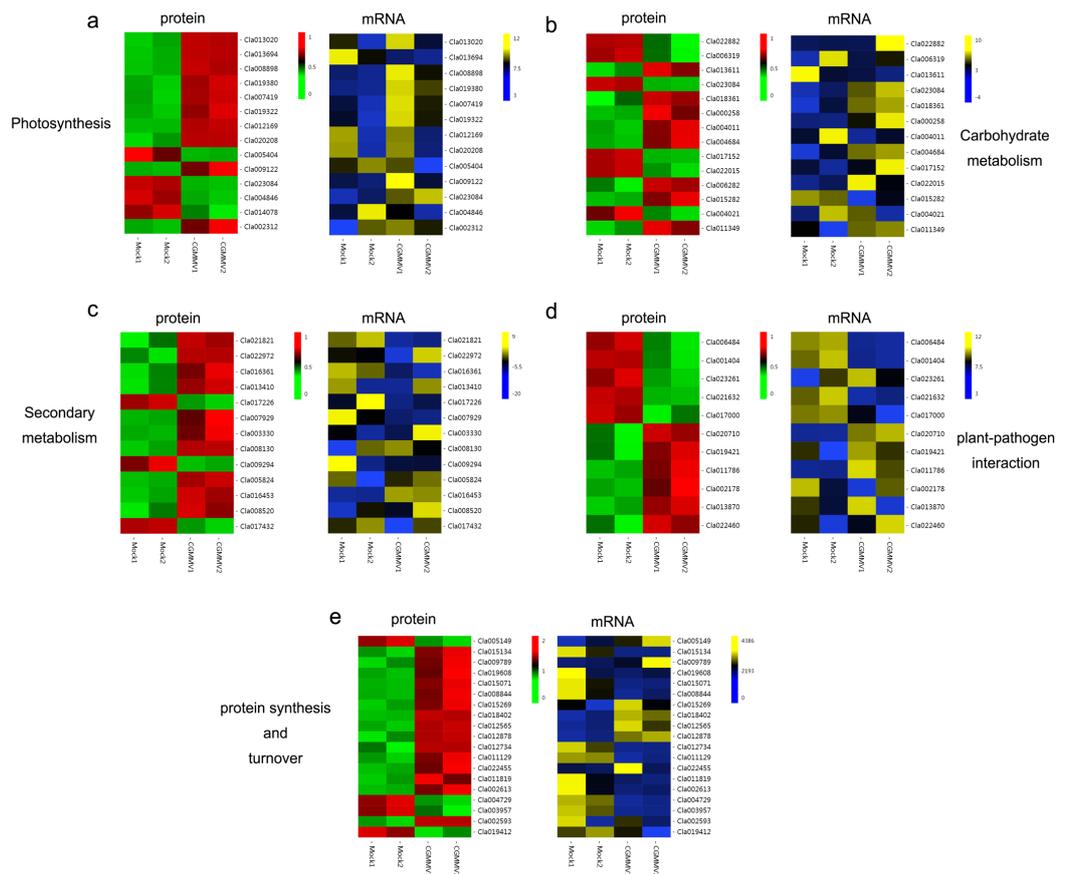
### Illustrations



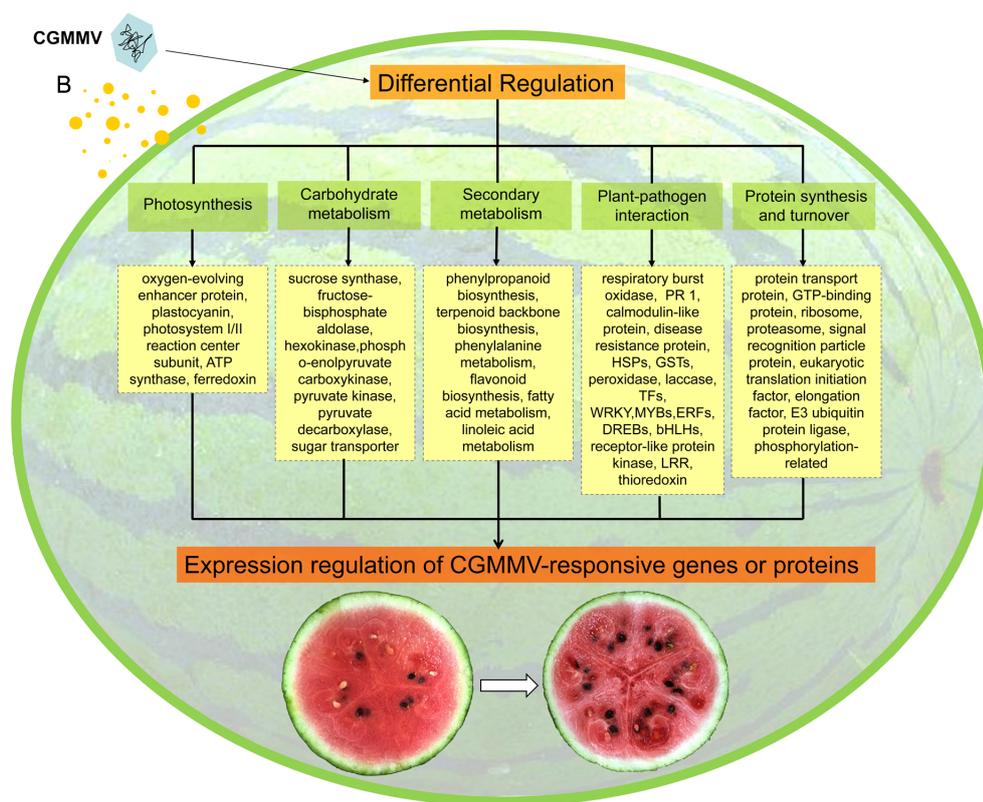
**Рис. 1.** The profiles of DAPs in CGMMV-inoculated watermelon fruits . (a) up-regulation and down-regulation of total DAPs; (b) volcano diagram of the distribution of CGMMV-inoculated and mock-inoculated proteins sets. More up-regulated proteins (red dots) were found than down-regulated proteins (blue dots); (c) hierarchical cluster of main DAPs in five groups between CGMMV-inoculated and mock-inoculated watermelon fruits libraries.



**Рис. 2.** GO function classification and KEGG pathway enrichment analysis of DAPs. (a) GO function classification of differentially accumulated proteins (DAPs). The three pie charts respectively show the functional annotation of DAPs in three major categories of GO database (“biological process”, “cellular component” and “molecular function”); (b) KEGG pathway enrichment analysis of differentially accumulated proteins (DAPs). Top 20 pathways with the smallest P-value were demonstrated. Each column represents the percentage of DAPs participated in each KEGG pathway. Asterisks indicate the significance of enriched pathways. (\*\*  $P < 0.01$ . \*  $P < 0.05$ )



**Рис. 3.** Hierarchical cluster of main DAPs in five groups between CGMMV-inoculated and boron-induced-CGMMV-inoculated watermelon fruits. (a) photosynthesis; (b) carbohydrate metabolism; (c) secondary metabolites biosynthesis; (d) plant-pathogen interaction pathway; (e) protein synthesis and turnover.



**Рис. 4.** Speculated regulation network of boron regulation CGMMV-responsive mechanism in watermelon fruits. The arrows represent the expression patterns of DEGs (red) or DAPs (blue) respectively.