

Comparative transcriptome and DNA methylation analyses of Phytoplasma infection Responses in Mulberry (*Morus multicaulis* Perr.)

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June 17, 2020

Abstract

To reveal whether the response of mulberry to phytoplasma infection is associated with DNA methylation changes, the methylome and transcriptome patterns of mulberry leaves in response to phytoplasma infection were explored. Though the average methylation level of infected leaves showed no significant difference with that of healthy leaves, there were 1253 differentially methylated genes and 1168 differentially expressed genes found in the infected leaves, and 215 genes were found simultaneously to be differently methylated and expressed. It was found that the expression of G-type lectin S-receptor-like serine/threonine protein kinase gene (Mu-GsSRK) was increased, but its methylation level was decreased in the infected leaves. Moreover, the expression of Mu-GsSRK was increased while its methylation level was reduced in mulberry treated with pathogen and SA. Expression of Mu-GsSRK in Arabidopsis enhanced transgenic plant disease resistance and the expressions of some defense genes when plants were inoculated with pathogens. In addition, the DNA methylation dynamic patterns and the roles of the differentially expressed and methylated genes were discussed. Our results suggested that DNA methylation has important roles in mulberry responses to phytoplasma infection, and the information provided there will facilitate to elucidate the epigenetic mechanisms underlying mulberry responses to phytoplasma infection.

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