DOI: https://doi.org/10.17816/ecogen112334

Overexpression of the *Ib-rolB/C* gene perturbs biosynthesis of caffeoylquinic acid derivatives in transgenic calli of sweet potato

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Ipomoea batatas is a root crop widely cultivated in South America, Africa, and Asia. This is also a source of caffeoylquinic acid derivatives (CQAs) with potential health-promoting benefits. Sweet potato genome carries two separate cellular T-DNA (cT-DNA) regions (*Ib*T-DNA1 and *Ib*T-DNA2). Especially, *Ib*T-DNA2 contains five ORFs homologous to the *Agrobacterium rhizogenes* T-DNA, namely ORF13, ORF14, ORF17n, ORF18/ORF17n, and RolB/RolC proteins [1]. Unfortunately, presently there is insufficient information on *Ib*T-DNA2 genes' function in the physiological processes of sweet potatoes.

In this study, expressional levels of the *Ib*T-DNA2 genes and the effect of *Ib-rolB/C* overexpression were examined using *I. batatas* cell culture. We discovered that *I. batatas* cT-DNA genes were not expressed in callus, and abiotic stresses and chemical elicitors affected their transcriptional levels weakly. Additionally, two *Ib-rolBC*-transgenic cell lines have been established though *Agrobacterium*-mediated transformation of *I. batatas* callus cells. Overexpression of *Ib-rolB/C* gene reduced biomass accumulation of transgenic cell lines by 1.2–1.6 times and increased the CQAs content by 1.5–1.9-fold. To justify the metabolic fluctuations, the study also looked into the expression patterns of the major biosynthetic genes, namely *bPAL*, *IbC4H*, *Ib4CL*, *IbHCT*, and *IbHQT*. The obtained data demonstrated that the overexpression of the *Ib-rolB/C* reduced the *IbPAL* transcript but considerable increase in the transcript levels of the *IbHQT*. We propose that this result was obtained through as-yet-uncharacterized signaling pathways activated by RolB/RolC.

REFERENCE

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