Amplified fragment length polymorphism and metabolomic profiles of hairy roots of Psoralea corylifolia L.

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Abstract
A reproducible protocol for establishment of hairy root cultures of Psoralea corylifolia L. was developed using Agrobacterium rhizogenes strain ATCC 15834. The hairy root clones exhibited typical sigmoid growth curves. Genomic and metabolomic profiles of hairy root clones along with that of untransformed control were analysed. Hairy root clones, Ps I and Ps II, showed significant differences in their amplified fragment length polymorphism (AFLP) profiles as compared to that of control, besides exhibiting Ri T-DNA-specific bands. These results amply indicate the stable integration of Ri T-DNA into the genomes of these clones. Further, the variations observed between clones in the AFLP profiles suggest the variable lengths and independent nature of Ri T-DNA integrations into their genomes. An isoflavonoid, formononetin, and its glycoside were present only in the hairy root clones while they were absent in the untransformed control. Variations observed in the metabolite profiles of these clones may be attributed to the random T-DNA integrations and associated changes caused by them in the recipient genomes. GC/MS analyses revealed the production of three and six clone-specific compounds in Ps I and Ps II, respectively, suggesting that the clones are dissimilar in their secondary metabolism. HPLC/UV–MS analyses disclosed substantial increases in the total isoflavonoids produced in Ps I (184%) and Ps II (94%) compared to untransformed control.

References


