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An expressed sequence tag database analysis of colchicine genes in *Gloriosa superba*

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Gloriosa superba can be used *in vitro* as a renewable biofactory for high-value pharmaceutical colchicine. However, one of the challenges in production is the lack of understanding of colchicine biosynthesis, and the genome remains largely unknown. Therefore, this study establishes a cDNA library for identifying key colchicine pathway genes. We will describe the cDNA library construction and expressed sequence tags (ESTs) analysis of colchicine pathway genes in *G. superba*. Some clones in the *G. superba* cDNA library showed high sequence homology to genes associated with colchicine biosynthesis. These genes could enhance the production of colchicine in *G. superba* via metabolic engineering.

Biography

Biography Sivakumar's research is primarily focused on biotech implications and applications of high-value natural products. He has extensively studied the plant-based small molecules pathway biochemistry, synthetic biology and metabolic & bioprocess engineering. He is internationally recognized in the field of biopharmaceuticals and a pioneer in industrial-scale production of bioactive molecules. He has over 40 publications. He is also on the editorial board of several journals. He serves as an expert of grant proposals as well as numerous scientific journals. His laboratory focuses on metabolic and bioprocess engineering of colchicine pathway and developing potential anticancer medicine. In addition, his group is interested in developing biofuels to address energy and environmental problems

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