

4th International Conference on

Bioprocess and Bio Therapeutics

October 20-21, 2016 Houston, USA

RNA-seq analysis of *Gloriosa superba* L.

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Gloriosa superba is the most important industrial crop for the biosynthesis of significant amounts of colchicine among the *Colchicaceae*. FDA-approved colchicine had been used in the treatment of gout. Gout pain is caused by elevated uric acid levels in the blood, which lead to the formation of crystals in bone joints. In order to improve cost-effective colchicine production from *G. superba* for drug manufacturing, understanding colchicine metabolism and elucidating its pathway is necessary. RNA-Seq is one of the next-generation sequencing methods in the analysis of gene expression patterns in *G. superba* and for mining colchicine pathway genes. Our initial *G. superba* bioinformatic analysis revealed that annotation of 31748 assembled publically available multi-tissue *G. superba* transcript sequences represents 14548 unique genes with homologs in known plant-specific Gene Ontology (GO) slims. This data could help identify colchicine pathway genes in *G. superba*.

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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