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## *De novo* analysis of *Gloriosa superba* and *Colchicum autumnale* transcription factors in Rhizome development

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The prime pharmaceutical colchicine producers such as *Gloriosa superba* and *Colchicum autumnale* are medicinal rhizomatous crops. *De novo* transcriptomic comparison between *G. superba* and *C. autumnale* is the first step in providing a resource to identify several transcription factor families involved in rhizome biomass biomanufacturing. Blast2GO led to the identification of transcription factors namely, *MADS-box, AP2-EREBP, bHLH, MYB, NAC* and *WRKY* candidate genes. These transcription factor families could potentially lead to the further understanding of the mechanisms involved in colchicine and biorhizome biomanufacturing.

### Biography

Ganapathy Sivakumar's research is primarily focused on biomanufacturing and biotech implications of biopharmaceuticals. He has extensively studied the plant-based small molecules pathway biochemistry, synthetic biotechnology and metabolic & bioprocess engineering. He is internationally recognized in the field of biopharmaceuticals and a pioneer in biomanufacturing of biorhizome-based colchicine. He has over 50 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.

**Notes:**

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