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Identification of genes related to the development of *Gloriosa superba* rhizome

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The pharmaceutical demand for plant-based colchicine is increasing because it is an effective FDA-approved gout medicine that also has potential for cancer therapeutics due to its ability to bind to microtubules and halt cell division. Understanding the biorhizome developmental genes are necessary to improve the biomanufacturing of colchicine. RNA-Seq was used to identify the rhizome developmental genes from *Gloriosa superba* and *Colchicum autumnale*. The transcriptome of both species were compared against NCBI and Swissprot protein databases. Python scripts were utilized to parse the transcriptome. Bioinformatics analysis revealed 60927 assembled multiple-tissue transcripts of *C. autumnale* represented 21948 unigenes and *G. superba* has 32312, which represented 15089 unigenes in known plant specific gene ontology (GO). Further GO analysis was used to identify known rhizome-specific and developmental genes in *G. superba*. This study could provide a foundation to enhance the biorhizome-based colchicine biomanufacturing in *G. superba*.

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Notes:

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