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# Transcriptome changes in *Polygonum multiflorum* Thunb. roots induced by methyl jasmonate

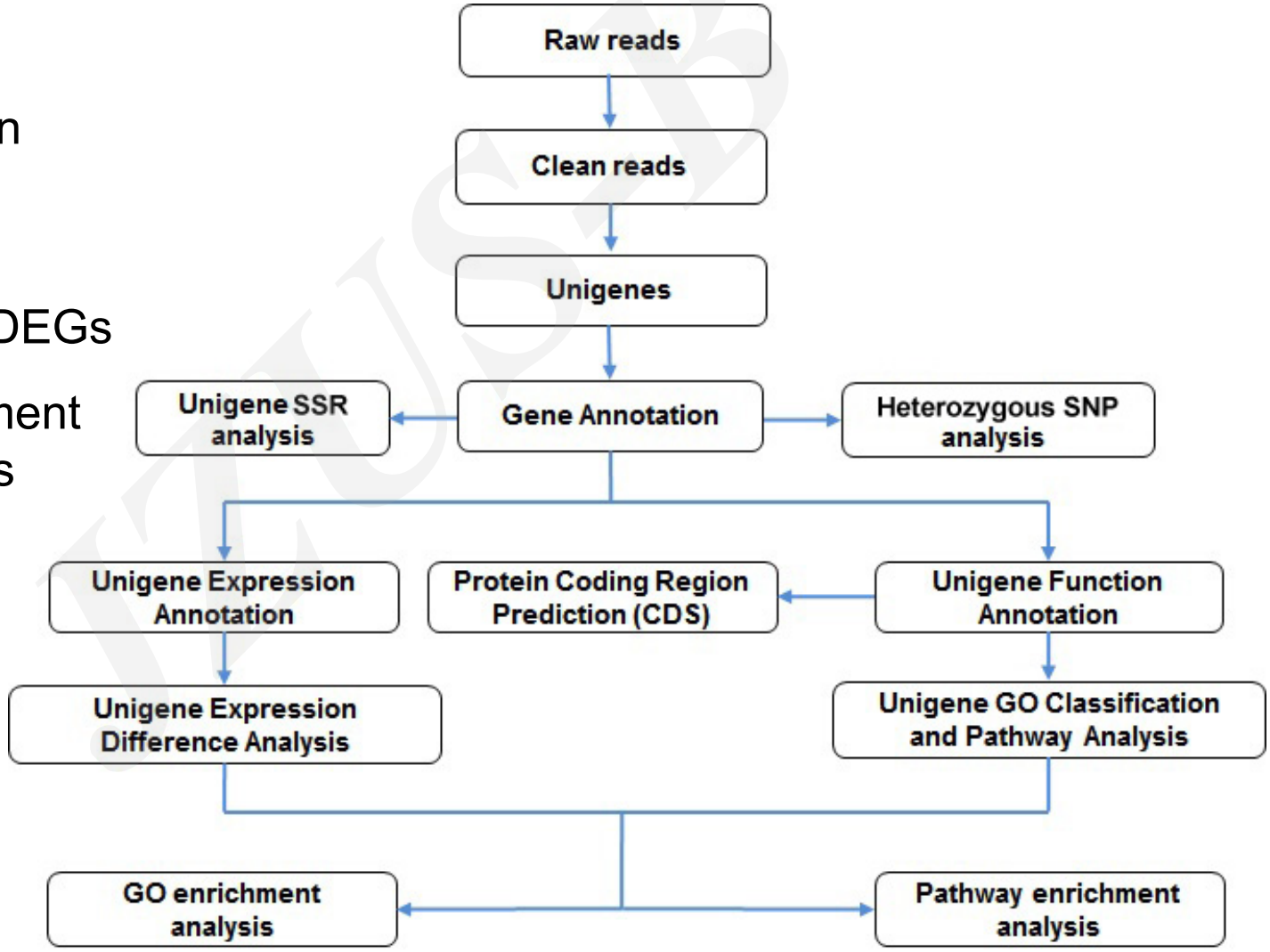
**Key words:** ***Polygonum multiflorum*** **Thunb., Methyl jasmonate, Transcriptome change, Differentially expressed genes**

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# Research Summary

**This paper mainly focused on the transcriptome changes in roots of *Polygonum multiflorum Thunb*. after MeJA treatment, and summarized the key transcritome changes in the following aspects:**

- Effect of MeJA on gene expression
- Go functional classification of DEGs
- Pathway enrichment analysis of DEGs



# *Innovation points*

- **First research for transcriptome changes in roots of *Polygonum multiflorum* Thunb. with method of exogenous MeJA root-irrigation.**

- **First application of transcriptome profiling to seek key enzyme gene which control the biosynthesis of active ingredient in *Polygonum multiflorum* Thunb..**

- **Many key enzyme genes of the secondary metabolic pathway in the root of *Polygonum multiflorum* Thunb. have been found, which will lay a solid foundation for the next research.**



*P.multiflorum* medicinal materials, which has been widely used in traditional medicine for treating various ailments, and is known for its diverse pharmacological properties.

| # | Pathway | DEGs with pathway annotation (2085) | All genes with pathway annotation (8986) | Pvalue | Qvalue | Pathway ID |
|---|---|---|---|---|---|---|
| 1 | Metabolic pathways | 307 (14.72%) | 1081 (12.03%) | 1.354119e-05 | 0.002911356 | ko01100 |
| 2 | Proteasome | 23 (1.1%) | 48 (0.53%) | 0.0001482570 | 0.015937627 | ko03050 |
| 3 | B cell receptor signaling pathway | 29 (1.39%) | 70 (0.78%) | 0.0005085341 | 0.036444944 | ko04662 |
| 4 | Apoptosis | 34 (1.63%) | 89 (0.99%) | 0.001018471 | 0.045737882 | ko04210 |
| 5 | Hematopoietic cell lineage | 31 (1.49%) | 80 (0.89%) | 0.001271905 | 0.045737882 | ko04640 |
| 6 | Primary immunodeficiency | 16 (0.77%) | 33 (0.37%) | 0.001276406 | 0.045737882 | ko05340 |
| 7 | Glycosylphosphatidylinositol(GPI)-anchor biosynthesis | 13 (0.62%) | 25 (0.28%) | 0.001618825 | 0.049721054 | ko00563 |
| 8 | N-Glycan biosynthesis | 18 (0.86%) | 40 (0.45%) | 0.001901140 | 0.051093137 | ko00510 |
| 9 | Huntington's disease | 60 (2.88%) | 187 (2.08%) | 0.003132988 | 0.074843602 | ko05016 |
| 10 | Other glycan degradation | 9 (0.43%) | 16 (0.18%) | 0.004361382 | 0.093769713 | ko00511 |
| 11 | Alzheimer's disease | 56 (2.69%) | 176 (1.96%) | 0.005133783 | 0.100342122 | ko05010 |
| 12 | Biosynthesis of steroids | 13 (0.62%) | 28 (0.31%) | 0.005747707 | 0.102979750 | ko00100 |
| 13 | Chronic myeloid leukemia | 27 (1.29%) | 74 (0.82%) | 0.006681019 | 0.110493776 | ko05220 |
| 14 | Epithelial cell signaling in Helicobacter pylori infection | 25 (1.2%) | 68 (0.76%) | 0.007943713 | 0.121992735 | ko05120 |

Part of Table 1

# *Innovation points*

**A series of comprehensive tables and figures were generated to summarize the latest knowledge about transcriptome changes in root of *Polygonum multiflorum* Thunb..**

**Table 1 | Significantly modulated pathways in root transcriptome of *P. multiflorum* subjected to MeJA treatment.**

**Table S1 | Statistical comparison of contigs and unigenes between control and treatment root transcriptome data of *P. multiflorum* seedlings.**

**Fig. 1 | GO function classification of DEGs.**

**Fig. 2 | "Stilbenoid, diarylheptanoid and gingerol biosynthesis" pathway induced by MeJA in root transcriptome of *P. multiflorum*.**

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