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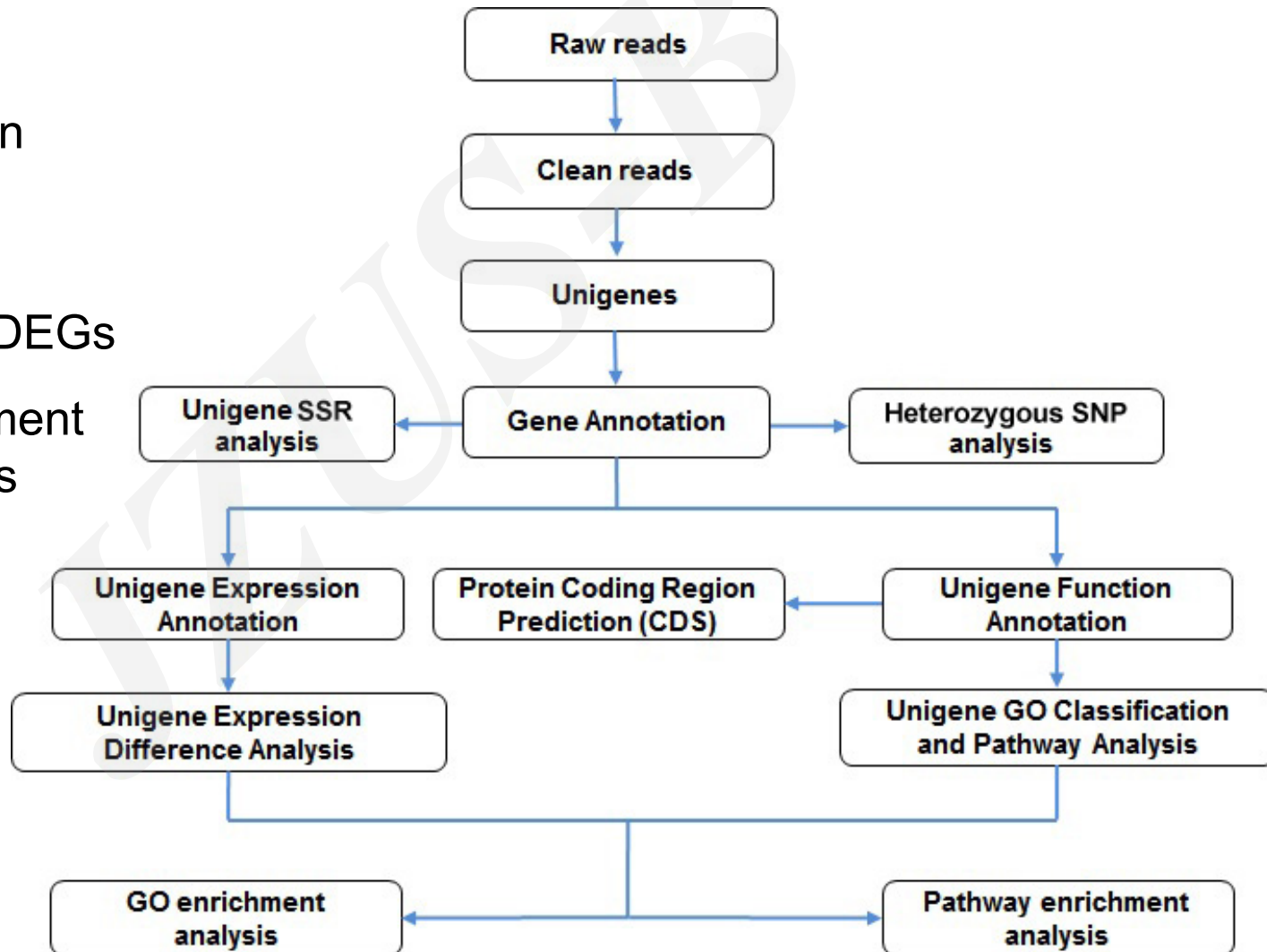
# Transcriptome changes in *Polygonum multiflorum* Thunb. roots induced by methyl jasmonate

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

# Research Summary

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