

The manuscript by Yang et. al, entitled " Full-length transcriptome profiling of *Gentiana straminea* Maxim provides new insights into iridoid biosynthesis pathway" attempts to shed light on detailed transcriptome analysis to identify genes that differentially expressed in five *G. straminea* tissues. Although the authors have done a commendable work in analysing and consolidating the research data still need to address the following points to improve the quality of current draft for suitability of publication in "Peer J".

Comments for the manuscript:

- The introduction provides a comprehensive background on *Gentiana straminea* and its bioactive compounds. However, it would be helpful to explicitly state the knowledge gap this study aims to address earlier in the introduction. Additionally, the transition from general background information to the study objectives could be smoother.
- Some figures (e.g., phylogenetic tree and gene expression heatmaps) contain valuable information but lack detailed explanations in the figure legends. Clarifying how branch support values were calculated in the phylogenetic tree and ensuring that heatmap color scales are clearly labeled would improve readability.
- The discussion provides insights into gene functions and their relevance to iridoid biosynthesis, but it could be expanded to discuss potential biotechnological applications of the findings. For example, how could the identified genes be used for metabolic engineering or plant breeding strategies?
- Include the completeness of assembled transcripts with BUSCO and discuss the sequencing depth.
- Compare the RNA seq and qRT-PCR expression result. Discuss it further in results.