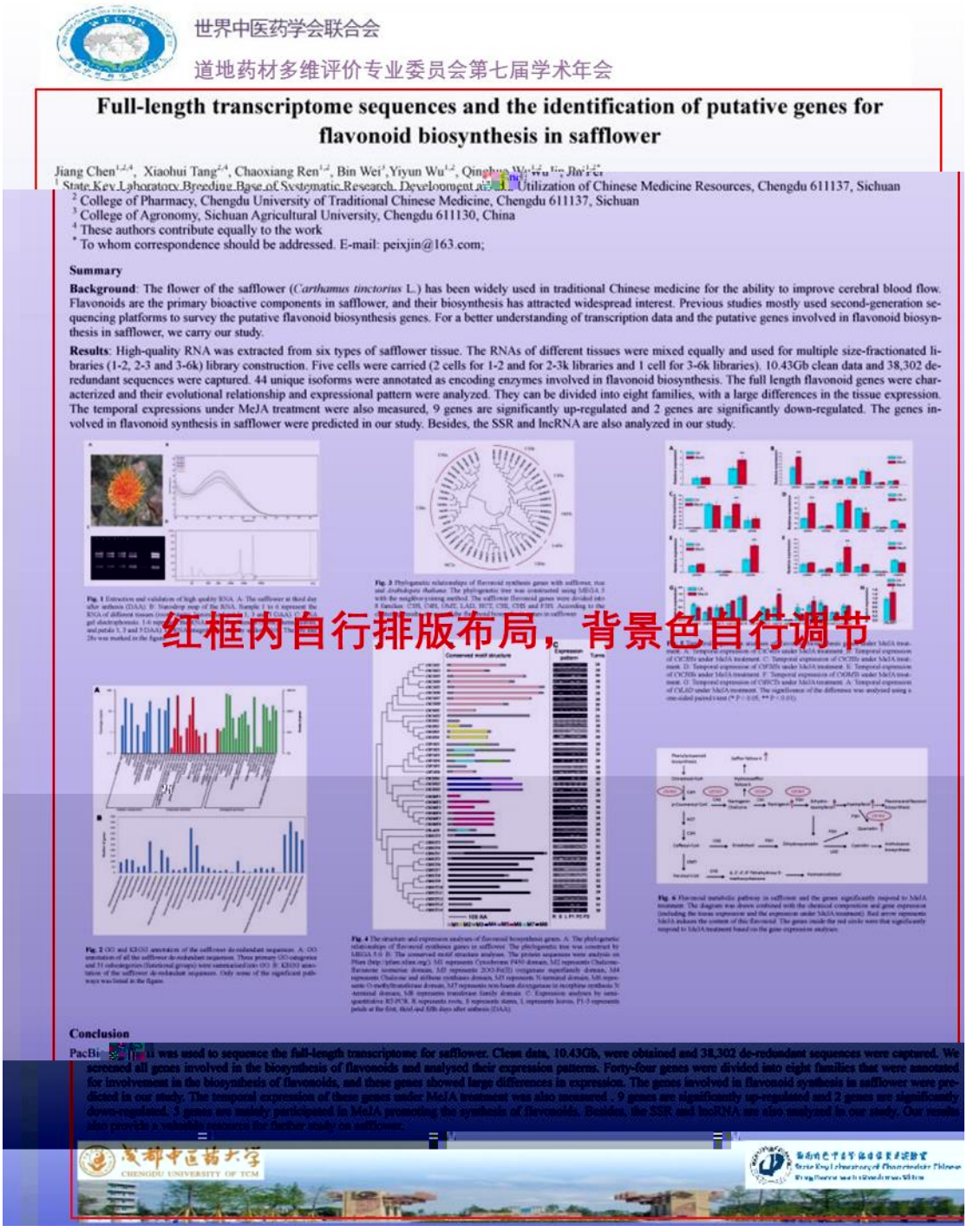
附件 1

壁报格式参考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Full-length transcriptome sequences and the identification of putative genes for flavonoid biosynthesis in safflower
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Summary
Background: The flower of the safflower (Carthamus tinctorius L.) has been widely used in traditional Chinese medicine for the ability to improve cerebral blood flow. Flavonoids are the primary bioactive components in safflower, and their biosynthesis has attracted widespread interest. Previous studies mostly used second-generation sequencing platforms to survey the putative flavonoid biosynthesis genes. For a better understanding of transcription data and the putative genes involved in flavonoid biosynthesis in safflower, we carry our study.
Results: High-quality RNA was extracted from six types of safflower tissue. The RNAs of different tissues were mixed equally and used for multiple size-fractionated libraries (1-2, 2-3 and 3-6k) library construction. Five cells were carried (2 cells for 1-2 and for 2-3k libraries and 1 cell for 3-6k libraries). 10.43Gb clean data and 38,302 de-redundant sequences were captured. 44 unique isoforms were annotated as encoding enzymes involved in flavonoid biosynthesis. The full length flavonoid genes were characterized and their evolutional relationship and expressional pattern were analyzed. They can be divided into eight families, with a large differences in the tissue expression. The temporal expressions under MeJA treatment were also measured, 9 genes are significantly up-regulated and 2 genes are significantly down-regulated. The genes involved in flavonoid synthesis in safflower were predicted in our study. Besides, the SSR and lncRNA are also analyzed in our study.
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Conclusion
PacBi
was used to sequence the full-length transcriptome for safflower. Clean data, 10.43Gb, were obtained and 38,302 de-redundant sequences were captured. We screened all genes involved in the biosynthesis of flavonoids and analysed their expression patterns. Forty-four genes were divided into eight families that were annotated for involvement in the biosynthesis of flavonoids, and these genes showed large differences in expression. The genes involved in flavonoid synthesis in safflower were predicted in our study. The temporal expression of these genes under MeJA treatment was also measured . 9 genes are significantly up-regulated and 2 genes are significantly down-regulated. 5 genes are notably participated in MeJA promoting the synthesis of flavonoids. Besides, the SSR and lncRNA are also analyzed in our study. Our results also provide a valuable resource for further study on safflower.
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