



Transcriptome Analysis of Male and Female Inflorescence of Medicinal Plant *Citrullus Colocynthis* to Identification the Effective Genes in Determination of Flower Sexuality

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Abstract: *Citrullus colocynthis* L. is a perennial plant, with male and female flowers on a monoecious [1]. In the Cucurbitaceae family, the profile of the transcriptome data of flower growth is limited to the determination of the flower sexuality and selective selection, which is regulated by biological agents and herbal hormones [2]. Primary genetic studies indicate that the three sexuality determine genes (F.A.M) in cucumber and melon are biosynthesizing a key enzyme in the hormone ethylene called 1-Aminositicopropane-1-carboxylic acid synthase (ACS) [3]. The APETALA3 gene has identified MADS that is associated with the expression of a specific male gender sequence in the squash (*Coccinia grandis*) [4]. In the present study, in order to evaluate the male and female inflorescence transcriptomes of *Citrullus colocynthis* L., RNA sequencing (RNA-seq) was performed on plant samples of *Citrullus colocynthis* which obtained from Khuzestan region. RNA extraction of inflorescence was done using RNeasy plant mini kit (cot.nos.74903 and 74904) and determination of quality and quantity of RNA was provided by agarose gel and electrophoresis were conducted in the Research Laboratory, Faculty of Agriculture, Islamic Azad University, Ahvaz Branch. RNA sequencing was done in Beijing Genomics Institute (BGI) Company in China. Illumina HiSeq 2500 instrument was used for a paired-end sequencing. Paired-end reads assembled into contigs using Trinity software. The results of this study were used to determine the genes expressed in the identification of inflorescence sexuality and SSR markers that are important in the research of medicinal plants.

Keywords: *Citrullus colocynthis* L., Inflorescence sexuality, Transcriptome, RNA sequencing

References

- [1] F. Zaree Mahmoudabadi, AB. Fallahhossini, F. Sharifabady, R. Nourouzzadeh, A. Emani, H. Ghoshouni, H, "The effect of *Urtica dioica* extract on preventing/reducing streptozotocin-induced diabetes in rat," *J. Kowsar Med.*, 12 (2007) 13-20.
- [2] S. Guo, J. Liu, Y. Zheng, M. Huang, H. Zhang, G. Gong, H. He, Y. Ren, S. Zhong, Z. Fei, Y. Xu, "Characterization of transcriptome dynamics during watermelon fruit development: sequencing, assembly, annotation and gene expression profiles," *BMC Genomics.*, 12 (2011) 454.
- [3] Z. Li, S. Huang, S. Liu, J. Pan, Z. Zhang, Q. Tao, Q. Shi, Z. Jia, W. Zhang, H. Chen, L. Si, L. Zhu, R. Cai, "Molecular isolation of the M gene suggests that a conserved-residue conversion induces the formation of bisexual flowers in cucumber plants," *Genetics.*, 182 (2009) 1381-1385.
- [4] B.K. Bhowmick, S. Nanda, S. Nayak, S. Jha, R.K. Joshi, "An *Apeta3* mads-box linked scar marker associated with male specific sex expression in *coccinia grandis* (L).," *Voigt. Sci. Hort. (Amsterdam).*, 176 (2014) 85-90.