

## Transcriptomic analysis for compactness of Sistan Yaghooti grape clusters

Yasoub Shiri<sup>a</sup>, Mahmood Solouki<sup>b\*</sup>, Esmail Ebrahimie<sup>c, d, e, f</sup>, Abbasali Emamjomeh<sup>g</sup>, Javad Zahiri<sup>h</sup>  
a. PhD student, Department of Plant Breeding and Biotechnology, University of Zabol, Zabol, 9861335856, Iran  
b. Department of Plant Breeding and Biotechnology, University of Zabol, Zabol, 9861335856, Iran  
c. Adelaide Medical School, the University of Adelaide, SA, Australia  
d. School of Information Technology and Mathematical Sciences, Division of Information Technology, Engineering and the Environment, University of South Australia, Adelaide, Australia  
e. Institute of Biotechnology, Shiraz University, Shiraz, Iran  
f. School of Biological Sciences, Faculty of Science and Engineering, Flinders University, Adelaide, Australia  
g. Laboratory of Computational Biotechnology and Bioinformatics (CBB Lab), Department of Bioinformatics, University of Zabol, Zabol, 9861335856, Iran  
h. Bioinformatics and Computational Omics Lab (BioCOOL), Department of Biophysics, Faculty of Biological Sciences, Tarbiat Modares University, Tehran, Iran  
\* mahmood.solouki@uoz.ac.ir

**Abstract:** Yaghooti grape of Sistan is the earliest ripening grape in Iran, which is harvested every May annually. It is compatible to dry conditions in Sistan region and its water requirement is less than other grape cultivars [1]. This study was done to identify the genes involved in compactness of Sistan Yaghooti grape clusters. Therefore, the result of this research is effective in producing grapes with low cluster compactness and this increases marketability and reduces disease damage. On the other hand, identifying the genes involved in the cluster formation process by RNA-Seq method can provide useful information. The transcriptional Complexity was studied in three stages of cluster development and the RNA was extracted [2]. Totally, 24121 genes were expressed in different cluster development steps (step 1: cluster formation, step 2: berry formation, step 3: final size of cluster) of which 3040 genes in the first stage, 2381 genes in the second stage and 2400 genes in the third stage showed a significant increment as their expression. The results of analysis based on GO terms indicated that when the clusters are ripening, activity of the nucleus, cytoplasmic, cytosol, membrane and chloroplast genes in the cluster peduncle and pedicels cells and activity of the endoplasmic reticulum, vacuole and extracellular region genes decrease and increase, respectively. When Yaghooti grape are growing and developing, some of metabolic pathways were activated in the response to biotic and abiotic stresses. The gene co-expression network reconstruction showed that *AGAMOUS* [3] is a key gene in compactness of Sistan grape cluster, because it influences on expression of *GA* gene which leads to increase cluster length and berries size.

**Keywords:** Transcriptome; Gene Co-expression Network; Gene Ontology; RNA-Sequencing

### References

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