



Transcriptome comparison of Shiraz (*Vitis vinifera*) grapevines in distinct sub-regions of the Barossa Valley

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Abstract

Studying the interaction between grapevines and the environment may provide insights of how terroir drives unique characters in wine. Analysing changes in gene expression between different environmental conditions provides a first step in understanding genes that may play a role in grapevine adaption. We, therefore, carried out RNA-seq analysis on Shiraz grapevine leaf tissue harvested from two sub-regions of the Barossa Valley to investigate whether gene expression changes occurred in response to two important environmental factors for plant growth, temperature and elevation. Young leaves from three vineyards in the Barossa central ground and three in the Eden Valley were sampled at budburst. The transcriptome profiling of all samples was clustered by vineyard and separated by region. In total, 429 genes showed significant changes in gene expression between two regions (FDR < 0.001). Among the differentially expressed genes, we found a subset of genes enriched in Gene Ontology (GO) terms that are related to environmental response, including abiotic stress and external biotic stress (Q-value < 0.05). Our study provides preliminary analysis of transcriptome changes in different sub-regions of Barossa Valley and identified potential candidate genes involved in adaptive responses under different environmental condition.

Keywords: transcriptome analysis, RNA-seq, Grapevine adaption, Barossa Valley, terroir, Shiraz