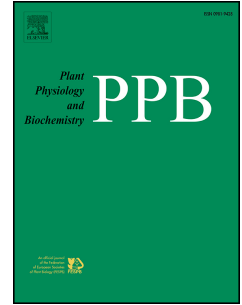


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Grapevine immune signaling network in response to drought stress as revealed by transcriptomic analysis

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1 **Grapevine immune signaling network in response to drought stress as revealed by**
2 **transcriptomic analysis**

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11 **Abstract**

12 Drought is a ubiquitous abiotic factor that severely impedes growth and development of
13 horticulture crops. The challenge postured by global climate change is the evolution of drought-
14 tolerant cultivars that could cope with concurrent stress. Hence, in this study, biochemical,
15 physiological and transcriptome analysis were investigated in drought-treated grapevine leaves.
16 The results revealed that photosynthetic activity and reducing sugars were significantly
17 diminished which were positively correlated with low stomatal conductance and CO₂ exchange
18 in drought-stressed leaves. Further, the activities of superoxide dismutase, peroxidase, and
19 catalase were significantly actuated in the drought-responsive grapevine leaves. Similarly, the
20 levels of abscisic acid and jasmonic acid were also significantly increased in the drought-stressed
21 leaves. In transcriptome analysis, 12,451 differentially-expressed genes (DEGs) were annotated,
22 out of which 8,021 DEGs were up-regulated and 4,430 DEGs were down-regulated in response
23 to drought stress. In addition, the genes encoding pathogen-associated molecular pattern (*PAMP*)
24 triggered immunity (*PTI*), including calcium signals, protein phosphatase 2C, calcineurin B-like
25 proteins, MAPKs, and phosphorylation (*FLS2 and MEKK1*) cascades were up-regulated in
26 response to drought stress. Several genes related to plant-pathogen interaction pathway (*RPML1*,
27 *PBS1, RPS5, RIN4, MIN7, PRI, and WRKYs*) were also found up-regulated in response to

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