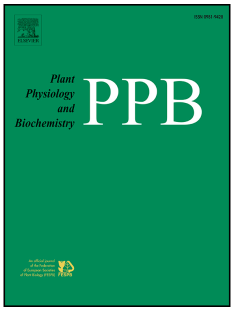

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Grapevine immune signaling network in response to drought stress as revealed by transcriptomic analysis

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Abstract

Drought is a ubiquitous abiotic factor that severely impedes growth and development of horticulture crops. The challenge postured by global climate change is the evolution of drought-tolerant cultivars that could cope with concurrent stress. Hence, in this study, biochemical, physiological and transcriptome analysis were investigated in drought-treated grapevine leaves. The results revealed that photosynthetic activity and reducing sugars were significantly diminished which were positively correlated with low stomatal conductance and CO_2 exchange in drought-stressed leaves. Further, the activities of superoxide dismutase, peroxidase, and catalase were significantly actuated in the drought-responsive grapevine leaves. Similarly, the levels of abscisic acid and jasmonic acid were also significantly increased in the drought-stressed leaves. In transcriptome analysis, 12,451 differentially-expressed genes (DEGs) were annotated, out of which 8,021 DEGs were up-regulated and 4,430 DEGs were down-regulated in response to drought stress. In addition, the genes encoding pathogen-associated molecular pattern (*PAMP*) triggered immunity (*PTI*), including calcium signals, protein phosphatase 2C, calcineurin B-like proteins, MAPKs, and phosphorylation (*FLS2 and MEKK1*) cascades were up-regulated in response to drought stress. Several genes related to plant-pathogen interaction pathway (*RPM1, PBS1, RPS5, RIN4, MIN7, PR1, and WRKYs*) were also found up-regulated in response to