Analysis of Physiological Response and Differential Protein Expression of *P. baillonii* Seedings Under Low Phosphorus Stress

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Abstract: 【Objective】*Paramichelia baillonii* is a rare and fast-growing tree species in subtropical China. The acidic red soil in southern China severely limits its growth as it lacks sufficient available phosphorus (P), resulting in declining soil fertility and nutrient availability. Previous studies only focused on *P. baillonii* geographical distribution, growth patterns, afforestation techniques, wood characteristics, and other related aspects. However, its response to low-P stress on growth, root attributes, and physiological response has not yet been reported. 【Method】We conducted a pot experiment on 2-year-old seedlings and treated them with 31 $mg \cdot L^{-1}$ (CK), 10 $mg \cdot L^{-1}$, 5 $mg \cdot L^{-1}$, 1 $mg \cdot L^{-1}$, and 0 $mg \cdot L^{-1}$ phosphorus stress. 【Result】It showed that compared to CK, low P stress (0-5 $mg \cdot L^{-1}$) decreased growth attributes, root morphological traits, and nutrient uptake of *P. baillonii seedlings*. Similarly, a respective reduction in chlorophyll a, b, total chlorophyll, Net photosynthetic rate (*Pn*), transpiration rate (*Tr),* and *Gs* by 86.23%, 17%, 64%, 62.96 %, 53%, and 47%, was recorded in low P stress compared to CK. Whereas, SOD, POD, MDA, acid phosphatase activity, and soluble protein content were increased with increasing low P-stress up to 5mg·L, although soluble sugar content increased under low P-stress treatments. Moreover, the proteomics analysis identified 2721 proteins, 196 showing differential expression, with 90 up-regulated and 106 down-regulated. Gene ontology and pathways analysis identified that 49.03% of transcripts were involved in molecular function, 34.77% in cellular components, and 16.2% in biological processes. The annotation of these genes provides a pathway analysis for their putative functions under P-stress conditions. The analysis focused on determining the subcellular localization of the identified proteins revealed that a significant proportion (32.14%), of the differentially expressed proteins were predicted to be located in the chloroplasts. This suggests that the chloroplast proteome is particularly susceptible to low phosphorus stress. Moreover, the differential expression of these proteins mainly contributed to the potential changes in redox homeostasis, cellular signalling, transport processes, and overall cellular organization. 【Conclusion】Our current research provides the basis for further revealing the molecular mechanism of *P. baillonii* in response to low P-stress. To understand the molecular mechanisms and metabolic processes involved under low p stress warrants further investigations.

Keywords: *P. baillonii*; Low Phosphorus; Growth; Physiological response, Protein expression