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Transcriptomic insights into phosphorus mobilization in the bacterium *Pantoea agglomerans* 33.1 under nutritional stress

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Phosphorus (P) is a vital element for plant development; however, its low availability in soluble forms on fields often limits agricultural productivity. Plant growth-promoting bacteria, such as *Pantoea agglomerans* 33.1 is able to mobilize insoluble P to plant host. Although the genetic regulation of these processes under different P availabilities remains to be fully elucidated. Therefore, this study aimed to uncover the transcriptional profile of *P. agglomerans* 33.1 under contrasting soluble P conditions (low vs. high concentration) using RNA-seq. Differential expression analysis revealed 1,254 differentially expressed genes (DEGs) (FDR < 0.05). Under low P availability (primary contrast), a robust survival response was observed, characterized by the systemic activation of the Pho regulon. The results highlighted a massive induction of phosphonate utilization pathways and high-affinity transport systems, which are essential for phosphorus scavenging in scarce environments. Additionally, there was a significant increase in the expression of enzymes dedicated to the mineralization of organic P sources, such as alkaline phosphatases and phosphodiesterases. Interestingly, pathways linked to PQQ-dependent organic acid production were also modulated, reinforcing the bacterium's role in the solubilization of inorganic sources. These findings demonstrate that *P. agglomerans* 33.1 possesses high metabolic versatility, prioritizing the exploitation of alternative phosphorus sources under nutritional stress. This study provides a solid molecular foundation for the development of optimized biofertilizers tailored for phosphorus-deficient agricultural systems.

KEYWORDS: Pho regulon, Phosphorus starvation, RNA-Seq, Plant growth-promoting bacteria

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