Label-free proteomics of Lemna aequinoctialis in response to Klebsiella pneumoniae infection

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Duckweed, also known as Lemnaceae, is an aquatic monocotyledonous angiosperm with rapid vegetative proliferation, common in still or slow-moving freshwater environments, including ponds, lakes and marshes. These plants have been considered a unique model system due to their biological characteristics and wide utility, including as a phytoremediation agent, biomass production and, recently, as a potential means of expanding biopharmaceutical production and ecological restoration, and their ability to respond to infection by human pathogenic bacteria. *Klebsiella pneumoniae* (Kp) is a bacterium with a multidrug resistance profile and is associated with most cases of hospital infection. Thus, the present study evaluated the differential proteomic response of *Lemna aequinoctialis* clone RDSC5570 under infection by carbapenem-resistant *Klebsiella pneumoniae* ATCC13883. Total soluble proteins were extracted using a phenolic method, followed by quantification and tryppinization. They were then injected into an LC-MS/MS system (Orbitrap Fusion Lumos Platform). The spectra obtained were processed in MaxQuant software, and the differentially accumulated proteins (DAPs) were identified and analyzed in Perseus software. The DAPs were characterized by gene ontology (Blast2GO/Panther) and evaluated for protein-protein interactions (Cytoscape/String). One hundred DAPs were obtained in the control condition (No Kp) and 129 DAPs positively regulated in response to Kp. Among the induced stress response proteins, the following stand out: DAP Beta-Fructofuranosidase, Long-chain-fatty acid-CoA ligase, NAD(p)H-quinone oxidoreductase, Peptide-methionine oxide reductase, L-ascorbate peroxidase, Lactoylglutathione lyase, Trehalose-6-Phosphate Synthase and Purple acid phosphatase. These proteins are associated with cellular defense, inhibiting or slowing down infection, in addition to acting throughout plant development and growth, cell wall thickening, phytohormone production, metabolite transport, cell signaling, control of xenobiotic compounds and antioxidant activity. These proteins together act to try to mitigate the damage suffered by the infection, as they are natural compounds, produced by the plant\'s protein synthesis, and are targets of biotechnological studies. Understanding these molecular mechanisms involved in infection and the identified induced proteins can help elucidate functional, metabolic and biochemical mechanisms of plants, in addition to prospecting compounds with potential antimicrobial activity.

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