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Profiling of differential expressed proteins from various explants in *Platycodon grandiflorum*

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Abstract

Though the *Platycodon grandiflorum*, has a broad range of pharmacologic properties, but the mechanisms underlying these effects remain unclear. In order to profile proteins from the nodal segment, callus, root and shoot, high throughput proteome approach was executed in the present study. Two-dimensional gels stained with CBB, a total of 84 differential expressed proteins were confirmed out of 839 protein spots using image analysis by Progenesis SameSpot software. Out of total differential expressed spots, 58 differential expressed protein spots (≥ 2-fold) were analyzed using MASCOT search engine according to the similarity of sequences with previously characterized proteins along with the UniProt database. Out of 58 differential expressed protein, 32 protein spots were up-regulated such as ribulose-1,5-bisphosphate carboxylase, endoplasmic oxidoreductin-1, heat stress transcription factor A3, RNA pseudourine synthase 4, cysteine proteinase, GntR family transcriptional regulator, E3 xyloglucan 6-xylosyltransferase, while 26 differential protein spots were down-regulated such as L-ascorbate oxidase precursor, late embryogenesis abundant protein D-34, putative SCO1 protein, oxygen-evolving enhancer protein 3. However, the frequency distribution of identified proteins using iProClass databases, and assignment by function based on gene ontology revealed that the identified proteins from the explants were mainly associated with the nucleic acid binding (17%), transferase activity (14%) and ion binding (12%). Taken together, the protein profile may provide insight clues for better understanding the characteristics of proteins and its metabolic activities in various explants of this essential medicinal plant *P. grandiflorum*.

Keywords: *Platycodon grandiflorum*, proteome profiling, functional categorization

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