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Proteome characterization of hormone-induced diploid and tetraploid roots of *Platycodon grandiflorum*

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Abstract

Plants, including *Platycodon grandiflorum* have been used globally across varied cultures as a safe natural source of medicines. From time immemorial, humans have relied on plants that could meet their basic necessities such as food, shelter, fuel and health. This study was executed to profile proteins from the hormone induced diploid and tetraploid roots using high throughput proteome approach. Two dimensional gels stained with CBB, a total of 64 differential expressed proteins were identified from the diploid root using image analysis by Progenesis SameSpot software. Out of total differential expressed spots, 20 differential expressed protein spots (≥ 1.5 -fold) were analyzed using LTQ-FTICR MS whereas a total of 13 protein spots were up regulated and 7 protein spots were down-regulated. However, in the case of tetraploid root, a total of 78 differential expressed proteins were identified from tetraploid root of which a total of 28 differential expressed protein spots (≥ 1.5 -fold) were analyzed by mass spectrometry whereas a total of 16 protein spots were up regulated and a total of 12 protein spots were down-regulated. However, proteins identified using iProClass databases revealed that the identified proteins from the explants were mainly associated with the nucleic acid binding, oxidoreductase activity, transporter activity and isomers activity. The exclusive protein profile may provide insight clues for better understanding the characteristics of protein function and its metabolic activity that can help for the development of the nutritional and breeding aspects of this economically important medicinal plant.

Keywords: hormonal effects, diploid root, tetraploid root, protein profiling, *Platycodon grandiflorum*

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