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Comparative proteome analysis of diploid and tetraploid root in *Platycodon grandiflorum*

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Abstract

In spite of the potential medicinal significance and a wide range of pharmacologic properties of *Platycodon grandiflorum*, the molecular mechanism of its roots is still unknown. The present study was conducted to profile proteins from 3, 4 and 5 months aged diploid and tetraploid roots of *Platycodon grandiflorum* using high throughput proteome approach. Two-dimensional gels stained with CBB, a total of 68 differential expressed proteins were identified from the diploid root out of 767 protein spots using image analysis by Progenesis SameSpot software. Out of total differential expressed spots, 29 differential expressed protein spots (≥ 2 -fold) were analyzed using LTQ-FTICR MS whereas a total of 24 protein spots were up-regulated and 5 protein spots were down-regulated. On the contrary, in the case of tetraploid root, a total of 86 differential expressed proteins were identified from tetraploid root out of 1033 protein spots of which a total of 39 differential expressed protein spots (≥ 2 -fold) were analyzed using LTQ-FTICR MS whereas a total of 21 protein spots were up-regulated and a total of 18 protein spots were down-regulated. It was revealed that the identified proteins from the explants were mainly associated with the nucleotide binding, oxidoreductase activity, transferase activity. Taken together, the identified proteins may be helpful to identify key candidate proteins for genetic improvement of plants.

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

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