

## Proteome characterization of the liquid cultured tetraploid roots in *Platycodon grandiflorum*

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### Abstract

The roots of *Platycodon grandiflorum* are commonly used for treating bronchitis, asthma, tuberculosis, diabetes, and other inflammatory diseases. Since the molecular mechanism underlying the roots of the plant is unclear. Therefore, the present study was conducted to profile proteins from liquid cultured tetraploid roots of *Platycodon grandiflorum* using high throughput proteome approach. Two-dimensional gels stained with CBB, a total of 659 differentially expressed proteins were identified from the liquid medium cultured tetraploid roots of which 32 proteins spots ( $\geq 1.5$ -fold) were sorted for mass spectrometry analysis. Out of these 32 proteins, a total of 15 proteins were up-regulated such as Serine carboxypeptidase-like 27, Transcription factor bHLH150, 60 kDa jasmonate-induced protein, Cytosolic Fe-S cluster assembly factor NBP35, Regulatory associated protein of TOR 2 and a total of 17 proteins were down-regulated such as Protein G1-like2, Phenylalanine ammonia-lyase, Fructokinase-2, Trihelix transcription factor GT-3a, Guanine nucleotide-binding protein alpha-1 subunit. However, the frequency distribution of identified proteins was carried out within functional categories based on molecular functions, cellular components, and biological processes. Functional categorization revealed that the most of the identified proteins from the explants were mainly associated with the nucleic acid binding, oxidoreductase, transferase activity, protein binding and hydrolase activity. In addition, the proteomic feedback of tetraploid roots of *P. grandiflorum* may potentially be used to understand the characteristics of proteins and their functions.

**Keywords:** *Platycodon grandiflorum*, proteome profiling; functional categorization; metabolic activity

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