



## BIOSYNTHESIS OF SECONDARY METABOLITES IN *Peperomia obtusifolia*: A PROTEOMIC APPROACH

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**Purpose of study:** *Peperomia obtusifolia*, an ornamental plant from Piperaceae family, accumulates bioactive secondary metabolites such as prenylated chromanes, lignans, amides, flavonoids and others phenolic derivatives [1,2]. Interestingly, this species seems to produce orsellinic acid-derived benzopyrans only, with some of them being isolated as racemic mixtures. The latter fact suggests either a chemical cyclization of the geranylated orsellinic acid precursor or the presence of two separate enzymatic systems devoted to the formation of each enantiomer. Therefore, *P. obtusifolia* represents an interesting plant for biosynthetic studies. Herein we report a comparison between the protein (soluble and microsomal fractions) and metabolic profiles of roots, stems and leaves of *P. obtusifolia* using shotgun proteomics and chromatographic methods.

**Methods:** Tryptic peptides were analyzed using an UFLC-DAD system coupled with mass spectrometry (ESI-IT-TOF). Proteins were identified from online databases (Swiss-Prot and NCBI) using the MASCOT protein search engine within Viridiplantae taxonomy. The metabolic profiles were determined by using HPLC-PAD-MS and GC-MS analyses.

**Results and Conclusions:** The shotgun proteomic analysis of the solution and microsomal fractions of different organs from *P. obtusifolia* led to the identification of more than 1500 proteins. Although the majority of these proteins were associated with the primary metabolism, a significant number of proteins involved in the secondary metabolism were also found (5% in soluble fraction and 20% in microsomal fraction), including enzymes related to the biosynthesis of prenylated chromanes, flavonoids and terpenes. These findings were corroborated by the metabolic profiles of the crude extracts of different organs from *P. obtusifolia* obtained via HPLC-PDA-MS and GC-MS analyses.

### References:

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