



**METABOLOMICS OF PSITTACANTHUS CORDATUS (HOFFMANN.) G. DON PARASITIZING
DIFFERENT HOST SPECIES**

Bruna Doimi Ortolan^{1*}, Mariana T. Hufnagel¹, Carlos A. Carollo², Flávio M. Alves³, Daniel P. Demarque¹

brunadoimi@usp.br

1- Pharmacognosy Laboratory, Department of Pharmacy, Faculty of Pharmaceutical Sciences, University of São Paulo, São Paulo, SP 05508-000, Brazil. 2- Laboratory of Natural Products and Mass Spectrometry (LaPNEM), Faculty of Pharmaceutical Sciences, Food and Nutrition (FACFAN), Federal University of Mato Grosso do Sul, Campo Grande, Mato Grosso do Sul 79070-900, Brazil. 3- Laboratory of Botany, Institute of Biosciences (INBIO), Federal University of Mato Grosso do Sul, Campo Grande, Mato Grosso do Sul 79070-900, Brazil.

Psittacanthus cordatus, also known as “erva-de-passarinho”, is a parasitic plant from the Loranthaceae family that uses a specific organ, the haustorium, to uptake water and nutrients from its hosts. Parasitic plants, as agricultural pests, can damage and decrease crop productivity, but also disturb ecosystems and biodiversity. Thus, understanding host–parasite interactions is crucial for developing effective control strategies. In this study, we investigated the phytochemistry based on a metabolomic profile of *P. cordatus* growing on four different host species. The plants (parasites, hosts and non-parasitized plants) were collected in Pantanal-Brazil, the leaves and stem methanolic extracts of those groups were analyzed by HPLC-ESI-qTOF-MS untarget metabolomics and networking (GNPS platform) to compound comparison between the plants. In those networks, we identified some nodes with a shared distribution between both the host plants and their parasite, suggesting a possible parasite-host metabolite transference. Another networking, with all parasites, were also built to investigate differences between them, showing nodes with different distributions in each group. Multivariate ANOVA one-way statistics were used on MetaboAnalyst 6.0 to compare parasites data, showing nine ions with significant differences in their distribution, depending on the host to which the parasite was associated. At last, in the annotation process of *P. cordatus*, the GNPS library matched with several flavonoids and flavonoid O-glycosides. Other compounds that were not able to identify and will be subjected to further investigation and isolation process. We concluded that, so far, it is possible to see differences in the chemical profile of the species, based on the host association. These findings contributed to a better understanding of the biochemical interactions between parasites and hosts plants. The authors acknowledge FCF-USP for providing the infrastructure and FAPESP (processes 2024/18203-0; 2022/08191-9) for financial support.

Keywords: Metabolomics, parasitic plant, phytochemistry, Loranthaceae, natural products

