METABOLITE PROFILING ANALYSIS IN SOYBEAN ROOTS INFECTED WITH THE BIOLOGICAL CONTROL FUNGUS Pochonia chlamydosporia AND ITS EFFECT ON DROUGHT TOLERANCE

IAN DE PAULA ALVES PINTO[1], Juliano Mendonça Rodrigues[1], Maria Goreti Almeida Oliveira[1], Humberto Josué de Oliveira Ramos[1,2], Monique Silva Bonjour[1], Leandro Grassi de Freitas [3]

[1.] DBB, Laboratory of Enzymology and Biochemistry of Proteins and Peptides, Department of Biochemistry and Molecular Biology, Universidade Federal de Viçosa,, Vila Matoso, 205 - Santo Antonio, Viçosa - MG, 36570-000;
[2.] NuBiomol, Laboratory of Enzymology and Biochemistry of Proteins and Peptides, Department of Biochemistry and Molecular Biology, Universidade Federal de Viçosa, UFV, BIOAGRO/INCT-IPP,, Vila Gianetti, 21 - Santo Antonio, Viçosa - MG, 36570-000;
[3.] DFP, Department of Phytopathology, UFV, Viçosa-MG, Brazil, Universidade Federal de Viçosa, Edifício Sylvio Starling Brandão - R. Purdue - Campus Universitário, Viçosa - MG, 36570-900;

Soybean is one of the most important grains in Brazil´s economy, being the world´s largest producer. However, climate change has led to fluctuations in rainy periods, reducing productivity due to drought. Therefore, it is necessary to employ various technologies to maintain efficient agriculture, such as the use of growth-promoting microorganisms. The fungus *Pochonia chlamydosporia* is known for its nematicidal action and beneficial association with plants. However, the relation between the fungal inoculation and drought tolerance has not been evaluated. To investigate this, soybean seeds of genotypes EMBRAPA 48 (tolerant) and BR 16 (sensitive) were grown in the presence of the fungus under both irrigated and drought conditions. When the plants reached a water potential of 1.0 MPa, fresh root material was collected and frozen in liquid nitrogen. Methanolic extracts were subjected to non-targeted LC/MS analysis, and the resulting profiles were aligned using the XCMS platform to identify metabolites responsive to the fungus-plant interaction and their relationship with drought tolerance. Subsequently, the spectra of metabolites altered in response to drought and fungal colonization were used for identification using the NIST library. Additionally, targeted LC/MS analysis was conducted for various compounds classified as phytohormones, proline, polyamines, and phenolic compounds. ABA concentrations in leaves and roots of both genotypes increased in response to water deficit, while JA and 1-aminocyclopropane-1-carboxylic acid responded to drought treatment. The metabolic response of plants in the presence of the fungus varied between evaluated genotypes. Fungal inoculation enhanced drought tolerance in both genotypes, maintaining leaf turgor. Changes in phenolic compound pathways correlated with alterations in xylem vessel caliber and hydraulic conductivity in fungus-exposed plants. Several pathways and compounds were significantly altered in response to drought and fungal interaction, including metabolites belonging to flavonoid, flavone, and flavonol biosynthesis pathways. These compounds may also be involved in various specialized metabolic functions, such as protection against oxidative stress damage and maintenance of redox homeostasis.

Agradecimentos: I thank the Minas Gerais Research Support Foundation (FAPEMIG), National Council for Scientific and Technological Development (CNPq) for the financial support. And I also thank the Federal University of Viçosa and the Biomolecule Analysis Center (NuBioMol).