Metabolomic analysis of the fungus Aspergillus niger cultivated in agri-food waste

Jhuly Wellen Ferreira Lacerda[1], Louis Pergaud Sandjo[1]

[1.] UFSC, Universidade Federal de Santa Cataria, Trindade, 88040-900, Florianópolis – SC, Brasil;

Aspergillus niger is a fungus of great biotechnological importance, used in fermentation processes to produce commercial substances, such as citric, gluconic, and oxalic acids, as well as enzymes. For its growth, a culture medium containing proteins, mineral salts and carbon is required. These components represent a cost, which can be reduced through the use of alternative sources, such as organic waste. According to the Food and Agriculture Organization (FAO), around 1.3 billion tons of food produced worldwide is lost or wasted each year. Thus, the use of these agri-food residues as a source of carbon and nutrients for the production of biomolecules through fermentation is not only economical, but also offers a more sustainable solution. The present work aims to carry out a metabolomic study of the fungus *A. niger* cultivated in banana peel residues. Two types of culture medium were applied: banana peel (BP) and banana peel enriched with starch (BPS), for both the fungus was cultivated for 14, 21 and 28 days. EtOAc solvent was used for extraction. All extracts obtained were analyzed by UPLC-ESI-QTOF-MS, acquiring data of the DIA and DDA types. The characterization of the chemical profile was performed by manual dereplication methods and the MS-DIAL and MS-Finder software. The multivariate statistical analysis PCA, PLS-DA and Heatmap were performed on the MetaboAnalyst. As a result, 44 metabolites were identified, belonging to the chemical classes of polyketides, phenolic acids, alkaloids, fatty acids and others. Some of these metabolites have already been reported in the literature as produced by the genus Aspergillus in conventional culture medium. A series of compounds from the naphtho-?-pyrone class were identified, which are predominantly produced by *A. niger* and present biological activities such as antituberculosis, antimicrobial and antitumor properties. Due to the large volume of data generated, multivariate statistical analyses were applied to better visualize the results. Due to the large volume of data generated, multivariate statistical analyses were applied to better visualize the results. The PCA plots, with 82.8 and 78% of the total data variance in the positive and negative modes, respectively, showed that there are variables (metabolites) that place the BPS28d culture medium in a clearly distinct group. The PLS-DA plots, with 75% and 68.8% of the variance in the positive and negative modes, respectively, reinforcing the clear distinction of the BPS28d medium. The heatmap plot revealed that some metabolites are more abundant in a specific type of culture medium. Compounds such as pyranonigrin A, nigerpyrone, aurasperone D, aspergilactone A, kotanin and versicolorin, already known to be produced by the genus Aspergillus, were shown to be predominant in the BPS28d. This suggests that these metabolites are responsible for the distinction of the BPS28d medium observed in the PCA and PLS-DA plots. It was observed that the fungus *A. niger* produced different metabolites when cultivated in each medium, as well as variations over the cultivation time. BPS28d stood out for favoring production rich in metabolites. Therefore, the use of agrifood waste as biomass for microbial cultivation proved to be a promising and low-cost opportunity for the production of biomolecules.

Agradecimentos: aos órgão de fomento CNPq e CAPES, a instituição UFSC e aos laboratórios LQPN e MIP.