D-157 (PMBqBM) - Identification and quantification of flavonoids in inoculated wheat with rizobacteria

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INTRODUCTION: Among the most studied plant exudates are flavonoids. Secondary water soluble phenolic compounds present in almost all plant organs, functions in antioxidant processes and stimulants benefiting the vegetable. They are involved in the communication of microorganisms with plants such as wheat, a second crop of grains most produced in the world, fundamental in human food OBJECTIVES: To evaluate quantitatively and qualitatively flavonoids produced in wheat roots inoculated with native rhizobacteria of biotechnological potential, in order to point out new strains favoring nitrogen fixation MATERIALS AND METHODS: *In vitro* experimental design will be composed of 8 treatments and 4 replicates of the CD 150 wheat inoculated with different microorganisms: *Azospirillum brasiliense; Herbaspirillum seropedicae, Enterobacter sp,* of different strains and their associations, being used two alternative solutions with and without addition of nitrogen. The roots of the plants are dehydrated in greenhouse and the extracts for the quantification of flavonoids collected through reflux for nutrient analysis For the identification and quantification of phenolic compounds, the extract will be submitted to high performance liquid chromatography (HPLC), nuclear magnetic resonance (NMR) and scanning electron microscopy (SEM). DISCUSSION AND RESULTS: Preliminary HPLC analyzes indicated 0.4455 µg g^{-1} of flavonoids present in the root. The treatments with the highest mean were Enterobacter sp. Nos. 203 and 493, differing statistically only from Witness N + and Herbaspirilum. The Witness N + also presented statistical difference of the inoculation with Enterobacter sp. in 208. Analyzing individually, the percentages found of two flavonoids are found, quercitina of 2,2 to 2,9% and rutin of 2,7 to 7,0%, depending on the treatment analyzed CONCLUSION: The discussion of the results evidenced the presence of specific flavonoids in the root, but it is not possible to point out the innocuous one that presents better plant / microorganism communication capacity favoring the biological fixation of nitrogen due to lack of tests. **Keywords:** NBF, Root, Bacteria

D-158 (PMBqBM) - Differential proteomic analysis of wheat variety roots which have distinct association with *Hesbaspirillum seropedicae*

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INTRODUCTION: The expression of proteins that may be related to the association for the benefit of the plant and of pathogenicity was observed in Crop plants seeded plant growth promoting rhizobacteria (PGPR). In wheat, it was shown two varieties, CD 120 and CD 104, that presented different productivity data when they were sown with *H. seropedicae* bacteria in greenhouse. They indicated beneficial association (CD 120) and non-association (CD 104). The roots of plants are the place by which PGPR begin their communication. In this way, to better understand how this association occurs, proteomic analysis can be an effective tool, as it has been to other studies. OBJECTIVES: It will be to know wheat varieties association potential through the study of total proteins expressed in roots of wheat seedlings grown *in vitro* with *H. seropedicae* in liquid medium in the absence of nitrogen source. MATERIALS AND METHODS: For this, wheat seeds of the CD 120 and CD 104 varieties will be grown in liquid medium in vitro. The treatments will be constituted in: seeds inoculated with *H. seropedicae*. For control seeds will be cultivated MS medium without nitrogen source and MS medium with nitrogen source. The best time will be evaluated for interaction through optical and scanning microscopy. Different protocols of total protein extraction will be assayed and, Shotgun proteomic analysis will be performed. DISCUSSION AND RESULTS: The work will produce quantitative expression data of proteins from each treatment that will be compared statistically. Data will also be compared in terms of biological function groups. CONCLUSION: The results intend to contribute to the discussion in the literature about the metabolic and physiological relationships in plant and bacterial interaction. And to observe which pathways of metabolism are relate to the interaction of plant bacteria to obtain biotechnological products. **Keywords:** Plant physiology, Proteomic analysis, Root / **Supported by:** FAP-PR Araucária Foundation

D-159 (PMBqBM) - Selection of Agro-industrial Waste to Produce Fungal Cellulase and Pectinase by Solid State Fermentation

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INTRODUCTION: Agro-industrial residues such as leaves, pods, barks, and bagasse have great potential to be used as a solid substrate in bioprocesses. Among the positive points for reuse of these residues are the low cost when compared to artificial substrates. Besides, through microorganism cultivation, the biomass volume that accumulates in the soil will reduce, and residues are converted into high-value metabolites, such as vitamins, organic acids and enzymes. Among the enzymes, hydrolases are of major industrial interest, due to their wide range of applications. OBJECTIVES: To use the residues of *Mangifera indica* (mango), *Theobroma grandiflorum* (cupuaçu), *Bertholletia excelsa* (Brazil nut), and *Ananas comosus* (pineapple) as solid substrate for the cultivation of *Aspergillus brasiliensis* to produce cellulase and pectinase. MATERIALS AND METHODS: The residues were acquired at popular markets in Manaus, Amazonas, dried at 45°C for 7 days and grounded to powder. The powder was supplemented with a solution containing NH_4NO_3, KH_2PO_4, and distilled water until 70% moisture was achieved. *Aspergillus brasiliensis* ATCC16404 was inoculated ($1x10^7$ spores/mL) and cultured at 28°C for 7 days. The enzymatic extract was obtained by filtration and the enzymatic activity was measured using the DNS method. DISCUSSION AND RESULTS: The shells of Brazil nut showed to be the best substrate for cellulose production, by reaching the higher enzymatic activity (0.686 U/mL), while the shells of cupuaçu showed to be suitable for pectinase production (1.01 U/mL). When the fungus was cultivated in the residues of mango and pineapple, no enzymatic activity was detected for either the enzymes. CONCLUSION: The residues of Brazil nut and cupuaçu were selected as substrates for the production of cellulose and pectinase, respectively. In the next phase of this work, we aim to optimize the production of these enzymes, identifying the most influential process variables, in order to increase enzyme activity. **Keywords:** Bioprocesses, hydrolases, fruit residues. **Supported by:** CAPES