

## **A25 - ANALYSIS OF PROTEIN EXPRESSION DIFFERENT AGENCIES: PRACTICE IN EXPERIMENTAL LABORATORY PROTEOMIC**

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### **Abstract:**

Proteomics is one of the currently existing technology platforms aimed to isolate, identify, characterize and quantify all proteins involved in a particular chain, organelle, cell, tissue, organ or organism. In the specific case of this study, emphasis was given to experimental approaches, the proprietor of the proteomics discipline that saw the need to understand the basic principles associated with each experimental approach, referring to methodologies and tools currently used in the analysis of protein expression in different tissues human, animal and plant. Thus experimental practice developed in this paper, aimed to apply / adapt / optimize / evaluate methodologies and tools proposed for the analysis of protein expression in plant tissue using seeds of the species *Myrciaria dubia* (Kunth) McVaugh, in proteomics laboratory of the Federal University of Amazonas (UFAM). Protocols for protein extraction and digestion in gel were applied, making the necessary adaptations, for the analysis of protein expression in seeds of *M. dubia*, originating from the state of Roraima. Since, due to the currently existing protocols and provided theoretical basis, 2D electrophoresis and mass spectrometry were selected for the experimental realization of practical techniques. These experiments were divided into, each containing two phases. In the case of seeds of *M. dubia*, how the sample was submitted prior to the drying process, it was possible the application of protocols provided, in part, to obtain information about the proteomic profile. Even so, some results were obtained. In the case of seed sample, one can see that among all the profiles obtained is the one who presented differently when visualized with Coomassie Brilliant Blue. M :molecular weight marker ( Page Ruler Prestained Protein Ladder Plus, Fermentas ). In proteomics quality, ways of collecting and conservation, the sample is critical for completion of the entire process. Because there is not yet a single extraction protocol or solvent, which can capture a complete proteome. Thus, the results obtained, it is necessary to make an adjustment to the protocol already described according to the characteristics of the tissue under investigation. A new collection and repeat the whole process is necessary if followed exactly the techniques of collecting and conservation.