Proteomic Analysis of Brain Tissue in Mice Exposed to a High-Fat Diet

Guilherme Ferraz Alvino de Santanna Costa[1], Michele Rodrigues Martins[1], Guillaume Nugue[1], Yara Martins da Silva [1], Livia Goto Silva[2], Fábio César Sousa Nogueira[1], Stevens Kastrup Rehen[2], Magno Junqueira[1]

[1.] UFRJ, Universidade Federal do Rio de Janeiro , Av. Athos da Silveira Ramos, 274 – Cidade Universitária;
[2.] IDOR, O Instituto D\'Or de Pesquisa e Ensino , Rua Diniz Cordeiro 30, Botafogo Rio de Janeiro ;

Introduction: The growing interest in neuroscience, along with current studies on how obesity is detrimental to a state of homeostasis, enhances the understanding of human behavior and physiology, driving a series of innovative studies. The field of proteomics, together with animal models, is a promising research alternative to understand how high-fat diets interfere with our system and metabolism. **Objective:** To analyze the proteomic profiles of brain tissue in mice under obesity conditions. **Methods:** In this project, two groups of samples were formed with biological triplicates: control mice and mice treated with "cafeteria food" (a high-fat diet). The samples were lysed and, after centrifugation, the proteins were extracted. These proteins were reduced, alkylated, and digested. The generated peptides were properly separated in each group condition and then taken for analysis by mass spectrometry using the Label-free method. The obtained data were processed by Proteome Discoverer 2.1 software and are also being analyzed by Perseus software. **Preliminary Results:** So far, a significant number of proteins have been identified for each condition. In total, we identified 4,347 proteins, some of them contaminants, allowing an interesting comparative view of the groups and their PCAs. **Perspectives:** The obtained data are still being analyzed. With this, we hope to gain more in-depth information about the relationship between the groups and a statistical view of them. We aim to solidify the results using software, identifying the biological and molecular enrichment pathways of the analysis group, allowing a comparative view that reveals the physiological and metabolic changes in the tested mice under their condition.Ultimately, this comprehensive analysis will help us understand the broader implications of these findings for a future potential therapeutic strategies.

Agradecimentos: