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IDENTIFICATION OF ENERGY HOMEOSTASIS SIGNALS FROM ADIPOSE TISSUES SECRETOME

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Introduction: A wide variety of endogenous systems regulating appetite, metabolism and energetic homeostasis have been traditionally studied in brain and peripheral tissues. However, there is still a need to improve our knowledge on the molecular mechanisms implicated in obesity development. The main objective of this work is the identification of new signalling systems from adipose tissues implicated in energy homeostasis regulation. We are applying proteomics as new emerging technology proven to be very useful for the identification of new disease target proteins, since it has been barely used for obesity studies.

Objectives: 1. To establish and characterize animal models for obesity proteomics: rats at sedentary, under voluntary exercise, activity-based anorexia (ABA) and obese conditions. 2. To standardize proteomics protocols for tissue secretion studies. 3. To obtain each tissue secretome reference map and to perform the differential secretome analysis in different nutritional status.

Methods: Animal models have been established in Sprague Dawley rats using activity wheels for voluntary exercise and ABA; obesity is being induced by high-fat diet (DIO). Animal models nutritional and metabolic status has been characterized by hormone determination, HOMA assays, body composition and metabolic enzyme profile expression. Fat subcutaneous, gonadal and visceral tissue explants have been incubated *in vitro* for secretome collection. Secretome samples have been submitted to bi-dimensional electrophoresis and mass spectrometry (MALDI-TOF/TOF).

Results: We have set and characterized sedentary, voluntary exercise and ABA animal models; the DIO model is currently being established. We have optimized the proteomics protocols for the tissue explants secretome studies. We are currently completing the reference maps for all tissue secretomes previous to the differential analysis. Preliminary results show known and novel proteins secreted by adipose tissue.

Conclusions: Proteomics technology proves to be a powerful tool for tissue secretome analysis and for the identification of new adipokines implicated in energy homeostasis.