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Proteomic white adipose tissue analysis of obese mice fed with a high-fat diet and treated with oral angiotensin-(1-7)

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The renin-angiotensin system (RAS) is recognized by its pivotal role on cardiovascular regulation and more recently also on metabolism. Angiotensin-(1-7) has been described as a new potential therapeutic tool on treating and preventing metabolic disorders by regulating several pathways in visceral white adipose tissue (vWAT). This tissue has an important role on the corporal and metabolic homeostasis. The aim of this study was to access the proteins differentially regulated by Ang-(1-7) using proteomic analysis of visceral white adipose tissue. Male FVB/N mice were divided into three groups and fed for 60 days, with each group receiving one of the following diets: Standard diet+HPβCD (ST), high fat diet + HPβCD (HFD) and high fat diet+Ang-(1–7)/HPβCD (HFD+Ang-(1-7)). Body weight, fat weight and food intake were measured. At the end of treatment, Ang-(1-7) induced a decreased in body and fat weight. Differential proteomic analysis using two-dimensional electrophoresis (2-DE) combined with mass spectrometry were performed to elucidate the molecular action of Ang-(1-7) on the antiobesity effect in visceral white adipose tissue. Results of protein mapping of mesenteric adipose tissue using 2-DE revealed the presence of about 450 spots in each gel (n=3/treatment) with a great reproducibility (>70%). Image analysis and further statistical analysis allowed the detection and identification of eight proteins whose expression were modulated in response to HFD when compared to ST. Among these, two proteins showed a sensitive response to Ang-(1-7) treatment (Enolase1 protein and aldehydedehydrogenase mitochondrial precursor). Besides, three proteins were statistically different expressed between HFD+Ang-(1-7) and HFD groups and four proteins were modulated compared to standard diet. In conclusion, comparative proteomic analysis of a mice model of diet-induced obesity allowed us to outline possible pathways involved in the response to Ang-(1-7), suggesting that Ang-(1-7) may be a useful tool for treat metabolic disorders.