## Transcriptomics expression analysis to unveil the molecular mechanisms underlying the cocoa polyphenol treatment in diet-induced obesity rats

## ABSTRACT

Cocoa polyphenol (CP), due to their biological actions, may be supplementary treatments for adipose tissue-fat gain. However, the molecular mechanism of CPs is still ambiguous. This study investigated the hypothesis that CP treatment modulates expressing of lipid metabolism genes in mesenteric white adipose tissue (MES-WAT). Sprague–Dawley (SD) rats were fed a low-fat (LF) or high-fat (HF) diet for 12 weeks. Thereafter, HFD rats (n = 10/group) were treated at a dose of 600 mg/kg bw/day CPs (HFD + CPs) for 4 weeks. DNA microarray analysis resulted in 753 genes of the 13,008 genes expressed. Bioinformatics tools showed CP treatment significantly decreased gene expression levels for lipogenic enzymes, while increased the mRNA levels responsible for lipolysis enzymes. CP administration differentially regulates gene expression involved in lipid metabolism in MES-WAT. These data unveil a new insight into the molecular mechanisms underlying the pharmacological effect of CPs on obesity biomarkers in obese rats.

Keyword: DNA microarray; Cocoa polyphenol; Transcriptomics; MES-WAT; Lipid metabolism; Obesity