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NMR METABOLOMICS TO STUDY THE REGULATION OF ENERGY METABOLISM ON CHICKEN LINES DIVERGENT FOR LOW OR HIGH ABDOMINAL FAT DEPOSITION

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The body fat content and partition of lipid stored in the different tissues of the carcasses are important phenotypic traits to be considered for the sustainability of farm animal production. Both genetics and non-genetic factors, including the distribution of diets formulated under the optimal requirements, are able to modify body fatness of growing animals, through their actions on lipid metabolism.

This project aimed to characterize the response of lipid metabolism and body fat based on two types of diets more or less rich in fiber (high and low fat) and in two chicken lines divergent for carcass fatness (4 experimental groups). The goal was to detect overall metabolic perturbations of 48 chicken plasma samples. A metabolomic approach using the 1D ^{1}H NMR experiments was recorded on a Bruker Avance 500 spectrometer with a cryoprobe. NOESY 1D NMR sequence including water presaturation was used to obtain plasma metabolic profile. After identifying metabolites, a statistical approach was applied on data for metabolites discrimination. The statistic tests included univariate (ANOVA, BoxPlot) and multivariate analysis (PCA, PLS-DA) using the free R software and SIMCA P+ (Umetric®), respectively. Plasma metabolic profiles were different in chickens fed with high and low fat diets. Lipid concentrations were significantly increased whereas LDL (Low Density Lipoprotein) levels were decreased in plasma of chickens fed high fat diet ($p<0.001$). A significant difference was also observed in plasma metabolites (glutamine, histidine and betaine) of chickens issued from fat or lean lines. These results confirmed previous data obtained on these lines and suggested the implication of methyl donors on the regulation of lipid metabolism. This study provided new information on circulating metabolites, which may help in elucidating key regulators associated to variations in body fat content.

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