TRANSCRIPTOMIC ANALYSIS OF GENES INVOLVED IN THE LIPID METABOLISM OF THE ALENTEJANO PIG

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Abstract: The Alentejano pig is an autochthonous breed scarcely selected, that due to its high trend for fat deposition present poorer lean yields than modern commercial breeds. However, its higher contents of intramuscular fat (IMF) increase pork sensory attributes and consumers' acceptability. Animal cells can obtain fatty acids (FA) from three distinct pathways: diet ingested fats, lipolysis of stored lipids in cells and through de novo synthesis. Betaine has been used as a dietary supplement in pig nutrition to reduce fat deposition and increase lean muscle mass with inconsistent results so far. This study compares the expression of genes involved in lipid metabolism from pigs consuming a control diet, and the control diet supplemented with betaine (WB). The expression of two genes involved in lipogenesis and lipolysis were evaluated in L. lumborum and B. femoris: ACC, which mediates the carboxylation of acetyl CoA into malonyl CoA concluding the first step of de novo synthesis, and MCPT1 which is responsible for the transport of acyl groups into the mitochondria for the start of β-oxidation. Our data suggest that the underlying mechanism regulating IMF deposition in Alentejano pigs supplemented with betaine is associated with the up-regulation of genes involved in lipid synthesis such as ACC, which increased ~190% in L. lumborum and 80% in B. femoris from WB-fed pigs. These results contradict some previous data, suggesting the inhibition of the lipolytic pathway as the elected mechanism for IMF accretion. Further genes' screening is required to better understand the effect of betaine on IMF deposition.

Keywords: Alentejano pig, betaine supplementation, lipid metabolism, gene expression.

PO - 1449