

GENDER STATUS AND MUSCLE TYPE MODULATES FATTY ACID COMPOSITION ASSOCIATED TO TRANSCRIPTS LEVELS OF ADIPOGENESIS-RELATED GENES IN BEEF

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I. OBJECTIVES

The goal of this study was to associate the fatty acid (FA) composition and adipogenesis related genes in *Longissimus* (LO) and *Triceps brachii* (TB) muscles of Angus × Nellore cattle from heifers, bulls, and steers.

II. MATERIALS AND METHODS

In the feedlot, 150 animals were separated by gender, fed with same diet, and subsequently harvested. The final mean weight was 431.3 ± 26.3 kg, 488.9 ± 30.7 kg, and 452.5 ± 24.9 kg for heifers, bulls, and steers, respectively. Lipids were extracted for the total lipid determination and FA composition from samples of LO and TB muscles. Total RNA from homogenous portions of samples was extracted using TRIzol[®]. The quantitative PCR reactions were analyzed in RT-PCR QuantStudio 6 (Applied Biosystems, Thermo Fisher Scientific, Foster City, CA). To calculate relative expression, target gene cycle threshold was normalized to the Ct values of the *GAPDH*, and the relative levels were represented as $2^{-\Delta Ct}$. The statistical analyses were performed by the PROC MIXED procedure of SAS (SAS Institute Inc., Cary, NC) for the meat FA analyses and JMP14[®] (SAS Institute Inc.) for gene expression. Nested gender was included as covariate for the final live weight and total lipid determination. The level of statistical significance was considered at $P \leq 0.05$.

III. RESULTS

There was a difference for the total saturated FA (SFA) for gender and muscle ($P < 0.01$). The meat from bulls (43.31%) had higher levels of SFA compared to heifers (41.09%) and had no differences in relation to meat from steers (42.42%). Among muscle type, total SFA increased in LO muscle (43%) compared with TB (41.6%). The FA 14:0 and 16:0 were affected by muscle type only, and the higher levels were detected in LO muscle ($P < 0.01$). There were differences in gender for total monounsaturated FA (MUFA; $P = 0.015$). Meat from bulls (42.65%) had lower levels of MUFA compared with other genders. The higher levels of MUFA observed in meat from heifers (48.04%) and steers (46.23%) is possibly due to the higher content of the major FA in this group (18:1 n-9c). The level of 18:1 n-9c was higher in the LO muscle (32.35%) than the TB (31.26%; $P = 0.022$). The total polyunsaturated FA (9.97%), total n3 (2.32%) and n6 (7.25%), polyunsaturated FA/SFA (0.24%) ratio, healthy index (1.65%), and the FA 18:2 n-6c (6.75%), 20:3-n3 (1.78%), and 22:4-n6 (0.26%) were higher ($P < 0.01$) in TB compared to LO muscle. Otherwise, the atherogenicity and thrombogenicity indexes were higher in the LO muscle ($P < 0.01$).

Regarding the transcript levels, there was an effect for muscle type on the expression of the *CEBPa* and *LPL* ($P < 0.01$) genes, both which had higher expression in TB muscle. Gender affected the transcript level of *ACC* ($P = 0.005$). This gene was increased in bulls, intermediated in steers, and decreased in heifers. Additionally, gender and muscle type interaction were observed on transcript levels of *FABP3*, *TPM2*, and *TPM3* ($P < 0.01$).

IV. CONCLUSION

The gender status and muscle type interact and modulate some transcripts levels related to the adipogenesis pathway by regulating the expression of enzymes and proteins involved in synthesis, transport, distribution, degradation, and oxidation of long-chain FA in adipose and muscle tissues. Therefore, these physiological and molecular changes are leading to different lipid profiles within each muscle, whereas LO muscle is more favorable to human health than TB, suggesting changes in consumer behavior based on healthy necessities and risk to develop different diseases.

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Keywords: gene expression, healthy index, beef cattle, crossbred, lipid accumulation