TRANSCRIPTOME PROFILE OF ANGUS-NELLORE CATTLE OF DIFFERENT SEX CLASSES ASSOCIATED WITH CARCASS TRAITS.

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I. INTRODUCTION

Over the last decade, there has been a growing shift in dietary intake patterns, creating a high demand for high-quality, nutritionally valuable meat products [1]. Consequently, studies utilizing advanced molecular techniques have been developed to characterize different meat profiles for a better understanding of the biological events involved in the meat desired by consumers. The use of castration to enhance carcass standardization and meat quality is widely employed. However, its effects on crossbred cattle still present discrepancies regarding their biochemical and molecular mechanisms, particularly in animals subjected to super-early production systems (< 24 months), finished in feedlots for 230 days. Therefore, the aim of this study is to characterize the meat of non-castrated and immune-castrated male cattle through the transcriptome profile of muscle tissue associated with carcass traits.

II. MATERIAL AND METHODS

This study involved twelve F1 Angus-Nellore crossbred animals, averaging 8 months old. Employing a fully randomized design, the animals were divided into two groups: six non-castrated males and six males subjected to GnRH-immunecastration, receiving three doses of the anti-GnRH vaccine at 250, 280, and 370 days of age. The animals were early weaned at 120 days old and housed in collective pens, where they were fed a growing diet until the start of the experiment. During the experimental period, the animals were housed in two pens according to treatment, with an average body weight of 292 kg ± 27 for non-castrated males and 289 kg ± 26 for immune-castrated males. Throughout the experiment, the animals received a growing diet for 110 days followed by a finishing diet for 120 days, totaling a 230-day experimental period. At the end of the experiment, the animals were slaughtered in a commercial slaughterhouse, and samples of the *Longissimus thoracis* muscle fresh were collected after the evisceration and stored in liquid N_2 for RNAseq analysis. After 48 hours of chilling, the carcasses were sectioned at the 12th rib for evaluation of loin muscle area (LMA) and backfat thickness (BFT). Muscle samples from three animals per treatment underwent RNA extraction using a commercial kit (RNeasy Mini Kit, Qiagen, Hilden, Germany). Libraries were prepared using the TruSeq Stranded mRNA kit (Illumina, USA) and sequenced on the NextSeq2000 platform (Illumina, San Diego, USA) with 2x100 bp reads. Only reads above 70 bp and a Phred score of 33 were used for mapping to the *Bos taurus* genome - ARS-UCD.1.2.1. Genes found exclusively in one of the treatments were identified using the DESeq2 package of the R statistical software. Additionally, transcription factor genes were identified through co-expression analysis using the CeTF package in contrast Non-castrated *versus* Immune-castrated. Phenotypic data were subjected to tests for normality of errors (Shapiro-Wilk) and variance homogeneity (Box-Cox) using SAS statistical software version 9.4.

III. RESULTS AND DISCUSSION

Male class significantly influenced carcass traits in the animals (Table 1). Immune castration reduced hot carcass weight by 12% ($P = 0.01$) and LMA by 14% compared to non-castrated males ($P = 0.01$). Conversely, immune-castrated males exhibited higher BFT compared to non-castrated males ($P = 0.02$). Non-castrated cattle showed higher expression of the genes *GH1* (log2FC = 0.47), *LDHC* (log2FC = 1.32), *IDH2* (log2FC = 0.021), *SDHC* (log2FC = 0.096), *UQCRFS1* (log2FC = 0.156), related to carcass traits phenotypes. While immune-castrated cattle had higher expression of the gene *ACOT12* (log2FC = -1.85).

The higher carcass weight and greater protein synthesis in non-castrated animals result from a better utilization of dietary N_2 by this animal category, conferred by testosterone hormone presence [2] associated with higher abundance of growth hormone, encoded by the upregulated *GH1* gene, identified as exclusive in non-castrated animals, demonstrating the intimate relationship between growth hormone and testosterone levels [3]. The greater efficiency and utilization of dietary nutrients are also evidenced by the upregulated gene *LDHC* responsible for lactate conversion to pyruvate, *IDH2* and *SDHC* belonging to the citric acid cycle, and the *UQCRFS1* gene belonging to cytochrome c reductase during oxidative phosphorylation. More productive and efficient animals have higher expression of genes involved in oxidative pathways.

Table 1 – Carcass traits of male non-castrated and castrated F1 Angus x Nellore, super early.

Traits	Male Class		SEM	*P*-value
	Non-castrated	Immune-Castrated		
Hot carcass weight - HCW, kg	353.0	310.0	9.40	0.01
Carcass yield - CY, %	59.0	58.4	0.40	0.51
Loin muscle area - LMA, cm^2	88.5	76.5	2.50	0.01
Backfat thickness - BFT, mm	9.4	12.1	0.64	0.02

On the other hand, animals with higher fat deposition, whether in the carcass, marbling, or both, are less efficient, as the energy cost for depositing 1 gram of fat is higher than that of protein due to its higher water content [4]. The greater backfat deposition in immune-castrated animals is supported by the exclusive gene *ACOT12* responsible for converting acetyl-CoA to acetate. Subcutaneous fat deposition has a greater preference for acetate as a substrate [5].

IV. CONCLUSION

The muscular metabolism of cattle from different male classes diverges in terms of substrate deposition and utilization from the diet. Non-castrated males exhibit greater protein synthesis due to their efficiency in utilizing dietary substrates, supported by higher expression of genes such as *GH1, LDHC, IDH2, SDHC*, and *UQCRFS1*. Conversely, immune-castrated males show increased carcass fat deposition via acetate, as evidenced by higher gene expression of *ACOT12*.

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