

**Abstracts - 35th Annual Meeting of the Brazilian Embryo Technology Society (SBTE)****OPU-IVF and ET****Transcriptional profile of lipid metabolism genes in OPU-derived oocytes from Gir (*Bos indicus*), Holstein (*Bos taurus*) and 1/2 Holstein × 1/2 Gir (*Bos taurus* × *indicus*) cows**

Ester Siqueira Caixeta Nogueira <sup>1</sup>, Asafe Costa Lopes <sup>1</sup>, Anthony César de Souza Castilho <sup>2</sup>, Mateus José Sudano <sup>4</sup>, Roniele Santana Valente <sup>5</sup>, Carlos Antônio C Fernandes <sup>3</sup>

<sup>1</sup> UNIFAL-MG - Universidade Federal de Alfenas (Alfenas, MG, Brasil), <sup>2</sup> UNOESTE - Universidade do Oeste Paulista (Presidente Prudente, SP, Brasil), <sup>3</sup> UNIFENAS - Universidade José do Rosário Vellano (Alfenas, MG, Brasil), <sup>4</sup> UFSCar - Universidade Federal de São Carlos (São Carlos, SP, Brasil), <sup>5</sup> UFABC - Universidade Federal do ABC (Santo André, SP, Brasil)

**Resumo**

*Bos taurus taurus* (*Bos taurus*) and *Bos taurus indicus* (*Bos indicus*) cattle are subspecies with remarkable differences related to production and reproduction. Moreover, it is known that differences in number and development potential of oocytes between breeds affect efficiency and economic viability of in vitro embryo production. Once lipids have a crucial role in oocyte development, we aimed to evaluate the mRNA abundance of genes involved in lipid metabolism in oocytes recovered from dairy breeds: Gir (*Bos indicus*), Holstein (*Bos taurus*), and their crossbreed (1/2 Holstein × 1/2 Gir). Cumulus oocyte complexes (COCs) were obtained by ovum pick-up procedure. The oocyte donor cows were from farms in Alfenas in the southern region of Minas Gerais state, Brazil. Part of COCs were submitted to in vitro maturation during 24h. Immature and in vitro matured COCs were processed to remove the cumulus, and denuded oocytes were stored for transcriptional analysis. Total RNA was extracted from pools of 20 immature oocytes (n = 4 pools per breed) and 20 in vitro matured oocytes (n = 4 pools per breed) using the RNeasy® Micro kit (Qiagen). The mRNA abundance of acetyl coenzyme A carboxylase (ACACA), carnitine palmitoyltransferase 1A (CPT1A), fatty acid binding protein 5 (FABP5), fatty acid translocase (CD36) and perilipin 2 (PLIN2), were assessed by real time RT-PCR using Power SYBR® green master mix (Applied Biosystems) and normalized by peptidylprolyl isomerase A (PPIA). Relative mRNA abundance was determined using the  $\Delta\Delta C_t$  method. The effects of breeds on expression of target genes in oocytes were tested by ANOVA, and means were compared using Tukey-Kramer HSD test. Differences were considered significant when  $P < 0.05$ . In immature oocytes, CD36 mRNA abundance was higher ( $P = 0.022$ ) in Gir compared to Holstein. Regarding in vitro matured oocytes, CD36 mRNA abundance was higher ( $P = 0.001$ ) in Gir and crossbreed cows compared to Holstein donors. Moreover, CPT1A mRNA abundance was higher ( $P = 0.03$ ) in in vitro matured oocytes from Gir compared to Holstein. In opposite, PLIN2 mRNA abundance was lower ( $P = 0.034$ ) in in vitro matured oocytes from Gir than in Holstein and 1/2 Holstein × 1/2 Gir. In conclusion, we reinforce that the different genetic groups impact expression of genes involved in lipid metabolism. Also, we figure out that differences could be more clearly discriminated between pure breeds: Gir vs Holstein. Furthermore, differential expression of CD36 in immature and in vitro matured oocytes, as well, CPT1A and PLIN2 in matured oocytes could suggest specific molecular mechanisms involved with  $\beta$ -oxidation of fatty acids and lipids accumulation during in vitro maturation.

**Acknowledgements**

CNPq 420581/2016-2, Fapemig APQ-02103-17.