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### G28 - SNPs and INDELS in genes involved in lipid metabolism of mammary gland of Zebu breeds identified by whole genome sequencing

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**Short Abstract:** Background: Guzerá and Gir are the main indicine breeds of cattle dairy that compound the Brazil herd. The milk produced by these indicine breeds contain higher concentration of fat in milk in comparison with taurine breeds. However, the genetic bases for these differences are unknown. In this context, the objective of this study was to sequence and to map the genome of three Guzerá bulls and three Gir bulls in order to identify zebu-specific variations involved in the lipid metabolism of the mammary gland.

Results: Genomes sequencing were performed using SOLiD and HiSeq platforms. The sequences obtained were mapped to the reference genome of *Bos taurus* (UMD 3.1) using the LifeScope and BWA-mem programs. The average depth of coverage achieved from mapping ranged from 10 to 26X for six samples and the genome coverage ranged from 87% to 98% of the reference genome. A list of putative SNPs and INDELS were generated using the LifeScope and SAMtools. We performed the selection of shared variations among the six samples and detected 2% of the SNPs and INDELS. These variations were classified functionally according to NSG-SNP and those located in genes involved in lipid metabolism of mammary gland were selected. We found potentially functional variations in genes involved in transport and secretion of cholesterol, activation of fatty acids and synthesis of sphingolipids.

Conclusions: This study identified potentially functional variations in genes that may be responsible for differences in the composition of lipids in the milk from indicine and taurine breeds.

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