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WholeGenome Sequencing of Guzerá Breed Revealed SNPs with Potential Implication for Milk Production

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Background: Guzerá is the second most important Zebu breed for milk production in Brazil. Genotyping chips with great potential to increase the efficiency of breeding programs do not include data from Guzerá. Thus, we aimed to identify Guzeráspecific SNPs in a newly sequenced genome of this breed.

Results: We sequenced and assembled the genome of Guzerá breed using matepaired libraries and SOLiD sequencer. Reads were mapped to the reference genome of *Bos taurus* Hereford breed (UMD 3.1) using LifeScope software. The average depth of coverage was 26X and 87% of the reference genome was covered. A list of putative SNPs was generated with diBayes SNP Detection module of LifeScope. Fiftyone percent of the 4,040,476 SNPs that passed the quality filter were new when compared to the dbSNP138. These new SNPs were mostly (93%) located in intergenic and intron regions. Only 5% (215,889) of SNPs that passed quality filter are represented in the commercial genotyping chips. Seven percent of the SNPs not represented in these chips were 3'UTR, 5'UTR, coding sequence, up and downstream gene, mature miRNA, splice and stop region. Important, we identified 2.496 SNPs in 23 genes involved in lipid metabolism of bovine mammary gland.

Conclusions: A large number of Guzeráspecific SNPs were identified. These differences may be associated with the production traits and adaptability that characterize the zebu breeds and may be useful in breeding programs.