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ZEBU GENOME SEQUENCING AND ANALYSIS USING SECOND GENERATION SEQUENCERS

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INTRODUCTION: The genetic structure of the Brazilian cattle is formed mainly by animals from zebu races and crossbreeds with taurine races. In Brazil, during the last decades, traditional genetic techniques have considerable gains in dairy production and resistance to infectious diseases. Although effective, these methods do not shed light at the biological processes underlying the observed results. The inclusion of genetic markers in the selection process has fostered the genetic gains and lowered the costs of traditional progeny tests. OBJECTIVE: To identify Single Nucleotide Polymorphisms (SNPs) markers in the zebu genome of Gir breeds. METODOLOGY: Mate paired libraries, with 1-2 kb inserts, were constructed. The reads generated (50bp long) were mapped into the publicly available reference genome of a female *Bos taurus* (NCBI Project ID: 10708) using SHRiMP. SamTools were used to generate the consensus sequence, and Varid to identify SNPs. The Y chromosome will be mapped into sequences from species phylogenetically more distant such as human, mouse, rat, etc. RESULTS: The first two runs using the SOLiD V3 plus platform yielded 203 million reads representing a theoretical 3,5 X coverage of the reference genome. Parameters such as observed coverage, gap sizes, number of mapped reads and number of SNPs will be used to evaluate the sequencing and the analysis process. PERSPECTIVES: The identification of SNPs in Brazilian Gir breed will improve the efficiency of the next version of genotyping chips for dairy zebu genetic selection in Brazil.