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3:00 pm - 4:30 pm

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Whole-Genome Sequencing of Guzerá Breed Revealed SNPs with Potential Implication for Milk Production #P561

Description:

**Presenters:** Izinara Rosse Cruz Federal University of Minas Gerais, Juliana A Geraldo Center for Excellence in Bioinformatics – FIOCRUZ-MG, Francison S. Oliveira Center for Excellent in Bioinformatics - FIOCRUZ-Minas, Laura Rabelo Leite Fundacao Oswaldo Cruz - CEBio, Flávio Araújo Genomics and Computational Biology Group - FIOCRUZ-MG, Adhemar Zerlotini EMBRAPA Informática Agropecuária - SP, Beatriz C. Lopes EPAMIG-MG, Wagner A. Arbex EMBRAPA Dairy Cattle – MG, Marco Antonio Machado Embrapa Dairy Cattle Research Center, Maria Gabriela C.D. Peixoto EMBRAPA Dairy Cattle – MG, Rui S. Verneque EMBRAPA Dairy Cattle – MG, Marta F.M. Guimarães EMBRAPA Dairy Cattle – MG, Marcos Vinicius G.B. Silva EMBRAPA Dairy Cattle – MG, Roney S. Coimbra Biosystems Informatics - FIOCRUZ-Minas, Maria Raquel S. Carvalho Federal University of Minas Gerais, Guilherme Oliveira Fundacao Oswaldo Cruz - CEBio

P561 - Whole-Genome Sequencing of Guzerá Breed Revealed SNPs with Potential Implication for Milk Production

**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 Guzerá-specific SNPs in a newly sequenced genome of this breed.

**Results:** We sequenced and assembled the genome of Guzerá breed using mate-paired 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. Fifty-one 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 Guzerá-specific 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.



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