

**P554****De Novo Assembly of a Nelore (*Bos indicus*) Bull Genome Based on Short Read Sequences**

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Room: Grand Exhibit Hall

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Zebu cattle breeds (*Bos indicus*) are widely used for milk and beef production in the tropics and show natural adaptations to biotic and abiotic stresses especially found in these regions. Advanced genomic tools will be essential to help unveil and explore the underlying genetic variations that distinguish taurine and indicine cattle and, at the same time, will facilitate the work of breeders striding towards incorporating genomic tools into breeding programs aiming to improve productivity and beef and milk quality. DNA extracted from a Nelore bull born in 1987, with an estimated cumulative inbreeding coefficient of 29.4%, and that can be traced to animals imported directly from India, was used to produce 100bp paired-end sequences from short and long insert (mate-pair) libraries, with an Illumina HiSeq platform. A total of 197Gbp of sequence were generated, corresponding to 76x of raw coverage of the genome. The SOAPdenovo assembler was used to build contigs and scaffolding. Several parameter sets were evaluated to obtain the best assembly based on the number of scaffolds, number of bases in scaffolds, N50, and total gap length, built with varying amounts of sequence. The best obtained assembly contains 2.7Gbp, 11,917 scaffolds with N50 and N90 of 607Kbp and 73Kbp, respectively. Sequence comparisons with the taurine reference sequence revealed >6 million SNPs, with 1.5%, 37.4% and 61.1% located in Exons, Introns and Intergenic regions, respectively. Additional data generation using different sequencing technologies is underway to improve sequence assembly quality before comprehensive comparisons with the *B. taurus* reference sequence and annotation are performed.

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January 10 - 15, 2014

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