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PARTIAL CHARACTERIZATION OF EXON 3 OF JY-1 GENE IN *Bos taurus indicus*

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The JY-1 is a protein present in monoovulatory species as cattle. It is an oocyte specific protein and it plays a key role in the regulation of the granulose cells functions. It also influences the early embryo development. The aim of this study was to characterize a region of the exon 3 of the JY-1 gene in Nelore cattle and investigate possible polymorphisms. DNA was extracted from tail hair of 20 unrelated Nelore heifers by the Phenol-Chloroform-Isoamyl Alcohol protocol. The primers 5'CCTGACCGTATCTCTTGCATACTT3' and 5'CACAGTGCTAATGAACTCTTCCA3' were designed to amplify a partial region of exon 3. The region amplified goes from the nucleotide 730 to the nucleotide 1355 of exon 3. It is a non-coding region. The fragment amplified by the Polymerase Chain Reaction (PCR) has 627 bp. After the PCR reactions, the samples were sequenced and analyzed by the CodonCode Aligner program. It was possible to identify four Single Nucleotide Polymorphisms (SNPs) and one nucleotide deletion. The positions of the SNPs (in the fragment amplified) and the substitutions are: 198T/A, 238G/A, 456T/C and 521G/A. The gap is located in the position 312 and corresponds to a deletion of a T. Moreover, the sequence obtained for *Bos taurus indicus* is different in one position compared with the sequence for *Bos taurus taurus*. In the position 476, the zebu cattle has a T and the european cattle has a G. The sequence of 627 bp of partial JY-1 gene was submitted to NCBI GenBank with accession number JN123736. Future studies of genotyping more samples must be done in order to verify the allelic and genotypic frequencies and also the possible influence of the SNP in reproductive traits.

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