



Report of a chimeric origin of transposable elements in a bovine-coding gene

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ABSTRACT. Despite the wide distribution of transposable elements (TEs) in mammalian genomes, part of their evolutionary significance remains to be discovered. Today there is a substantial amount of evidence showing that TEs are involved in the generation of new exons in different species. In the present study, we searched 22,805 genes and reported the occurrence of TE-cassettes in coding sequences of 542 cow genes using the RepeatMasker program. Despite the significant number (542) of genes with TE insertions in

exons only 14 (2.6%) of them were translated into protein, which we characterized as chimeric genes. From these chimeric genes, only the FAST kinase domains 3 (FASTKD3) gene, present on chromosome BTA 20, is a functional gene and showed evidence of the exaptation event. The genome sequence analysis showed that the last exon coding sequence of bovine FASTKD3 is ~85% similar to the ART2A retrotransposon sequence. In addition, comparison among FASTKD3 proteins shows that the last exon is very divergent from those of *Homo sapiens*, *Pan troglodytes* and *Canis familiares*. We suggest that the gene structure of bovine FASTKD3 gene could have originated by several ectopic recombinations between TE copies. Additionally, the absence of TE sequences in all other species analyzed suggests that the TE insertion is clade-specific, mainly in the ruminant lineage.

Key words: Cow; Genome; Exaptation; Domestication; Transposon; FASTKD3