OFFICIAL ABSTRACT and CERTIFICATION

Bioinformatic Investigation of the Peculiarities of Long Intron Splicing in Hominidae

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Recursive splicing is an RNA maturation phenomenon wherein transcripts are matured during multiple splicing reactions, first discovered in long Drosophila melanogaster introns of genes involved in morphogenesis and development. Human chromosome 2 was formed during an ancestral fusion event of two smaller chromosomes present in bonobos and chimpanzees. Recursive splicing can be detected by computationally parsing genomic DNA for recursive sequences. Scaled samples of Hominidae chromosomes 2 were executed in a python program written to score genomic sequences for matches to recursive sites. After the entire D. melanogaster genome (control), bonobo chromosome 2a and chimpanzee chromosome 2a had the highest scores, with both chromosomes 2b having the lowest scores. Considering that human chromosome 2 had a middle score, the fusion event may have been favored by natural selection to offset the difference in recursive site concentration between chromosomes 2a and 2b, supporting the hypothesis that recursive splicing functions as a more accurate mechanism. WebLogo analysis revealed that the recursive sequences of the three Hominidae species resemble each other far more closely than they resemble those of Drosophila and the recursive motif, indicating potential for an alternative mechanism. LiftOver analysis also contributed that chimpanzee chromosomes had the highest number of total motif matches to the recursive pattern, and that the coordinates of the recursive sites found in human chromosome 2 are most similar to those of the chimpanzee. This study offers novel evolutionary data regarding the conservation of recursive splicing in Hominidae and the genomic basis of developmental variation.

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