Chimeric RNAs and Proteins

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If adjacent genes in the same direction (Tail-to-Head, T2H) are located very close to each other (at a distance of several hundred base pairs) or partially overlapping, chimeric transcripts (RNAs) can occur as a result of their joint transcription and splicing. The chimeric RNAs can serve as mRNAs and a further translation of these chimeric mRNAs may produce chimeric proteins. The purpose of the project is the genome-wide identification of the closely located T2H gene pairs in humans, some mammalian animals, and higher plants, estimation of their potential to produce chimeric RNAs. T2H gene pairs with the potential to produce chimera RNAs have been identified in the genomes of humans, 4 mammals (rhesus monkey, chimpanzee, house mouse and Norwegian rat) and 6 higher plants (soybean, barrelclover, black cottonwood, tomato, wine grape, and corn). Number of all T2H gene pairs (regardless a distance between genes) in analyzed genomes varies from 9700 to 19900, and number of close (d=300 bp or partially overlapping) T2H gene pairs varies from 100 to 640. Each of the analyzed genomes contains T2H gene pairs with a potential to produce chimeric transcripts. In particular, transcription of partially overlapping T2H genes pairs into alternative chimeric mRNAs seems to be obvious. Analysis of DNA regions containing gene pairs that could produce potential chimeric RNA using the FGENESH program shows that at least some of these chimeric transcripts can be translated into chimeric proteins. At present, these studies are continuing.

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