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## Is there any intron sliding in vertebrata?

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## Abstract

I hree main evolutionary events in eukaryotic gene structures are intron gain, loss and sliding. The last one means the change of intron position over several nucleotides. Due to its ambiguous molecular mechanism and rarity of occurrence, the existence of intron sliding could still be debatable. Here we analyzed 36 genome pairwise alignments of vertabrates, including human, rat, chicken and zebrafish in search of intron sliding events. The thorough comparison of exon-intron boundaries in the pairwise genome alignments from UCSC Genome Browser showed that the sliding is indeed very rare the maximum number of hits for each analyzed pair of organisms does not exceed 20. In addition, comparison of gene annotations from different databases called into question almost half of all cases. To confirm that the found sliding events are not being the result of gene annotation errors we used transcriptome data from UCSC Genome Browser. We found out that majority of sliding events predicted by alignments seemed to happen in the low frequency isoforms, as we were not able to confirm them by transcriptome data. Only several cases were partially supported by transcriptome (e.g. sliding in EIF1AX gene between human and sheep) which leaves the question open whether the sliding occurs at all. The study was funded by RFBR according to the research project № 18-34-



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Irina Poverennaya had completed her Specialist's Diploma and graduated with honors in Lomonosov Moscow State University, Faculty of Bioengineering and Boinfromatics in 2013. Currently she works as bioinformatician and young researcher in Vavilov Institute of General Genetics of Russian Academy of Science and Institute of Mathematical Problems of Biology RAS.

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