

P63

Gene Diversification and Transcript Variants by Retroelements

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During the primate evolution, many different retroelement had integrated into the primate genome and followed by the diversification of gene. Among various retroelements, LTR and LINE have been reported to have polyadenylation signal for their transcription. SINE also has a potential ability providing the polyadenylation signal if it inserted in 3' UTR region of gene. The integration of retroelement which control capacity of the transcription termination results in different transcripts. We found various fused transcripts with retroelement at transcript terminal region, indicating that retroelements are associated with transcription termination for the alternative splicing. Fusion types were divided by the four types (Type I, Type II, Type II, Type III, and Type IV). Known 12 canonical polyadenylation signals were used for the analysis of final exon fused by retroelements. Most of candidate fusion genes were revealed to have more than two polyadenylation signals. Our data suggests that retroelements seem to be main resources to make different splicing pattern in the transcript termination region by providing the polyadenylation signals.

P64

Bioinformatic application for the analysis of evolutionary dynamics
of genus *Oncorhynchus* species using SINE elements.

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For the abundance of sequence data available from the higher animals to lower animals, bioinformatic application could be a powerful tools. Here, we introduced the application of bioinformatic tools for the analysis of SINE elements in genus *Oncorhynchus* species. First, we collected published sequence data related to SINE elements for the establishment of consensus SINE elements (Sma I, Hpa I) and sequence data (246949 sequences) from the Genbank database. Second, we analyzed those sequence data using modified library of repeatmasker program. Finally, we found various SINE elements in different *oncorhynchus* genome and transcriptom. Taken together, the transcriptom of genus *oncorhynchus* showed many insertion events in their mRNA sequences as shown in the mammalian genes. We suggest that SINE elements have a significant role in the evolutionary dynamics and diversification of *oncorhynchus* genes.