085

IDENTIFICATION AND ANALYSIS OF ANCESTRAL HOMINOID TRANSCRIPTOME INFERRED FROM NON-HUMAN PRIMATE GENOMIC SEQUENCES

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Comparative transcriptomics studies in hominoids are difficult for lack of EST information in the great apes. Nevertheless, processed pseudogenes (PPGs), which are reverse transcribed ancient transcripts present in the current genome, can be regarded as a virtual transcript resource that may compensate for the paucity of ESTs in non-human hominoids. We have showed that chimpanzee PPGs can be applied to identification of novel human exons/alternatively spliced variants (ASVs) and inference of the ancestral hominoid transcriptome and chimpanzee exon loss events. We developed a method for comparatively extracting novel transcripts from PPGs (designated "CENTP"), and identified 643 novel human exons/ASVs. RT-PCR-sequencing experiments confirmed >50% of the tested exons/ASVs, supporting the effectiveness of the CENTP pipeline. With reference to the ancestral transcriptome inferred by CENTP, exon loss events were identified. Furthermore, by combining outgroup, paralogue, and PPG information, we can identify lineage-specific exon loss/gain events. We also demonstrated that the ancestral transcriptome and exon loss/gain events inferred based on comparisons of current transcripts may be incomplete (or occasionally inappropriate) because ancestral transcripts may not be represented in the ESTs of existing species.

Keywords: comparative and evolutionary genomics, transcriptome, processed pseudogene, alternative splicing