Pseudo? Regulation of Young Duplicated Genes in Human

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Abstract

Gene duplication, believed to play a major role in the origination of new genes, is majorly derived from either segmental duplications or retro-transposition events. Unlike retrogenes, the newly segmental duplicated genes share nearly identical genomic features, like the promoter sequences and the intron-exon structure. Therefore, these young duplicated genes might retain original functions and express similar transcripts. However, their transcripts are too similar to be distinguished from each other in current measure using assays of northern blot, quantitative real time polymerase chain reaction (qPCR), spotted cDNA arrays, and oligonucleotide arrays. The activity of those duplicated loci remains enigmatic. In this study, we have identified 4,149 segmental duplicated loci. Their transcripts share at least 99 percent sequence identity which is high enough for them to be undistinguishable in experiments. We have analyzed the sequence conservation status of those loci and discovered that indels might play an important role in speeding up their divergence process. Besides, the preservation is distance dependent to functional regions. For instance, exon's conservation is higher than intron's and close promoter regions are more conserved than distant ones. Aside from that, over 90 percent of duplicated loci possess histone modification signals. Both reflect that those duplicated loci might be functional preserved even though they have accumulated mutations after duplication. Generally, their histone modification profiles are highly positive correlated to the sequence conservation of promoter regions. It supports that genomic sequence is an important feature for histone modifications related to gene expression. However, we also show that some duplicated loci are not conserved in promoter regions but possess similar histone modification patterns, and vice versa. Furthermore, our biological experiments display that there are locus-specific isoforms derived from duplicated loci and expressed differentially in either cell types or drug treatments. In sum, we have performed sequence conservation analysis, histone modification profiles, and case studies in expression of duplicated loci to provide insight into the regulation of young duplicated genes.

Key words: duplicated gene; gene expression; histone modification