

Non-coding sequences conserved independently in four different mammalian orders

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Conserved noncoding sequences (CNSs) of vertebrates are considered to be closely linked with protein-coding gene regulatory functions. We examined the abundance and genomic distribution of CNSs in four mammalian orders: primates, rodents, carnivores, and cetartiodactyls. We defined the two thresholds for CNS using conservation level of coding genes; using all the three coding positions and using only first and second codon positions. The abundance of CNSs varied among lineages, with primates and rodents having highest and lowest number of CNSs, respectively, whereas carnivores and cetartiodactyls had intermediate values. These CNSs cover 1.3-5.5% of the mammalian genomes and have signatures of selective constraints that are stronger in more ancestral than the recent ones. Evolution of new CNSs as well as retention of ancestral CNSs contribute to the differences in abundance. The genomic distribution of CNSs is dynamic with higher proportions of rodent and primate CNSs located in the introns compared with carnivores and cetartiodactyls. In fact, 19% of orthologous single-copy CNSs between human and dog are located in different genomic regions.

If CNSs can be considered as candidates of gene expression regulatory sequences, heterogeneity of CNSs among the four mammalian orders may have played an important role in creating the order-specific phenotypes. Fewer CNSs in rodents suggest that rodent diversity is related to lower regulatory conservation. With CNSs shown to cluster around genes involved in nervous systems and the higher number of primate CNSs, our result suggests that CNSs may be involved in the higher complexity of the primate nervous system. This study was published in *Genome Biology and Evolution* (Babarinde and Saitou, 2013; vol. 5:2330-2343).

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