

NEWS

Press release



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The tale of the telomeres – Facts in the “theory” of evolution

San Diego – October 24, 2007. The tips of each chromosome are protected by regions called telomeres that include repeated sequences of DNA. Just interior of telomere repeats lie *subtelomeric* sequences. In many organisms, including primates, subtelomeres are composed of duplicated DNA sequences common to many different chromosome ends. As a result of duplications, deletions, and inter-chromosomal exchanges that have occurred in recent evolutionary history, the content of subtelomeres varies greatly among different individuals. The sequences found in subtelomeres, which can include active genes, vary extensively among individuals in the numbers of copies of repeated DNA sequences. Subtelomeres are also incredibly variable in the genomes of closely related primates.

In order to track the evolutionary history of just one subtelomeric region, Dr. Katie Rudd, Fred Hutchinson Cancer Research Center, Seattle and colleagues have constructed genomic maps for the chromosome 15 subtelomere in the genomes of human, chimpanzee, gorilla, orangutan and rhesus macaque. In the common ancestor of these species, this region was in the middle of a chromosome. That chromosome broke into two parts after the species split between macaque and the other higher primates, placing this region at the end of what is now chromosome 15 in humans. In this study, every primate examined has a different chromosome 15 subtelomeric structure, due to rampant DNA sequence transfers and deletions. Among the five species examined, there have been gains and losses of genes, especially in the olfactory receptors affecting the sense of smell.

Changes in gene copy number and gene location can lead to species diversity. This in-depth comparative analysis of a single primate subtelomere demonstrates that subtelomeres are one of the most rapidly evolving regions of the genome. While this research focused on the study of variability within and among species, the investigation of such variability may also lead to better understanding of subtelomeric rearrangements in the human genome that, in some cases, can lead to mental retardation and other developmental disorders.

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