

DIVERSIFICATION OF BITTER TASTE RECEPTOR GENE FAMILY IN CHIMPANZEES

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Comparative genomic analyses using reference sequences in various vertebrates revealed that the evolution of *T2R* genes, bitter taste receptor genes, is likely to reflect their dietary changes. In humans, analyses of DNA polymorphisms in the entire repertoire of 25 putatively functional *T2R* genes showed that nucleotide diversity in the *T2R* genes is relatively high, and results in a large number of amino acid substitutions, suggesting that multiple and functionally divergent alleles are likely found at *T2R* loci due to relaxation of functional constraints on these genes. These raise the question of whether the large number of amino acid substitutions reflect a low level of selective constraint on bitter taste receptors in general, or if they reflect dietary changes during human evolution. Here, we report the analysis of polymorphisms in the entire repertoire of *T2R* genes in chimpanzees, the closest extant relatives of humans. The numbers of functional genes were different among individuals, but most chimpanzees had 2 or 3 more functional genes than those of humans. Evolutionary analysis of the chimpanzee *T2R* genes revealed that nucleotide diversity is also high, along with a high rate of amino acid substitutions, suggesting that a selective constraint on these genes was weak as seen earlier in human *T2R* genes. The weak functional constraint in both species has resulted in the occurrence of various functionally divergent alleles within the populations, and in heterozygous individuals who might have the ability to taste a broader range of substances.

Keywords: chimpanzees, *T2R*, polymorphisms, evolution