

## INTRASUBSPECIFIC POLYMORPHISMS AND INTERSUBSPECIFIC DIVERGENCE OF BITTER TASTE RECEPTOR GENES IN CHIMPANZEES

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Human (*Homo sapiens*) and western chimpanzee (*Pan troglodytes verus*) genome have ~25 and ~28 intact bitter taste receptor genes, *T2Rs*, respectively. It has been revealed that they have a lot of single nucleotide polymorphisms (SNPs), including ones that can cause inactivation of the genes (pseudogenization). However, biological meaning of the high diversity in *T2Rs* is little elucidated. In this study, we sequenced putative intact *T2Rs* in eastern chimpanzees (*P. t. schweinfurthii*) and compared them with homologous regions in western chimpanzees, which have been geographically isolated and thus genetically differentiated at some level from eastern chimpanzees. We found that *T2Rs* of each subspecies as a whole tend to have nucleotide diversities comparable to autosomal noncoding regions and that there are several polymorphisms resulting in pseudogenes unique to each subspecies. There are also polymorphic mutations in chromosomal level unique to eastern chimpanzee (chromosomal deletion and gene conversion) which may drastically alter the senses of bitter taste in each individual. Chimpanzees intake many plants which are bitter for humans and often utilize them as "drugs" in some local groups. Hence, our results suggest that the different senses of bitter taste between these subspecies are likely to enable chimpanzees to evaluate different dietary sources from each habitat, including such "bitter" compounds.

Keywords: Chimpanzees, Bitter Taste Receptor Genes, SNPs, Diets