

REGION-SPECIFIC DISTRIBUTION OF NON-TASTER JAPANESE MACAQUES

N. Suzuki, T. Sugawara, A. Matsui, Y. Go, H. Hirai, H. Imai

Kyoto University, Inuyama, Aichi, Japan,

Presenter's Email: suzukin@pri.kyoto-u.ac.jp

Bitter taste perception has evolved as a key defense mechanism against the ingestion of harmful substances, and is mediated by *T2R* gene families in vertebrates. The best studied bitter substance is phenylthiocarbamide (PTC), which is recognized by T2R38 and has a similar molecular structure to glucosinolates contained in Brassica plant species. The “non-taster” phenotypic polymorphism (i.e., not sensitive to PTC-containing foods) has been identified in many primates including humans. However, only human and chimpanzee genotypes that caused to the “non-taster” phenotype have been identified thus far. It is important to identify the responsible genotype in other primates and to understand molecular, behavioral and ecological relevance. For this purpose, we investigated the sequences of *T2R38* of 388 Japanese and rhesus macaques which are from several region in Japan and Asia, respectively. As a result, we identified several genotypes and one genotype of Japanese macaque showed a mutation in the initiation codon, suggesting the coding protein of this genotype is not functional. Interestingly, the genotype was found in a specific region. In order to examine the phenotype of this genotype, we conducted behavior test and found that the homozygote individuals could not recognize PTC. Furthermore, comparison of the sequences of Japanese and rhesus macaques suggested that the genotype appeared after the divergence of these species, independently from the appearance of human and chimpanzee “non-tasters”. This finding provides new insights into the ecological and evolutionary biology of primates, as related to the plants in their environment that they sometimes use as foods.

Keywords: genome, bitter, behavior, diet