



# Molecular cloning and evolutionary analysis of captive forest musk deer bitter taste receptor gene *T2R16*

G.J. Zhao<sup>1</sup>, N. Wu<sup>2</sup>, D.Y. Li<sup>2</sup>, D.J. Zeng<sup>1</sup>, Q. Chen<sup>1</sup>, L. Lu<sup>2</sup>, X.L. Feng<sup>1</sup>, C.L. Zhang<sup>1</sup>, C.L. Zheng<sup>3</sup> and H. Jie<sup>1</sup>

<sup>1</sup>Laboratory of Medicinal Animal, Chongqing Institute of Medicinal Plant Cultivation, Chongqing, China

<sup>2</sup>Institute of Animal Genetic and Breeding, Sichuan Agricultural University, Ya'an, China

<sup>3</sup>Sichuan Institute of Musk Deer Breeding, Dujiangyan, China

Corresponding author: H. Jie  
E-mail: jiehangisgood@126.com

Genet. Mol. Res. 14 (4): 16185-16195 (2015)

Received June 18, 2015

Accepted September 20, 2015

Published December 8, 2015

DOI <http://dx.doi.org/10.4238/2015.December.8.8>

**ABSTRACT.** Sensing bitter tastes is crucial for most animals because it can prevent them from ingesting harmful food. This process is mainly mediated by the bitter taste receptors (T2R) that are largely expressed in the taste buds. Previous studies have identified some *T2R* gene repertoires. Marked variation in repertoire size has been noted among species. However, research on *T2Rs* is still limited and the mechanisms underlying the evolution of vertebrate *T2Rs* remain poorly understood. In the present study, we analyzed the structure and features of the protein encoded by the forest musk deer (*Moschus berezovskii*) *T2R16* and submitted the gene sequence to NCBI GenBank. The results showed that the full coding DNA sequence (CDS) of musk deer *T2R16* (GenBank accession No. KP677279) was 906 bp, encoding 301 amino acids, which contained ATG start codon and TGA stop codon, with a calculated molecular weight of 35.03 kDa and an isoelectric point of 9.56. The T2R16 protein receptor

had seven conserved transmembrane regions. Hydrophobicity analysis showed that most amino acid residues in T2R16 protein were hydrophobic, and the grand average of hydrophobicity (GRAVY) was 0.657. Phylogenetic analysis based on this gene revealed that forest musk deer had the closest association with sheep (*Ovis aries*), as compared to cow (*Bos taurus*), *Tursiops truncatus*, and other species, whereas it was genetically farthest from humans (*Homo sapiens*). We hope these results would complement the existing data on *T2R16* and encourage further research in this respect.

**Key words:** Forest musk deer; Bitter taste receptor; *T2R16*; Structure analysis; Phylogenetic analysis