



Sequence characterization and phylogenetic analysis of toll-like receptor (*TLR*) 4 gene in the Tibetan macaque (*Macaca thibetana*)

Q.X. Dai^{1,2*}, Y.F. Yao^{1*}, Z.C. Qi^{3*}, Y. Huang¹, Q.Y. Ni¹, M.W. Zhang¹
and H.L. Xu¹

¹College of Animal Science and Technology, Sichuan Agricultural University, Ya'an, China

²Forestry College, Sichuan Agricultural University, Ya'an, China

³College of Veterinary Medicine, Sichuan Agricultural University, Ya'an, China

*These authors contributed equally to this study.

Corresponding author: H.L. Xu

E-mail: huailxu@yahoo.com

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ABSTRACT. In this study, the complete coding region sequence of an innate immune-related *TLR4* gene was obtained from the Tibetan macaque (*Macaca thibetana*) genome via PCR and direct sequencing. The sequence had a total length of 2481 bp, contained 3 complete exons, and encoded 826 amino acids (AAs); its isoelectric point was 5.703, and the molecular weight was 94.72 kDa. The high structure prediction showed that the protein was comprised of one extracellular region, one transmembrane region, and one intracellular region. There were 48 potential functional sites in the protein, including glycosylation, phosphorylation, and acetylation sites. A homology analysis among 9 primate species, including the Tibetan macaque, human, chimpanzee, gibbon, rhesus macaque, cynomolgus monkey, pig-tailed monkey, squirrel monkey, and small-eared galago, showed that the homology

of the nucleotide and AA sequences ranged from 60.9-99.5% and 51.4-99.0%, respectively. Higher variability was identified in the extracellular region of the TLR4 protein, and its variable sites accounted for 88.79% (AA) of the total variable sites. Additionally, the number of AAs at the 3' end of the intracellular region was notably different among the primate lineages. The phylogenetic tree based on *TLR4* gene exons of 9 primate species showed that the Tibetan macaque clustered with the rhesus macaque, cynomolgus monkey, and pig-tailed monkey; it was most distant from the small-eared galago. This study will provide an important basis for further study on the expression, regulation, and polymorphism of the *TLR4* gene and the relationship between polymorphisms and host disease susceptibility.

Key words: Innate immunity; *Macaca thibetana*; Phylogenetic analysis; Toll-like receptor; *TLR4* gene