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Evolutionary analysis of the short-type peptidoglycan-recognition protein gene (*PGLYRP1*) in primates

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ABSTRACT. Short-type peptidoglycan (PGN)-recognition protein 1 (PGLYRP1), an innate immunity protein that directly breaks down the structure of microbial cell wall PGNs, plays an important role both in antibacterial defenses and several inflammatory diseases. To explore the adaptive evolution of the *PGLYRP1* gene in primates and provide insight into the function of this antibacterial protein, we sequenced the entire *PGLYRP1* gene from *Macaca thibetana* and *Rhinopithecus roxellana*, identified the corresponding sequences from the draft genome of 8 other primates, including humans, and conducted related statistical analyses. Homology analysis showed that the identity of nucleotide and deduced amino acid sequences of *PGLYRP1* among 10 primates ranged from 82.0 to 99.0% and 74.5 to 98.5%, respectively. The R value (transition/

transversion) and disparity index per site also presented relatively low-base composition biases. Selective pressure analysis for the *PGLYRP1* sequences among major primates revealed that both the whole gene and the substructure of *PGLYRP1* are under strong purifying selection at similar levels of selective pressure among 6 major primate lineages (human, great ape, lesser ape, Old World monkey, New World monkey, and prosimian monkey). Using the Bayes empirical Bayes procedure, we also detected 2 positively selected codons (121L and 141T sites) that are independent of PGN-binding and PGLYRP-specific regions, implying 2 potential key sites for the functional effect of the PGLYRP1 protein. These results demonstrated that *PGLYRP1* was highly conserved at the molecular level and subjected to strong functional constraints during primate evolution.

Key words: Innate immunity; Molecular evolution; *PGLYRP1* gene; Primate; Purifying selection; Positive selection

