



***Toxoplasma gondii* rhopty protein 38 gene: sequence variation among isolates from different hosts and geographical locations**

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ABSTRACT. *Toxoplasma gondii* is an obligate intracellular parasite that is able to infect almost all mammalian species, and may lead to toxoplasmosis of the host. In the present study, we examined sequence variation in rhopty protein 38 (ROP38) genes among *T. gondii* isolates collected from different hosts and geographical regions. The complete ROP38 gene from 13 *T. gondii* isolates was amplified and sequenced. The results of sequence alignments showed that the lengths of the entire ROP38 gene ranged from 2646 to 2650 bp, with a sequence variation of 0.2-1.1%, among the 13 *T. gondii* isolates. This result

indicated low sequence variation in the ROP38 gene. Phylogenetic analysis of ROP38 sequences using Bayesian inference showed that the clustering of the 13 *T. gondii* isolates was not consistent with their respective genotypes. This result indicates that the ROP38 gene is not a suitable genetic marker for population genetic studies of different *T. gondii* genotypes from different hosts and geographical locations, but may represent a potential vaccine candidate against toxoplasmosis, and hence worthy of further research.

Key words: *Toxoplasma gondii*; Rhoptry protein 38 (ROP38); Toxoplasmosis; Sequence variation