



Sequence variation in ROP8 gene among *Toxoplasma gondii* isolates from different hosts and geographical localities

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ABSTRACT. The protozoan parasite *Toxoplasma gondii* has a worldwide distribution; it can cause serious diseases in humans and almost all other warm-blooded animals. Different genotypes of *T. gondii* result in different lesions in the same host. *T. gondii* rhoptry protein 8 (TgROP8) is a major factor of *T. gondii* acute virulence. We examined sequence variation in the TgROP8 gene among *T. gondii* isolates from different hosts and geographical localities. The TgROP8 gene was amplified from individual isolates and sequenced. A phylogenetic tree was constructed using Bayesian inference, maximum parsimony, and maximum likelihood based on the sequences obtained plus TgME49 from the ToxoDB database. The TgROP8 gene was 1728 bp in length for all the examined *T. gondii* strains, and their A+T contents were 45.37-45.95%. Sequence analysis detected 140 (0.06-

5.56%) variable nucleotide positions resulting in 96 (0-10.78%) amino acid substitutions. Sequence variations in the TgROP8 gene resulted in polymorphic restriction sites for endonucleases *Bst*BI, *Bsa*I, and *Xho*I, which allowed the differentiation of the three classical genotype strains (types I, II, and III) by polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP). However, phylogenetic analyses indicated that the TgROP8 gene is not a suitable genetic marker for population studies of *T. gondii*.

Key words: *Toxoplasma gondii*; Toxoplasmosis; ROP8; Genotyping; Sequence diversity