



Characterization of the *Toxoplasma gondii* *hsp60* gene sequences from different hosts and geographical locations

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Genet. Mol. Res. 13 (3): 6906-6911 (2014)

Received July 10, 2013

Accepted February 10, 2014

Published August 29, 2014

DOI <http://dx.doi.org/10.4238/2014.August.29.13>

ABSTRACT. The intracellular protozoan *Toxoplasma gondii* is one of the most successful parasites, with the ability to invade all warm-blooded animals, including humans. *T. gondii* heat shock protein 60 (TgHSP60) plays an important role in intracellular survival and in the differentiation of the parasite, and is also recognized as being associated with its virulence. In the present study, we examined sequence variation in the *hsp60* coding region among five *T. gondii* isolates from different hosts and geographical regions, which were compared with the corresponding sequences of strains ME49, 76K, and GT1 available in the ToxoDB databases. The length of the *T. gondii hsp60* sequence was 1728 bp for all strains, and the A+T content ranged from 41.96 to 42.13%. The sequence alignment of the 8 *T. gondii* strains identified 20 variable positions (0-1.44%) and showed 1.16% overall sequence

variation, suggesting a relatively considerable sequence diversity. Phylogenetic analysis of *hsp60* sequences using Bayesian inference and maximum parsimony differentiated the two major clonal lineage types into their respective clusters, and thus separated atypical strains from classical genotypes. The results of the present study suggested that the coding region of the *hsp60* gene may represent a novel genetic marker for intraspecies phylogenetic analyses of *T. gondii*.

Key words: *Toxoplasma gondii*; Toxoplasmosis; Sequence variation; Heat shock protein 60; Phylogenetic analysis