



## Sequence variation in the *Toxoplasma gondii* *eIF4A* gene among strains from different hosts and geographical locations

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**ABSTRACT.** *Toxoplasma gondii* is an opportunistic protozoan parasite that infects a wide range of animals, including humans. The *T. gondii* eukaryotic translation initiation factor 4A (eIF4A) protein is expressed in the tachyzoite, but its expression is markedly downregulated in the bradyzoite, and it is therefore considered to be associated with tachyzoite virulence. The present study examined sequence variation in the eIF4A gene among nine strains of different genotypes from different hosts and geographical localities using polymerase chain reaction amplification, sequence analysis, and phylogenetic reconstruction by Bayesian inference. The complete

genomic sequence of the eIF4A gene was 3156 bp in length in the strain TgCgCaI, 3153 bp in the strain MAS, 3152 bp in the strain TgPNY, and 3154 bp in the other six strains. Sequence analysis identified 29 (0-0.8%) variable nucleotide positions among all strains, with 16 of these variations located in the coding region, while the other 12 were distributed between the two introns. Phylogenetic analyses revealed that these eIF4A sequences were not effective molecular markers for intra-species phylogenetic analysis and differential identification of *T. gondii* strains from different hosts and geographical locations. This study demonstrated the existence of low sequence variation in the eIF4A gene, suggesting that *T. gondii* eIF4A may represent a suitable candidate vaccine against toxoplasmosis.

**Key words:** *Toxoplasma gondii*; Toxoplasmosis; Sequence variation; Eukaryotic translation initiation factor 4A protein; Phylogenetic analysis