



PARASITO2025

29º CONGRESSO BRASILEIRO DE PARASITOLOGIA

INHIBITORY POTENTIAL OF ISOPRENOID BIOSYNTHESIS IN *TOXOPLASMA GONDII* BY LIMONENE: AN *IN SILICO* STUDY

CARLOS VINICIUS BARROS OLIVEIRA¹, MARIA ELENILDA PAULINO DA SILVA², LAURA DE SOUZA RODRIGUES SIQUEIRA¹, ROMÁRIO MATHEUS CONCEIÇÃO DE OLIVEIRA³, ALISSON JUSTINO ALVES DA SILVA³, JOSÉ ELIÚ SOUSA DA SILVA³, MARIA SIMONETE DE SOUSA CRUZ³, ANA KAROLINE FERREIRA DE ALBUQUERQUE¹, ANA LÍVIA ALCÂNTARA³, MARIA JÉSSICA MENDES BRITO⁴

¹AGGEU MAGALHÃES INSTITUTE, RECIFE, PERNAMBUCO, BRAZIL, ²FEDERAL UNIVERSITY OF PERNAMBUCO, ³REGIONAL UNIVERSITY OF CARIRI, ⁴DOCTOR LEÃO SAMPAIO UNIVERSITY CENTER

Abstract

Toxoplasmosis is a pathology caused by the apicomplexan *Toxoplasma gondii*, and in pregnant women or immunocompromised individuals, it can cause severe symptoms, including mental confusion, lack of coordination and seizures. Protein prenylation is a ubiquitous covalent post-translational modification found in all eukaryotic cells, comprising the attachment of a farnesyl or a geranylgeranyl isoprenoid. It is essential for the proper cellular activity of numerous proteins in apicomplexans. Considering the inhibition of prenylation already documented for *Plasmodium* sp. by the monoterpene limonene, the present study aimed to determine the inhibitory potential of this terpene also on the activity of the farnesyl/geranylgeranyl diphosphate synthase of *T. gondii* through modeling of this protein and subsequent docking procedures. The modeling of the protein of interest was performed in the *AlphaFold 2* software, a program for modeling protein structures based on artificial intelligence available in Colab. The entire amino acid sequence provided in the ToxoDB database (identifier: TGME49_224490) was used for structural prediction. After modeling, the model was refined in the YASARA server and used for simulations (in triplicate), with magnesium divalent cations (*MIB2*); and with small molecules in the SwissDock server (*Autodock Vina*): dimethylallyl diphosphate (DMAPP), DMAPP+isopentenyl diphosphate (IPP), limonene, and DMAPP+limonene. The conformations most similar to the 1rqi model and stable were subsequently analyzed. The 2D interaction diagram generated by the *Discovery Studio* software shows that the stability of the DMAPP+limonene model (-5.278 kcal/mol) is quite similar to that of DMAPP+IPP (-5.550 kcal/mol), which may indicate an inhibitory potential due to competition at this binding site. Future *in vitro* results should further clarify the mechanism associated with the effect of limonene on isoprenoid synthesis in *T. gondii*.

Keywords: Toxoplasmosis, Prenylation, Inhibition.

 (11) 93232-3976

 www.parasito2025.com

 info@parasito2025.com

60 SBP
ANOS
SOCIEDADE BRASILEIRA DE PARASITOLOGIA