In silico anticoccidial activity of Fermented Maize Supernatant against *Eimeria tenella* of chickens

Gbolahan Oladipupo Oduselu[1,2*], Oluwayomi Oluwatoyin Adeyemi[3*], Olufemi Isaac Sotayo[4], Olamide Daniel Shoyinka[2]

[1]West African Centre for Cell Biology of Infectious Pathogens (WACCBIP), University of Ghana, P.O. Box LG 54, Legon, Accra, Ghana
[2]Drug Discovery Innovation Hub, Ota, Ogun State, Nigeria
[3]Department of Zoology, University of Lagos, Lagos, Nigeria
[4]Department of Microbiology, University of Lagos, Lagos, Nigeria

Presenting/Corresponding author: Oluwayomi Oluwatoyin Adeyemi (yadeyemi@unilag.edu.ng; +2348033954967)

Chicken coccidiosis, caused by *Eimeria* parasites is a major cause of economic losses in the global poultry sector. Control success is currently limited by widespread drug resistance and the high cost of vaccines. This underscores the urgent need for sustainable alternatives, with growing interests in natural products and traditional remedies in developing countries. Fermented Maize Supernatant (FMS), an organic waste product from maize slurry production, is rich in lactic acid bacteria metabolites and organic acids and is traditionally used in West Africa to manage gastroenteritis. Its anticoccidial potential, however, remains largely unexplored. This study employed *in silico* approaches to evaluate the activity of bioactive compounds from FMS against molecular targets in *Eimeria tenella*. Eight protein targets implicated in parasite development were retrieved from the Protein Data Bank, including dihydroorotate dehydrogenase (DHODH), apical membrane antigen 1 (AMA1), calmodulin-like domain protein kinase, phosphotransferase, microneme protein 3, microneme protein 5 precursor, SAG family member (SAG19), and enoyl-acyl carrier protein reductase. Thirteen previously reported FMS compounds were docked against these targets using Maestro Schrödinger, and binding affinities and free energies were analyzed. Results varied across the targets, with most interactions exhibiting moderate binding affinities. Notably, 2-methoxy-4-vinylphenol demonstrated the most favorable overall binding profile across multiple targets and exhibited a stronger binding affinity than the co-crystallized ligand of AMA 1. Three other phenolic compounds, including phenol-2,6-dimethoxy (-6.78 kcal/mol; -34.42 kcal/mol), 2′,4′-dimethoxyacetophenone (-6.03 kcal/mol; -39.33 kcal/mol), and 2,4-di-tert-butylphenol (-5.87 kcal/mol; -27.80 kcal/mol) showed particularly strong binding against the calmodulin-like domain protein kinase. Furthermore, squalene, a non-phenolic compound, showed considerable binding affinity toward the DHODH target (-5.63 kcal/mol; −46.61 kcal/mol). Overall, these compounds exhibited relatively stronger and more stable interaction profiles compared to other evaluated candidates. Our findings provide preliminary computational evidence of potential anticoccidial activity in FMS, warranting further in vitro and in vivo validation.