



## REVIEW

# Novel Antimalarial Drug Targets as Potent Tools to Accelerate Drug Discovery: A Short Review

Eze SC<sup>1\*</sup>, Isioma M<sup>2</sup>, Ugorji CC<sup>2</sup> and Ozota GO<sup>3</sup>.

<sup>1</sup>Faculty of Pharmaceutical Sciences, University of Nigeria Nsukka, Enugu State, Nigeria; <sup>2</sup>Faculty of Pharmaceutical Sciences, University of Nigeria Nsukka, Enugu State, Nigeria; <sup>3</sup>Federal Neuropsychiatric Hospital, Yaba, Lagos State, Nigeria.

### Address for correspondence:

Mr. Shadrach C. Eze  
Faculty of Pharmaceutical Sciences, University of Nigeria Nsukka, Enugu State, Nigeria  
Email: shadrachchinecheremeze@gmail.com

**To cite this article:** Eze SC, Isioma M, Ugorji CC and Ozota GO. Novel antimalarial drug targets as potent tools to accelerate drug discovery: A short review. *Journal of Basic and Social Pharmacy Research*, 2022;2(5):21-29  
**ISSN: 2705-3245**

## ABSTRACT

**Introduction:** Malaria is a significant tropical disease and the greatest killer of all time. The molecular pathways of known antimalarial drugs have been extensively elucidated. However, the emergence of resistant plasmodium species, especially that of *P. falciparum*, further threatens the prospects of its eradication. The advancement in proteomics and genomics has taken us a step further. Mere serendipity and pharmacology-based approaches can no longer take the lead in drug discovery. Newer and better antimalarial drug targets need to be sought.

**Objectives:** This study presents the need and problems in identifying and validating novel antimalarial drug targets to accelerate drug discovery.

**Methods:** Relevant literature was retrieved from Google Scholar, PubMed, and ScienceDirect. An exploratory search for traditional antimalarial drug targets and their shortcomings were reviewed, and the problems in identifying and validating novel drug targets. Possible solutions were proposed.

**Body:** Emerging resistance and advances in proteomics drive the need for newer targets. Significant problems include the lack of crystal structure of some targets and determining the essentiality of genes and their cognate proteins. The in-silico approach using phylogenetic comparison can quickly determine the essentiality of genes, and Protein Interference Assay (PIA) is potent in validating newer targets.

**Conclusion:** Identifying and validating novel antimalarial drug targets will effectively drive the search for and discovery of newer drugs.

**Keywords:** Malaria; Antimalaria; Drug discovery; Drug target; Target identification; *Plasmodium falciparum*