CHARACTERISATION OF *Plasmodium falciparum PFMDR1* GENE MUTATIONS IN MALARIA PATIENTS FROM SELECTED HOSPITALS IN OTA, OGUN STATE, NIGERIA

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AUGUST, 2024

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A DISSERTATION SUBMITTED TO THE SCHOOL OF POSTGRADUATE STUDIES IN PARTIAL FULFILLMENT OF THE REQUIREMENTS FOR THE AWARD OF MASTER OF SCIENCE (M. Sc) DEGREE IN MICROBIOLOGY IN THE DEPARTMENT OF BIOLOGICAL SCIENCES, COLLEGE OF SCIENCE AND TECHNOLOGY, COVENANT UNIVERSITY, OTA, OGUN STATE, NIGERIA

AUGUST, 2024

ACCEPTANCE

This is to attest that this dissertation is accepted in partial fulfilment of the requirements for the award of the degree of Master of Science in Microbiology in the Department of Biological Sciences, College of Science and Technology, Covenant University, Ota, Nigeria

Miss. Adefunke F. Oyinloye
(Secretary, School of Postgraduate Studies) **Signature and Date**

Prof. Akan B. Williams
(Dean, School of Postgraduate Studies) **Signature and Date**

DECLARATION

I, **ARIRIGUZOH, VICTORIA-GRACE ONYEKACHI (22PCQ02456)** declare that this research was carried out by me under the supervision of Professor Olayemi O. Akinnola of the Department of Biological Sciences, College of Science and Technology, Covenant University, Ota, Nigeria. I attest that the dissertation has not been presented either wholly or partially for the award of any degree elsewhere. All sources of data and scholarly information used in this dissertation are duly acknowledged.

ARIRIGUZOH VICTORIA-GRACE ONYEKACHI

Signature and Date

CERTIFICATION

We certify that this dissertation titled "**CHARACTERISATION OF Plasmodium *falciparum* PFMDR1 GENE MUTATIONS IN MALARIA PATIENTS FROM SELECTED HOSPITALS IN OTA, OGUN STATE, NIGERIA**" is an original research work carried out by **ARIRIGUZOH, VICTORIA-GRACE ONYEKACHI** in the Department of Biological Sciences, College of Science and Technology, Covenant University, Ota, Ogun State, Nigeria under the supervision of Professor Olayemi O. Akinnola. We have examined and found this work acceptable as part of the requirements for the award of Master of Science in Microbiology.

Professor Olayemi O. Akinnola
(Supervisor) **Signature and Date**

Dr Isaac O. Ayanda
(Head of Department) **Signature and Date**

Professor Segun I. Oyedeji
(External Examiner) **Signature and Date**

Professor Akan B. Williams
(Dean, School of Postgraduate Studies) **Signature and Date**

DEDICATION

For my dear mom, without whom my academic achievements would not have been possible. Your unwavering support, encouragement, and sacrifices have been the driving force behind my success. Thank you for always believing in me and pushing me to be my best self. This project is dedicated to you with all my love and gratitude.

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TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

FIGURES **TITLES** **PAGES**

ABSTRACT

Malaria continues to be a significant global health problem, especially in tropical and subtropical areas. The 2023 World Malaria Report by the World Health Organization reveals that there were 249 million cases of malaria and 608,000 fatalities in 2022. A significant obstacle in malaria control is the rise and spread of resistance to antimalarial drugs, which endangers the efficacy of current therapies and undermines worldwide endeavours to eradicate the illness. The efficacy of routinely used antimalarial medicines, such as artemisinin-based combination treatments (ACTs), is increasingly endangered by the formation and spread of multi-drug resistance (MDR). The *Plasmodium falciparum* multidrug resistance 1 gene (*Pfmdr1*) is frequently linked to multi-drug resistance. This study was conducted to detect the presence and prevalence of the *Pfmdr1* gene in *Plasmodium falciparum* isolated from malaria-positive blood samples to understand its role in anti-malaria drug resistance within Ota, Ogun State, Nigeria. Ethical approval was obtained from the Covenant Health Research Ethics Committee, Ogun state, Nigeria, before the commencement of the study. Three hundred and fifty-six blood samples were obtained from outpatients attending Covenant University Medical Centre and the General Hospital, Ado-Odo Ota, Ogun State. Microscopy was used to identify *P. falciparum* in all samples. The prevalence of malaria was recorded at 66%, with the age group of children ≤ 10 having the highest prevalence at 80%. DNA extraction was performed to isolate *P. falciparum* from 50 malaria-positive blood samples. Nested PCR was performed to identify and amplify the *Pfmdr1* gene and determine its mutations. The prevalence of the *Pfmdr1* was recorded at 66% among samples amplified using two-step Nested PCR. Sanger Sequencing was carried out on 10 samples to provide a detailed genetic characterization of the *Pfmdr1* gene and three mutations of the *Pfmdr1* gene the F74L, Y184F and S164S were identified.

KEYWORDS: Malaria, Multidrug resistance, Gene Mutations, Prevalence