MOLECULAR EPIDEMIOLOGY AND SOME FACTORS ASSOCIATED WITH GENITAL HUMAN PAPILLOMAVIRUS INFECTION AMONG WOMEN IN OYO STATE, NIGERIA

BY

YEWANDE TOLULOPE, NEJO

Matric Number: 130636 B. Sc. Microbiology (Ilorin), M. Sc. Virology (Ibadan)

A Thesis in the Department of Virology, Submitted to the Faculty of Basic Medical Sciences,College of Medicine, inpartial fulfillment of the requirements for the award of Degree of

DOCTOR OF PHILOSOPHY

of the

UNIVERSITY OF IBADAN.

MARCH, 2019

ABSTRACT

Genital Human Papillomavirus (HPV) infection is a well-established causative agent of cervical cancer; a major cancer in most developing countries.Persistent infection with high-risk HPV, especially types 16 and 18 have been associated with cervical cancer. Two HPV vaccines (Cervarix and Gardasil) are currently available in Nigeria, targeting two (16 and 18) and four (6, 11, 16 and 18) types, respectively. However, the distribution of HPV types varies greatly across geographical regions with little information on the circulating types among Nigerian women, thus raising concerns about the effectiveness of the available vaccines in the country. This study was therefore designed to determine the circulating HPV types among women in Oyo State, Nigeria and identify some factors associated with the infection.

A total of 295 endocervical swab samples were collected from consenting women attending routine cervical cancer screening, STI clinics and community-based outreach programme. The participants were enrolled from University College Hospital, Ibadan; Baptist Medical Centre, Saki and during an outreach in Molete community, Ibadan.Structured questionnaire was used to capture demographic, medical information and sexual history.Genomic DNA was extracted from samples using commercial extraction reagents. The presence of HPV was detected by PCR using two sets of consensus primers targeting the L1 and E6/E7 genes. Six pairs of HPV type-specific primers (16, 18, 31, 33, 35 and 6/11) were then used to genotype the HPV isolates in a nested PCR. Samples not identified by the primers used were sequenced and typed by phylogenetic analysis. Data were analysed using Chi-square at $\alpha_{0.05}$.

Fifty five (18.6%) individuals were positive for HPV infection. Primers targeting E6/E7 region detected more HPV infections (17.3%) than those targeting L1 region (9.2%). Five HPV types were detected using type-specific primers (HPV 16, 18, 31, 33 and 35), while 14 HPV types (HPV 6, 16, 18, 31, 35, 42, 43, 44, 52, 58, 66, 74, 81, 86) were identified by sequencing. In all, 15 HPV types were detected with HPV 31 being the most predominant (32.8%), followed by HPV 35 (17.2%) and HPV 16 (15.5%). About 21.0% of individuals had dual infections while high-risk HPV genotypes were found among 86.2% of HPV-

positive individuals. Highest nucleotide substitutions (n=32) were found in HPV 44 genotype while the only HPV 74 isolate had three nucleotide (CCT) insertionsat E7 gene that translated into amino acid proline. Some factors including divorce (p=0.019), illiteracy (p=0.003), polygamy(p=0.027), unemployment (p=0.023), low income earnings (p=0.018), younger age (<18years)at sexual debut (p=0.039) and passive smoking (p=0.017) were associated with HPV infection.

Multiple Human Papillomavirus types co-circulated in Oyo State, Nigeria. Most of the circulating Human Papillomavirus are high-risk type with type 31 being the most predominant. Although the implication of the rare HPV 74 with proline insertion detected for the first time in Nigeria is unknown, it may have effect on the transformation potential of the virus. Primers targeting E6/E7 region may be more appropriate for the detection of Human Papillomavirus circulating in Oyo State, Nigeria.

Keywords: Circulating Human Papillomavirus types, High-risk Human
Papillomavirus, E6/E7 genes, Human Papillomavirus associated factors
Word count: 492

ACKNOWLEDGEMENTS

I express my immense gratitude to my supervisor, Professor Georgina N. Odaibo whose thorough supervision, advice and scrutiny in every step of this work has led to its success. I am also very grateful to the Head of Department, Professor O. D. Olaleye for the advice and necessary guidance provided during the course of this work.

To my lovely husband, James Oladipupo, thanks for your care, love, and support throughout this programme. To my wonderful princesses, Oluwadolabomi and Oluwademilade, and my niece Osundahunsi Folasade; thanks for your support and understanding in making this work a reality, God bless you and I love you all.

My heartfelt appreciation goes to my father, Dr. P. A. Ajayi for his care, love and support towards making my Ph.D. programme a remarkable one, and to my dear mother, Mrs E. T. Ajayi, a jewel of inestimable value. Mummy, I will never forget your prayers and labour of love.

In a distinctive way, I appreciate my eldest brother and his wife, Dr and Mrs A. F. Ademola whose love and support has contributed to the success of this study, and to my niece, Aderinsola, Foyinsola, and my nephew, Damisola; you've being a great company to me, I love you all. My gratitude and love goes to my other brothers; the Engineer: Akintunde, the Accountant General: Adeolu, and the Barrister: Femi and their families, thanks to you all for your love and being there always whenever I called.

All the participants who took part in this study are gratefully acknowledged. Thanks to the Nurses of the cytology unit of the Department of Obstetrics and Gynaecology in University College Hospital, Ibadan for their support during sample collectionespecially Mrs Payne, God bless you ma. Thanks to the staff of Baptist Medical Centre, Shaki, Oyo State especially Miss Funke and Mr Kunle Fagade, you are all appreciated for your assistance in sample collection.

I owe a lot of thanks to Dr. O. A. Faneye whose support and advice have contributed to the reality of this work,God bless you real good. My appreciation goes to Dr.M. O. Adewumi, and Mr. A. B. Olusola for their useful advice and contributions; thanks so much for being there always. To my colleagues; Mr. Olukunle Oluwasemowo, Mr.Tunde Motayo,Mr Austin, Dr. Tekky, Mr, Shittu, Mr. Babalola and Mrs. Shenge, thanks for your encouragement and support;I will never forget your great company and useful advice. Thanks to all the postgraduate students who have contributed in one way or the other to the success of this work. I appreciate Dr and Mrs Emmanuel Donbraye, andalso Dr Bakarey for their encouragement and support, you've inspired me a great deal. My deep gratitude goes to all the Departmental, MEPIN, and Polio project staff who have contributed to the success of this work; you are all wonderful people, God bless you all.My appreciation also goes to the Bowen University, Iwo Management and the staff of Department of Biological Sciences for their support during the course of this study.

Above all, I am gratefulto the Almighty God;my all in all, for His wisdom, protection, direction and provision throughout this programme and my entire life;I give Him all the glory, honour and thanks.

CERTIFICATION

We certify that this work was carried out by Mrs. Yewande Tolulope NEJO in the Department of Virology, Faculty of Basic Medical Sciences, College of Medicine, University of Ibadan, Ibadan, Nigeria.

Supervisor Georgina N. Odaibo, Ph.D. Professor and Head, Department of Virology, College of Medicine,

University of Ibadan, Ibadan, Nigeria.

Co-supervisor O. D. Olaleye, DVM, Ph.D. Professor and Consultant Virologist, Department of Virology, College of Medicine, University of Ibadan, Ibadan, Nigeria.

DEDICATION

This work is dedicated to my Heavenly Father, the Author and Finisher of my faith. He is my portion and the reason for my existence. To Him be glory, honour, majesty, dominion, power, wisdom, and might forever, Amen.

TABLE OF CONTENTS

CONTENT		PAGE
Title Page		i
Abstra	act	ii
Ackno	owledgements	iv
Certifi	ication	vi
Dedic	ation	vii
Table	of Contents	viii
List of	f Tables	xii
List of	f Figures	xiv
List of	f Appendices	xvi
Acron	lyms	xvii
CHAI	PTER ONE	1
1.0.	INTRODUCTION	1
1.1.	Justification for the Study	5
1.2.	Research Questions	6
1.3.	Aim of the Study	6
1.4.	Objectives of the Study	6
CHAPTER TWO		8
2.0.	LITERATURE REVIEW	8
2.1.	History of Human Papillomavirus	8
2.2.	HPV Structure and Genome Organization	9
2.2.1.	Morphology of Human papillomavirus	9
2.2.2.	Genome Organization of Human papillomavirus	10
2.3.	Classification of Human Papillomavirus	14
2.4.	Properties of Human Papillomavirus	17
2.5.	Transmission of HPV Infection	17
2.5.1.	Horizontal Transmission of HPV Infection	18
2.5.2	Vertical Transmission of HPV Infection	18

2.6.	Clinical Presentation of HPV Infection		19	
2.7.	Replication of Human Papillomavirus		19	
2.8.	Pathogenesis of Human Papillomavirus Infection		23	
2.8.1.	Natural History of Genital HPV Infection		25	
2.8.2.	HPV Infection and Cervical Cancer		26	
2.9.	Epidemiology of HPV			28
2.9.1.	Risk Factors for HPV Infection and Cervical Cancer			30
2.9.2.	Molecular Epidemiology of HPV			32
2.10.	Host Immune Response to HPV Infection		34	
2.11.	Methods for the Detection of HPV Infections	34		
2.11.1.	Target Amplification Systems (Polymerase Chain Reaction)		34	
2.11.1.	1. Detection and Analysis of Amplification Products			35
2.11.2.	Serological Testing		36	
2.11.1.	Non-Molecular Techniques			36
2.12.	Prevention and Control Measures		39	
2.12.1.	Human Papillomavirus Vaccines		39	
2.13.	Treatment of clinically manifested HPV infections		42	
CHAPTER THREE				43
3.0.	MATERIALS AND METHODS		43	
3.1.	Study Area		43	
3.2.	Study Population		43	
3.3.	Study Design			44
3.3.1.	Sample size determination			44
3.3.2.	Inclusion/Exclusion criteria			44
3.4.	Ethical consideration and consent			44
3.5.	Sample Collection		44	
3.5.1	Data collection using Questionnaire			45
3.6.	Sample Analysis			45
3.7.	Extraction of Viral DNA		45	
3.7.1.	Principle of the DNA Extraction kit			46
3.7.2.	Procedure for DNA Extraction		46	

3.8.	Polymerase Chain Reaction (PCR)	47	
3.8.1.	Principle of Polymerase Chain Reaction		47
3.8.2.	Primers Used for HPV screening	47	
3.8.3.	Detection of HPV DNA using PCR	48	
3.8.4.	HPV Genotyping by PCR	48	
3.9.	Identification of PCR Products by Gel Electrophoresis	55	
3.9.1	Principle of Agarose Gel Electrophoresis		55
3.9.2.	Preparation of Reagents for Gel Electrophoresis	55	
3.9.3.	Preparation of Agarose Gel	56	
3.10.	Purification of PCR Product	56	
3.10.1.	Procedure for Purification of Amplicons	57	
3.11.	Quantification of the Amplicons	57	
3.11.1	Preparation of Reagentsfor Quantification	57	
3.11.2.	Quantification of the purified DNA (Amplicons)	57	
3.12.	Sequencing ofPurified PCR Products	58	
3.12.1.	Principle of Sanger's sequencing method	58	
3.12.2.	Sanger's sequencing Procedure	(60
3.13.	Analysis of the Sequences Generated	60	
3.14.	Data Analysis		60
СНАР	TER FOUR	(62
4.0.	RESULTS	62	
4.1.	Socio-demographic Characteristics of Participants	62	
4.2.	Detection of HPV DNA	624	.2.1.
	Detection of HPV DNA by Primers used in PCR	,	70
4.3.	Prevalence of HPV Infections	,	70
4.4.	Distribution of HPV Infection by sexual and smoking history of Par	ticipants	76
4.5.	Prevalence of HPV by some clinical history of Participants	76	
4.6.	Factors associated with HPV Infection by location of sample collect	ion 79	
4.7.	Sequenced isolates	79	
4.8.	Distribution of HPV Genotypes	83	
4.9.	Multiple Alignments and Phylogenetic analysis of Study isolates	87	

4.9.1.	. Multiple Alignments and Phylogenetic analysis of sequences of	
	High-risk HPV study isolates and other existing isolates	874.9.2
	Multiple Alignments and Phylogenetic analysisof sequences of	
	Low-risk HPV study isolates and other existing isolates	87
4.9.3.	Multiple Alignments and Phylogenetic analysis HPV-74 and HPV-86	87
4.9.4.	Nucleotide Substitutions and Amino Acid Variations in Sequences of Str	udy
	Isolates	107
CHAI	PTER FIVE	110
5.0.	DISCUSSION	110
CHAI	PTER SIX	126
6.0.	SUMMARY AND CONCLUSIONS	126
6.1.	Recommendations	127
REFE	CRENCES	128
APPE	NDICES	151

LIST OF TABLES

TAB	LE TITLE	PAGE
2.1.	The Human papillomavirus proteins and functions	13
2.2.	Clinical manifestations of HPV infections and associated HPV types	20
2.3.	Characteristics of the three Human papillomavirus vaccines licensed for	
	use in the United States	41
3.1.	Nucleotide sequence of the Consensus primers used for HPV screening	49
3.2.	Nucleotide Sequence of E6/E7 Type-specific primers used for HPV	
	Genotyping	50
3.3.	Constitution of master mix for PCR using PGMY09/11primers	51
3.4.	Thermo-cycling condition for PCR using PGMY09/11 Primer	52
3.5.	Constitution of master mix for nested PCR for HPV Genotyping	53
3.6.	Thermo-cycling condition for HPV Genotyping nested PCR 54	
3.7.	Quantification result of the Purified Amplicons	59
4.1.	Socio-demographic characteristics of study participants	63
4.2.	Rate of detection of HPV DNAby PGMY09/11 and E6/E7 Primers 71	
4.3.	Prevalence of HPV types by type-specific primers among study population	on72
4.4.	Prevalence of HPV infection by location of sample collection and study	
	population	73
4.5.	HPV Prevalence by some socio-demographic factors	74
4.6.	HPV Prevalence among participants by their State of Residence, Ethnic	
	groupand Travel history	75
4.7.	Distribution of HPV infection by sexual and smoking history of study part	rticipants
	77	
4.8.	Prevalence of HPV by Clinical history of participants	78
4.9.	Factors associated with HPV infection by location of sample collection	80
4.10.	List of sequenced isolates, location of Isolation and Genbank Accession	number
	81	
4.11.	Distribution of HPV Genotypes bytheir Risk type	84

4.12.	Distribution of HPV Genotypes by the type of Infection	85
4.13.	Distribution of HPV types by health status of individuals tested	86
4.14.	HPV E6 sequences of study isolates with some nucleotide substitutions	
	andamino acid changes	108
4.15.	HPV E7 sequences of study Isolates with their nucleotide substitutions	
	and amino acid changes	109

LIST OF FIGURES

FIGU	RE TITLE	PAGE
2.1.	The Structure of Human papillomavirus	10
2.2.	HPV Genome organization	12
2.3.	Phylogenetic tree inferred from the L1 nucleotide sequences of 189	
	papillomaviruses types	
	16	
2.4.	Productive Life Cycle of Human papillomavirus	21
2.5.	Degradation and inactivation of tumor suppressor p53 and pRb by HPV	
	E6 and E7 binding respectively	
	24	
2.6.	HPV-mediated progression to cervical cancer	27
2.7.	Estimated Contribution of HPV to Cancer	29
2.8.	Cervical Morphological Lesions	38
4.1.	Agarose gel electrophoresis Image of DNA detection by beta-globin gene	with the
PC04	and GH20 primers 64	
4.2.	Agarose gel electrophoresis Image of HPV DNA amplification with	GP-
E6/E7	Consensus Primers 65	
4.3.	Agarose gel electrophoresis Image of HPV DNA amplification with	
	PGMY09/11 Consensus Primers	
	66	
4.4.	Agarose gel electrophoresis Image of HPV DNA genotypingwith	
	HPV 16 (457bp) and 18 (322bp) E6/E7 Specific Primers	67
4.5.	Agarose gel electrophoresis Image of HPV DNA genotypingwith	
	HPV 31 (263bp) E6/E7 Specific Primer	
	68	
4.6.	Agarose gel electrophoresis Image of HPV DNA genotyping with	
	HPV 6 (334bp), 35 (358bp) and 33 (398bp) E6/E7 Specific Primer	S
	69	

4.7.	Sequence Electropherographs showing Peak and Length ofRead	
	(between 120 and 520 bases) of Isolate NGSk271-74	82
4.8.	Multiple E6/E7 Nucleotide Sequence Alignment of Study Isolates	88
4.9.	Multiple Amino acid sequence alignment of study isolates	89
4.10.	Estimates of Evolutionary Divergence between Sequences of Study	
	Isolates	90
4.11.	Phylogenetic Tree of Sequences of Study Isolates with HPV Reference	
	Sequences (REF)	
	91	
4.12.	Multiple Nucleotide Sequence Alignment of HPV 16 Study Isolates	
	withReference Sequence and Existing HPV sequences	92
4.13.	Phylogenetic Tree of HPV-16 Isolates	93
4.14.	Phylogenetic Tree of HPV-18 Isolates	94
4.15.	Phylogenetic Tree of HPV-31 Isolates	95
4.16.	Phylogenetic Tree of HPV-35 Isolates	96
4.17.	Phylogenetic Tree of HPV-52 Isolates	97
4.18.	Phylogenetic Tree of HPV-58 Isolates	98
4.19.	Phylogenetic Tree of HPV-66Isolates	99
4.20.	Phylogenetic Tree of HPV-6 Isolates	100
4.21.	Phylogenetic Tree of Sequences of HPV-42 and HPV-43 Isolates	101
4.22.	Phylogenetic Tree of Sequences of HPV 44 Isolates	102
4.23.	Phylogenetic Tree of HPV 81 Isolates	103
4.24.	Nucleotide Sequence Alignment of HPV-74 Isolate with Reference	
	Sequence and Sequence from France, showing insertion of CCT	
	104	
4.25.	Multiple Nucleotide Sequence Alignment of HPV-86 Study Isolates with	
	Reference Sequence	105
4.26	Phylogenetic Tree of HPV-74 and HPV-86 Isolates	106

LIST OF APPENDICES

APPENDIX	TITLE	PAGE
1	Ethical Approval	151
2.	Questionnaire	152
3.	Informed Consent Form (English Version)	154
4.	Informed Consent Form (Yoruba Version)	155
5.	Reagents for DNA Extraction	156
6.	Reconstitution of Reagents for DNA Extraction	156
7.	Purification Kit Contents	156
8.	Reconstitution of Reagent for Purification	157
9.	Reagents for DNA Quantification	157
10.	Reconstitution of Reagents for DNA Quantification	157
11.	Sequences of Study Isolates	158

ACRONYMS

ACOG- American College of Obstetricians and Gynecologists

AIDS- Acquired Immunodeficiency Syndrome

AIN- Anal Intraepithelial Neoplasia

BLAST- Basic Local Alignment Search Tool

BPV- Bovine Papillomavirus

CDC- Center for Disease Control

CIN- Cervical Intraepithelial Neoplasia

CMV- Cytomegalovirus

CRPV- Cottontail Rabbit Papillomavirus

DC- Dendritic cells

DNA- Deoxyribonucleic acid

DVI- Direct visual inspection

EDTA- Ethylene di-amine tetra acetic acid

ELISA- Enzyme-Linked Immunosorbent Assay

EV- Epidermodysplasia verruciformis

FDA- Food and Drug Administration

HHV- Human herpesvirus

HIV- Human Immunodeficiency Virus

HPV- Human papillomavirus

HR-HPV- High-risk types

HSIL- High-grade cervical lesions

IARC- International Agency for Research on Cancer **ICC-** Invasive Cervical Cancer ICTV- International Committee on the Taxonomy of Viruses **IFN-** Interferon LC- Langerhans cells LCR- Long control region LR-HPV- Low-risk types LSIL- Low-grade cervical lesions MCL- Maximum Composite Likelihood NCBI- National Centre for Biotechnology Information **NC-Negative Control** NCR- Non-coding region **NHS-** National Health Service NK- Natural killer cells, **NKT**- Natural killer T NMPCR- Nested Multiplex Polymerase Chain Reaction **OC-** Oral Contraceptives **ORFs-** Open reading frames **PC-** Positive Control **PCR-** Polymerase Chain Reaction **PG-**Pico Green PIN- Penile Intraepithelial Neoplasia **PV-** Papillomaviruses SPSS- Statistical Package for Social Sciences **STI-** Sexually Transmitted Infection **TBE-** Tris Borate EDTA **UCH-** University College Hospital **URR-** Upstream regulatory region VIA- Visual inspection with acetic acid VIN- Vulvar Intraepithelial Neoplasia **VLPs-** Virus-like particles

WHO- World Health Organization