Research Article

iMedPub Journals
http://www.imedpub.com/

Journal of HIV & Retro Virus
ISSN 2471-9676

2016
Vol.2 No.3:26

DOI: 10.21767/2471-9676.100026

Transmitted HIV-1 Drug resistance and the Role of Herpes Simplex Virus-2 Co-infection among Fishermen along the Shores of Lake Victoria, Kisumu, Kenya

Victor Mburu Macharia[1], Caroline Ngugi[1], Raphael Lihana[2] and Musa Otieno Ngayo[3]

[1]College of Health Sciences, Jomo Kenyatta University of Agriculture and Technology, Nairobi, Kenya

[2]Centre for Virus Research, Kenya Medical Research Institute, Nairobi, Kenya

[3]Centre for Microbiology Research, Kenya Medical Research Institute, Nairobi, Kenya

Corresponding author: Musa Otieno Ngayo, Centre for Microbiology Research Kenya Medical Research Institute: Nairobi, Kenya, Tel: 254202720038226; E-mail: musaotienoy@yahoo.com

Received date: October 17, 2016; **Accepted date:** October 24, 2016; **Published date:** October 29, 2016

Citation: Macharia VM, Ngugi C, Lihana R, et al. Transmitted HIV-1 drug resistance and the role of herpes simplex virus-2 co-infection among fishermen along the shores of lake Victoria, Kisumu, Kenya, J HIV Retrovirus. 2016, 2:3.

Abstract

Introduction: Herpes simplex virus type 2 (HSV-2) infection has been associated with a 3-fold risk of HIV-1 acquisition. The prevalence of HIV-1 and HSV-2 in the fishing communities along the shores of Lake Victoria in Kisumu have been reported to be high. This may contribute to the growing HIV epidemic in Kenya including the spread of transmitted drug resistance (TDR). We report data on the association of HSV2/HIV-1 co-infection and TDR in this antiretroviral (ARV)-naïve population.

Methods: Blood samples were obtained from 249 consenting fishermen from 5 beaches and a detailed sociodemographic questionnaire was administered. Blood samples were analyzed for HIV-1/HSV2 co-infection. The HSV-2 serology was performed using Kalon HSV type 2 enzyme-linked immunosorbent assay (ELISA). The HIV-1 counselling and serology were carried out according to local standards of practice in Kenya, using two parallel rapid assays (Alere Determine HIV-1/2 and Trinity Biotech Uni-Gold), with a third ELISA-Vironostika HIV Uni-Form II Ag/Ab for resolving discrepancies. All HIV positive samples were tested for TDR using an in house HIV-1 pol-RT genotyping protocol.

Results: Of the 249 recruited fishermen (mean age 35.1 years), 134 (53.8%) were positive for HSV-2, 59 (23.7%) were HIV positive while 48 (19.3%) were HIV/HSV-2 co-infected. Twenty-three of 59 (38.9%) HIV positive men had TDR, with the majority (19/23, 82.6%) in HIV/HSV-2 co-infected fishermen. Among the 48 HIV/HSV-2 co-infected fishermen, 9 had nucleoside reverse-transcriptase inhibitor (NRTI) resistance mutations with NRTI- associated mutations [NAMS], M184V (77.8%) and K65R (11.1%) being the highest. Nineteen (19) fishermen had Non-NRTI (NNRTIs) mutations including; four (21.1%) each of K103N, Y181C and G190A. Three (15.7%) V179T, two V901V and single A98G and Y188L mutations. Among the 11 fishermen who had HIV-1 mono-infection, four (36.4%) had drug resistant mutations. One fisherman had NRTI resistance mutation M184V. In addition, three men (3/4) had NNRTI resistance; K103N, G190A and Y181C mutations each. In the regression model, HIV/HSV-2 co-infection was independently associated with TDR [OR 4.1 (95% CI 1.4 to 11.9)].

Conclusion: The level of TDR to NNRTIs in these ARV-naive fishermen was significantly high especially among those co-infected with HSV-2. HSV-2 infection may increase the risk of TDR in this population.

Keywords: HIV; AIDS; HIV-1; Drug resistance

Introduction

Fishing communities along the shore of Lake Victoria in Kenya comprise young, highly migratory men who spend long periods away from their families and local communities and engage in high risk sexual behaviour [1-3]. This community has one of the highest prevalence of sexually transmitted infection (STI) and HIV in East Africa [4]. In Kenya, higher HIV prevalence 25.6% and 19.6% HSV-2/HIV co-infection was reported among fishermen along Lake Victoria in Kisumu [5, 6] compared to the national prevalence of 5.3% and 16%, respectively [7, 8]. This fishing community therefore qualifies as a high priority groups for HIV intervention programs [1].

Herpes simplex virus type-2 (HSV-2) is a chronic sexually transmitted infection [STI] responsible for genital ulcer disease worldwide [9, 10]. The HSV-2 infection constitutes a substantial public health problem because it increases the risk of HIV acquisition up to about four fold [11, 12]. Many studies have demonstrated a synergistic relationship between HSV-2 and HIV; HSV-2 infection increases the susceptibility to and transmission of HIV, while HIV infection increases the susceptibility to HSV-2 infection and HSV-2 genital shedding [10, 13]. HSV-2 therefore contributes in the HIV epidemic in Kenya and may also enhance the transmission of drug-resistant HIV variants to newly infected individuals termed transmitted drug resistance (TDR) [14].

Sub-Saharan African countries in the past decade, has been marked with substantial scale up in the access to antiretroviral therapy (ART) [15]. Unfortunately, significant increase in patients failing ART and HIV resistance to some ART medications is being observed [16]. Consequently, cases of ART-naïve individuals infected with TDR, associated with treatment failure [17, 18] are on the rise. Studies across Kenya are beginning to show widespread resistance in ART-naïve persons [19-21]. In this study, we determined the prevalence of drug-resistant mutations as well as evaluated the association of HSV-2 co-infection in the prevalence of TDR among ARV-naive men working in the fishing industries along the shores of Lake Victoria in Kisumu, Kenya.

Methods

Study design and population

This cross sectional study was conducted among men working in the fishing industry in the beaches along Lake Victoria in Kisumu Kenya. The description of these beaches has been described elsewhere [3]. Formula for estimating the population proportion with specified absolute precision by Lemeshow et al. [22] was used to determine the number of fishermen recruited in this study. Setting α at 0.05 and fishermen HSV-2/HIV co-infection rate of 19.6% [8], a total of 249 fishermen were recruited to achieve 0.95 power.

Four beaches, namely Nyamware, Dunga, Kichinjio and Kobudho were chosen based on the population size, the level of fishing activity and mobility. From each beach, the beach management unit (BMU) provided us with the list of registered boats and the number of fishermen on the boat. Men who were 18 years old or more and worked in the fishing industry for at least 3 months were eligible to participate. Informed consent was sought before they were enrolled in the study.

Counselling and sample collection

The enrolled fishermen underwent HIV counselling according to the guidelines in Kenya before blood samples were collected for testing. The risk and benefits of testing and meaning of test results were explained. About 5 ml of blood were collected for HIV-1 and herpes simplex virus (HSV) testing. This study was approved by the ethical review committee of Kenyatta National Hospital and University of Nairobi.

Laboratory procedures

Serology

Serology was carried out according to local standards of practice in Kenya, using two parallel rapid assays (Alere Determine HIV-1/2 and Trinity Biotech Uni-Gold), with a third enzyme-linked immunosorbent assay (ELISA) assay using Vironostika HIV Uni-Form II Ag/Ab (Biomerieux, Marcyl'Etoile, France) to resolve discrepancies. The HSV-2 serology was tested by Kalon HSV type 2 IgG ELISA (Kalon Biological Ltd, Surrey, United Kingdom) according to the kit manufacturer's instructions [23].

Genotypic testing

All HIV positive samples were evaluated for genotypic drug resistance using an in-house population-based sequencing method as described previously [24]. Briefly, viral RNA was extracted from 140 µl of plasma using a QiAmp viral RNA kit (Qiagen, Valencia, CA) according to the manufacturer's instructions. A nested reverse transcriptase-polymerase chain reaction (RT-PCR) was performed to amplify 645 base pairs of HIV-1 pol [24]. The PCR products of correct size were confirmed by gel electrophoresis and purified and sequenced by dideoxynucleoside-based analysis using a Big Dye terminator kit (Applied Biosystems) and ABI Prism 3100 equipment (Applied Biosystems, Foster City, US).

Ethical considerations

This study was conducted according to the Declaration of Helsinki and International Conference on Harmonization Guideline on Good Clinical Practice (ICH-GCP). The protocol and informed consent form were reviewed and approved by the Kenyatta National Hospital and University of Scientific Steering Committee and the Ethical Review Committee prior to commencement of field activities (KNH-ERC/RR/707-P545/08/2015 on 16th September 2015). Written informed consent was obtained from each participant. Confidentiality was maintained by assigning all participants with a unique identification number and all paper research records stored in a locked cabinet stationed in a secured room only accessible to the principal investigator. This research adhered to the STROBE guidelines for observational studies as outlined.

Drug resistance mutation analysis and statistical methods

Genotypic resistance was defined as the presence of resistance mutations associated with impaired drug susceptibility using the Stanford Genotypic Resistance Interpretation Algorithm. Codons included major NNRTI mutations at K103N, Y188L, Y181C, and G190A, and major NRTI mutations, M184V, K65R, and thymidine analog mutations (TAMs). HIV-1 subtypes were determined using the NCBI subtyping tool and phylogenetic trees were constructed from pol sequences with PAUP version 4.0 Beta10 [25] by creating a neighbour-joining phylogenetic tree with reference sequences from the Los Alamos National Laboratory HIV Database.

Data were analysed using STATA 13 (StataCorp, College Station, TX, USA). Descriptive statistics, frequency (%), mean, standard deviation was used to present the quantitative data. Bivariate and multivariate analyses were done using Poisson regression to evaluate factors that were associated with TDR (at $P \leq 0.05$).

Results

Characteristics of the study participants

Between September 2015 and February 2016, 249 fishermen were enrolled. The characteristics of the fishermen are shown in **Table 1**. The mean age (SD) was 35.1 (7.8) years. The HIV infected 34.7 (8.3) years, HSV-2 infected 35.6 (8.98) years and

HIV-1/HSV-2 34.3 (7.49) years. Overall, the majority (68.3%) of participants were married and 78.7% worked as fishermen. Majority (93.2%) had their age of sexual debut below 18 years, 85.9% were uncircumcised, while 42.2% had more than one sexual partner. For the fishermen who travelled away from their fishing beaches, 11.6% had at least one sexual act and 20.9% used condoms. Of the 249 fishermen, 134 (53.8%) were HSV-2 positive, 59 (23.7%) were HIV-1 positive while 48 (19.3%) were HIV/HSV-2 co-infected.

Table 1 Participants characteristics by infection type (Data on beach, marital status, No of wives, education, occupation, income, circumcision, No. of sexual partner, No. travelled in past month, sexual acts during last travel, sexual partner and condom use last two act was presented as absolute numbers (n) and percentages (%) while age and Age of sexual debut was shown as mean ± standard deviation (SD) in years).

Variable	Mono or co-infection							
	Total		HIV-1		HSV-2		HIV-1/HSV-2	
	N	%	N	%	N	%	N	%
Beach								
Dunga	63	25.3	20	33.9	39	29.1	20	41.7
Kichinjio	62	24.9	15	25.4	24	17.9	6	12.5
Kobudho	62	24.9	7	11.9	17	12.7	5	10.4
Nyamware	62	24.9	17	28.8	54	40.3	17	35.4
Age								
Mean (SD) (Years)	35.1	7.8	34.7	8.3	35.6	8.98	34.3	7.49
Range (Years)	40	26 to 66	36	26 to 66	40	26 to 66	31	26 to 66
21-30	80	32.1	24	40.7	46	34.3	20	41.7
31-40	127	51	24	40.7	60	44.8	19	39.6
>41	42	16.9	11	18.6	28	20.9	9	18.8
Marital status								
Single	71	28.5	19	32.2	42	31.3	18	37.5
Married	170	68.3	38	64.4	90	67.2	29	60.4
Divorced/Widowed	8	3.2	2	3.4	2	1.5	1	2.1
No. of wives								
1	160	64.3	35	59.3	83	61.9	26	54.2
2	10	4	3	5.1	7	5.2	3	6.3
Not applicable	79	31.7	21	35.6	44	32.8	19	39.6
Education Level								
Primary	144	57.8	32	54.2	69	51.5	22	45.8
Secondary	104	41.8	27	45.8	64	47.8	26	54.2
Tertiary	1	0.4	0	0	1	0.7	0	0
Occupation								
Fisherman	196	78.7	33	55.9	93	69.4	25	52.1
Fish trader	53	21.3	26	44.1	41	30.6	23	47.9
Income (Ksh)								
<10000	223	89.6	53	89.8	117	87.3	43	89.6
>10001	26	10.4	6	10.2	17	12.7	5	10.4

Age sex debut								
Mean (SD) (Years)	15.1	2.6	14.7	1.9	15.3	2.7	14.8	1.999
Range (Years)	19	7 to 26	8	10 to 18	19	7 to 26	8	10 to 18
<18	232	93.2	59	100	123	91.8	48	100
>18	17	6.8	0	0	11	8.2	0	0
Circumcised								
Yes	35	14.1	12	20.3	25	18.7	10	20.8
No	214	85.9	47	79.7	109	81.3	38	79.2
No of sexual partner								
1	140	56.2	32	54.2	76	56.7	23	47.9
>1	105	42.2	23	54.2	54	40.3	21	43.8
None	4	1.6	4	6.8	4	3	4	8.3
No travelled in past month								
1	58	23.3	14	23.7	34	25.4	13	27.1
>1	72	28.9	20	33.9	40	29.9	14	29.2
None	119	47.8	25	42.4	60	44.8	21	43.8
Sexual acts during last travel								
None	220	88.4	51	86.4	116	86.6	40	83.3
At least once	29	11.6	8	13.6	18	13.4	8	16.7
Sexual partner								
Girlfriend	124	49.8	28	47.5	71	53	22	45.8
Wife	5	2	3	5.1	4	3	3	6.3
Casual partner	106	42.6	21	35.6	48	35.8	17	35.4
Not applicable	14	5.6	7	11.9	11	8.2	6	12.5
Condom use last two act								
Yes	52	20.9	19	32.2	33	24.6	18	37.5
No	183	73.5	33	55.9	90	67.2	24	50
Not applicable	14	5.6	7	11.9	11	8.2	6	12.5

Genotypic Profiles

A genotype result was obtained for all the 59 HIV infected fishermen. Subtype analysis of the pol region showed that HIV-1 subtype A was most common 28/59 (47.5%) [78.6% in HIV-1/HSV-2 co-infection verses 21.4% in HIV-1 mono-infection], followed by subtype D 16/59 (27.1%) [93.8% in HIV-1/HSV-2 co-infection verses 6.3% in HIV-1 mono-infection], subtype C 3/59 (5.1%) [66.7% in HIV-1/HSV-2 co-infection verses 33.3% in HIV-1 mono-infection], subtype B 3/59 (5.1%) [All in HIV-1/HSV-2 co-infection], subtype G 2/59 (3.4%) and possible unique recombinants 7/59 (11.9%) **(Table 2)**.

Table 2 HIV-1 Subtype and Transmitted Drug Resistance Mutations (TDRM) among Antiretroviral - naive HIV mono and HIV/HSV-2 co-infected fishermen.

HIV-1/HSV-2 co-infected					**HIV-1 Mono-infected**				
Age	**Beach**	**Subtype**	**NRTI**	**NNRTI**	**Age**	**Beach**	**Subtype**	**NRTI**	**NNRTI**

31	Dunga	A	Susc	V179T	29	Kichinjio	G	Susc	V90I, K103N, F227FL
47	Kobudho	B	K65KR	V106AV, F227FL, M230I	62	Kichinjio	CRF01_AE	Susc	Y181CY
30	Nyamware	D	M184V	V106A	57	Kichinjio	C	M184V	Susc
35	Dunga	C	M184V	K103KN	29	Kichinjio	A	Susc	G190A
30	Dunga	C	M184V	K103KN	37	Kichinjio	CRF01_AE	Susc	Susc
30	Nyamware	A	Susc	K103KN	32	Kobudho	D	Susc	Susc
40	Dunga	D	M184V	A98G, Y181C, H221HY	32	Kobudho	A	Susc	Susc
28	Dunga	D	M184V	Y188L	36	Kichinjio	A	Susc	Susc
26	Dunga	D	Susc	G190AG	33	Kichinjio	A	Susc	Susc
42	Kichinjio	A	Susc	K103N	30	Kichinjio	A	Susc	Susc
38	Dunga	CRF01_AE	Susc	G190AG	29	Kichinjio	A	Susc	Susc
28	Dunga	CRF01_AE	M184V	E138Q, G190A					
33	Nyamware	D	Susc	V90IV					
36	Kichinjio	A	M184V	G190A					
37	Nyamware	D	Susc	V179DV					
31	Nyamware	D	V75MV	Y181CY					
30	Nyamware	CRF01_AE	Susc	V90IV, Y181FINY					
33	Kobudho	G	Susc	Y181C, H221Y					
35	Nyamware	A	Susc	V179T					
32	Dunga	A	Susc	Susc					
28	Dunga	A	Susc	Susc					
41	Dunga	A	Susc	Susc					
31	Dunga	D	Susc	Susc					
30	Kobudho	D	Susc	Susc					
30	Dunga	B	Susc	Susc					
37	Dunga	D	Susc	Susc					
37	Dunga	A	Susc	Susc					
30	Kobudho	A	Susc	Susc					
29	Dunga	A	Susc	Susc					
41	Dunga	A	Susc	Susc					
43	Dunga	A	Susc	Susc					
38	Nyamware	D	Susc	Susc					
35	Dunga	D	Susc	Susc					
45	Kichinjio	A	Susc	Susc					
28	Dunga	A	Susc	Susc					
27	Nyamware	A	Susc	Susc					
33	Kichinjio	D	Susc	Susc					

28	Nyamware	B	Susc	Susc					
28	Nyamware	A	Susc	Susc					
28	Nyamware	A	Susc	Susc					
32	Kichinjio	A	Susc	Susc					
27	Nyamware	A	Susc	Susc					
56	Kichinjio	A	Susc	Susc					
26	Nyamware	D	Susc	Susc					
51	Nyamware	A	Susc	Susc					
27	Nyamware	CRF01_AE	Susc	Susc					
32	Nyamware	D	Susc	Susc					
57	Kobudho	CRF01_AE	Susc	Susc					

Twenty-three of 59 (38.9%) sequenced samples had TDR. Majority, 19/23 (82.6%) were among HIV/HSV-2 co-infected fishermen. Among the 59 HIV infected fishermen, 10 had NRTI resistance mutations with NAMS M184V (80%) and K65R (10%) were among mutations observed (about 90% found in the HIV/HSV-2 co-infected fishermen). Twenty-two (22) had NNRTI mutations; five (22.7%) fishermen had K103N, Y181C and G190A each. Three13.6%) fishermen had V179T, two fishermen had V901V while A98G, Y188L mutations were also detected. About 81.8% of these NNRTI mutations were found in the HIV/HSV-2 co-infected fishermen **(Table 3)**.

Table 3 Factors associated with TDR variant.

Variable	Sample size	TDR infected fishermen		Bivariate cOR (95% CI)	Multivariate aOR (95% CI)
		Frequency	Percentage		
HSV-2 infection					
Positive	134	19	14.2	4.1 (1.4-11.9)	NS
Negative	115	4	3.5	1	
Beach					
Dunga	63	8	12.7	1.1 (0.4-3.1)	
Kichinjio	62	6	9.7	0.9 (0.3-2.6)	NS
Kobudho	62	2	3.2	0.3 (0.1-1.4)	
Nyamware	62	7	11.3	1	
Age					
21-30	80	9	11.3	0.8 (0.3-2.7)	NS
31-40	127	10	7.9	0.7 (0.3-1.7)	
>41	42	4	9.5	1	
Marital status					
Single	71	5	7		NS
Married	170	18	10.6	ND	
Divorced/Widowed	8	0	0		
No of wives					
1	160	17	10.6	1.7 (0.6-4.6)	NS
2	10	1	10	1.5 (0.2-13.5)	

Not applicable	79	5	6.3	1	
Education Level				ND	
Primary	144	8	5.6		ND
Secondary	104	15	14.4		
Tertiary	1	1	100		
Occupation					
Fisherman	196	15	7.7	1.9 (0.8-4.7)	NS
Fish trader	53	8	15.1	1	
Income (Ksh)					
<10000	223	21	9.4	1.2 (0.3-5.2)	NS
>10001	26	2	7.7	1	
Age sex debut				ND	
<18	232	23	9.9		ND
>18	17	0	0		
Circumcised					
Yes	35	5	14.3	1.7 (0.6-4.6)	
No	214	18	8.4	1	
No of sexual partner					NS
1	140	16	11.4	0.5 (0.06-3.4)	
>1	105	6	5.7	0.2 (0.03-1.9)	NS
None	4	1	25	1	
No travelled in past month					NS
1	58	5	8.6	1.8 (0.3-9.9)	
>1	72	8	11.1	0.6 (0.1-2.6)	
None	119	10	8.4	1	
Sexual acts during last travel					NS
At least once	29	3	10.3	0.9 (0.3-2.9)	
None	220	20	9.1	1	
Sexual partner					
Girlfriend	124	13	10.5	0.7 (0.2-3.3)	
Wife	5	0	0	ND	
Casual partner	106	8	7.5	0.5 (0.1-2.4)	NS
Not applicable	14	2	14.3	1	
Condom use last two act					NS
Yes	52	7	13.5	1.7 (0.7-4.1)	
No	183	14	7.7	1	

Table 3 summarizes the bivariate and multivariate analysis of factors associated with the prevalence of TDR. In the regression model, HSV-2 co-infection was the only factor independently associated with TDR; OR 4.1 (95% CI 1.4-11.9).

Discussion

The prevalence of HIV TDR in this population was 38.9%. According to WHO surveillance criteria, this level is high [26]. This is not surprising because this region is not only marked with highest prevalence of HIV in Kenya but has also experienced significant ART treatment roll-out over the last 10 years. The emergence of TDR in communities has been largely attributed to the longer availability of ARVs [27]. It has also been stipulated that the higher the ARV coverage, the higher the risks of the emergence and spread of TDR [28]. Previous studies of TDR in Kenya showed a prevalence ranging from 1.1% to as high as 13.3% [20, 29, 30]. In Uganda a prevalence of 6% TDR among fishermen along the shore of L. Victoria in Uganda has been reported [31].

The mutations seen in our study were associated with resistance to both NNRTIs (K103N, Y181C, V106A and G190A) and NRTI (M184V and K65KR). These mutations confer resistance to drugs used as standard first line ART regimens in Kenya. Reports show that some NNRTI mutants are relatively fit and may therefore be more likely to be transmitted and to persist over time [32]. Other studies among ART naïve individuals in Kenya have identified either only NNRTI mutation [20] or mutations to NRTIs and PIs [21]. A multisite study in 6 sub-Saharan Africa countries (Kenya, Nigeria, South Africa, Uganda, Zambia, and Zimbabwe), identified K103N, thymidine analogue mutations, M184V, and Y181C/I as the most common drug-resistance mutations [27]. With the initiation of ART in Kenya, levels of HIVDR seem to increase with time [33], a trend that is yet to be confirmed everywhere [34].

Most TDR mutations seen in our study were among fishermen who were co-infected with HSV-2. The synergistic relationship between HIV and HVS-2 has been established [35]. Studies consistently demonstrate higher plasma viral loads and increased genital tract HIV during episodes of HSV-2 reactivation, which may increase the risk for sexual and mother-to-child transmission and accelerate HIV disease progression [36, 37]. The HIV/HSV-2 coinfection has been shown to potentiate the clinical severity and infectiousness of the two viruses [38]. Whether it's the synergistic relationship between HIV and HVS-2 or TDR viral fitness that was associated with the high prevalence of TDR in HVS-2 infected men, is an area for further investigation.

Our findings of high TDR in HSV-2 infected fishermen, poses a significant challenge not only in treatment but also the need for drug resistant testing prior to ART initiation among the naïve individuals [39]. Further, it is important to intensify monitoring the development and propagation of drug resistance. Intensive health education, counseling and monitoring of patients on ART are some of the suggested interventions to achieve maximal ART adherence [31]. Currently, monitoring of TDR in developing countries is often opportunistic and depends on individual initiatives. Surveillance strategies are needed to systematically screen populations (especially the high risk) in Kenya and other countries that are currently rolling out and or scaling up ART programs.

Some of the limitations in our study include, first the population sequencing as used in our study. Resistance variants are likely to remain undetected. Secondly, although this study was conducted prior to the increasing availability of ARVs, we were not able to report increases in TDRs over time. A longitudinal design would give better data.

Conclusion

In conclusion, the level of TDR in this high risk population was high (38.9%). This is a concern given their high mobility which limit access to healthcare services. With increasing ARV therapy availability in sub-Saharan Africa and the recent WHO recommendations for earlier treatment, it follows that the prevalence of TDRs will also increase, highlighting the importance of TDR monitoring. Although the synergetic relationship between HIV and HSV-2 has been continuously reported, the role of HSV-2 co-infection in the transmission of TDR require further investigation.

Acknowledgement

We acknowledge all of the volunteers who participated in this study. We would also like to thank Brian Khasimwa of Nairobi University for offering technical support during HIV genotyping. This study was funded by student's loan.

Author's Contributions

This work was part of Master of Science degree for VMM in Medical Virology at the Jomo Kenyatta University of Agriculture and Technology. MON and VMM conceived and designed the study. MON and VMM conducted field work and laboratory assays. MON conducted data analysis. RL and CN guided the design of the study and provided general supervision. All authors read and approved the final manuscript.

Nucleotide Sequence Accession Numbers

The gene sequences determined in this study were deposited in Gen Bank under accession numbers KX505314-KX505372.

References

1. Seeley JA, Allison EH (2005) HIV/AIDS in fishing communities: Challenges to delivering antiretroviral therapy to vulnerable groups. AIDS Care 17: 688-697.
2. Kissling E, Allison E, Seeley J, Russell S, Bachmann M, et al. (2005) Fisher folk are among groups most at risk of HIV: Cross-country analysis of prevalence and numbers infected. AIDS 19: 1939-1946.
3. Kwena ZA, Bukusi EA, Ng'ayo MO, Buffardi AL, Nguti R, et al. (2010) Prevalence and risk factors for sexually transmitted infections in a high-risk occupational group: The case of fishermen along Lake Victoria in Kisumu, Kenya. Int J std aids 21: 708-713.
4. Seeley J, Kamali A, Mpendo J, Asiki G, Abaasa A, et al. (2012) High HIV incidence and socio-behavioural risk patterns in fishing communities on the shores of Lake Victoria. Sex Trans Dis 39: 433-439.
5. Ng'ayo M, Bukusi E, Rowhani-Rahbar A, Koutsky L, Feng Q, et al. (2008) Epidemiology of human papillomavirus infection among fishermen along Lake Victoria Shore in the Kisumu District, Kenya. Sexually Transmitted Infections 84: 62-66.
6. Kwena ZA, Bukusi EA, Ng'ayo MO, Buffardi AL, Nguti R, et al. (2010) Prevalence and risk factors for sexually transmitted infections in a high-risk occupational group: The case of fishermen along Lake Victoria in Kisumu, Kenya. Int J STD AIDS 21: 708-713.
7. (2016) Ministry of health and national AIDS control council. The 2014 Kenya HIV county profiles.
8. Mugo N, Dadabhai SS, Bunnell R, Williamson J, Bennett E, et al. (2011) Prevalence of herpes simplex virus type 2 infection, human immunodeficiency virus/herpes simplex virus type 2 co-infection and associated risk factors in a national, population-based survey in Kenya. Sexually Transmitted Diseases 38: 1059-1066.
9. World Health Organization (2016) Herpes simplex virus type 2 programmatic and research priorities in developing countries, World Health Organization 2001, London.
10. Paz-Bailey G, Ramaswamy M, Hawkes SJ, Geretti AM (2007) Herpes simplex virus type 2: Epidemiology and management options in developing countries. Sex Transm Infect 83: 16-22.
11. Celum C, Levine R, Weaver M, Wald A (2004) Genital herpes and human immunodeficiency virus: Double trouble. Bulletin of the World Health Organization 82: 447-453.
12. Freeman EE, Weiss HA, Glynn JR, Cross PL, Whitworth JA, et al. (2006) Herpes simplex virus 2 infection increases HIV acquisition in men and women: Systematic review and meta-analysis of longitudinal studies. AIDS 20: 73-83.
13. Okuku HS, Sanders EJ, Nyiro J, Ngetsa C, Ohuma E, et al. (2011) Factors associated with herpes simplex virus type 2 incidence in a cohort of human immunodeficiency virus type 1-seronegative Kenyan men and women reporting high-risk sexual behavior. Sex Transm Dis 38: 837-844.
14. Bennett DE, Camacho RJ, Otelea D, Kuritzkes DR, Fleury H, et al. (2009) Drug resistance mutations for surveillance of transmitted HIV-1 drug-resistance: 2009 update. PLoS One 4: e4724.
15. Jahn A, Floyd S, Crampin AC, et al. (2008) Population-level effect of HIV on adult mortality and early evidence of reversal after introduction of antiretroviral therapy in Malawi. Lancet 371: 1603-1611.
16. Gupta RK, Jordan MR, Sultan BJ (2012) Global trends in antiretroviral resistance in treatment-naive individuals with HIV after rollout of antiretroviral treatment in resource-limited settings: A global collaborative study and meta-regression analysis. Lancet 380: 1250-1258.
17. Heneine W (2010) When do minority drug-resistant HIV-1 variants have a major clinical impact? J Infect Dis 201: 647-649.
18. Wittkop L, Gunthard HF, de Wolf F (2011) Effect of transmitted drug resistance on virological and immunological response to initial combination antiretroviral therapy for HIV (EuroCoord-CHAIN joint project): An European multicohort study. Lancet Infect Dis 11: 363-371.
19. Chung MH, Beck IA, Dross S, Tapia K, Kiarie JN, et al. (2014) Oligonucleotide ligation assay detects HIV drug resistance associated with virologic failure among antiretroviral-naive adults in Kenya. J Acquir Immune Defic Syndr 67: 246-253.
20. Hassan AS, Mwaringa SM, Obonyo CA (2013) Low prevalence of transmitted HIV type 1 drug resistance among antiretroviral-naive adults in a rural HIV clinic in Kenya. AIDS Research and Human Retroviruses 29: 129-135.
21. Budambula V, Musumba FO, Webale MK (2015) HIV-1 protease inhibitor drug resistance in Kenyan antiretroviral treatment-naive and -experienced injection drug users and non-drug users. AIDS Research and Therapy 12: 27.
22. Lemeshow S, Hosmer DK, Klar J, Lwanga SK (1990) World Health Organization. Adequacy of samples size in health studies.
23. Ng'ayo MO, Friedrich D, Holmes K, Bukusi E, Morrow RA (2010) Performance of HSV-2 type specific serological tests in sera from fishermen in Kisumu district, Kenya. Journal of Virological Methods 163: 276-281.
24. Lehman DA, Chung MH, Mabuka JM, John-Stewart GC, Kiarie J, et al. (2009) Lower risk of resistance after short-course HAART compared with Zidovudine/Single-Dose nevirapine used for prevention of HIV-1 mother-to-child transmission. J Acquir Immune Defic Syndr 51: 522-529.
25. Swofford D (2000) Phylogenetic analysis using parsimony and other methods. Sinauer Associates, Sunderland, p: 4.
26. Bennett DE, Myatt M, Bertagnolio S, Sutherland D, Gilks CF (2006) Recommendations for surveillance of transmitted HIV drug resistance in countries scaling up antiretroviral treatment. Antivir Ther 13: 25-36.
27. Hamers RL, Wallis CL, Kityo C, Siwale M, Mandaliya K, et al. (2011) HIV-1 drug resistance in antiretroviral-naive individuals in sub-Saharan Africa after rollout of antiretroviral therapy: A multicentre observational study. Lancet Infect Dis 11: 750-759.
28. Baggaley RF, Garnett GP, Ferguson NM (2006) Modelling the impact of antiretroviral use in resource-poor settings. PLoS Med 3: e124.
29. Sigaloff KC, Mandaliya KN, Hamers RL, Otieno FP, Jao IM, et al. (2012) High prevalence of transmitted antiretroviral drug resistance among newly HIV-1 diagnosed adults in Mombasa, Kenya. AIDS Res Hum Retroviruses 28: 833-837.
30. Onsongo S, Abidi SH, Khamadi S, Shah R, Kageha S, et al. (2016) Prevalence of transmitted drug resistance mutations in HIV-1-infected drug-naive patients from urban and suburban regions of kenya. AIDS Res Hum Retroviruses 32: 220-225.
31. Nazziwa J, Njai HF, Ndembi N (2013) Short communication: HIV type 1 transmitted drug resistance and evidence of transmission clusters among recently infected antiretroviral-naive individuals from Ugandan fishing communities of lake Victoria. AIDS Research and Human Retroviruses 29: 788-795.

32. Koval CE, Dykes C, Wang J, Demeter LM (2006) Relative replication fitness of efavirenz-resistant mutants of HIV-1: Correlation with frequency during clinical therapy and evidence of compensation for the reduced fitness of K103N+L100I by the nucleoside resistance mutation L74V. Virology 353: 184-192.

33. Gupta HA, Haley T, Hamers RL, Pillay D (2011) Transmitted drug resistance in low and middle income settings-a meta regression analysis. XX International Drug Resistance Workshop Mexico, Los Cabos, pp: 7-11.

34. Manasa J, Katzenstein D, Cassol S, Newell ML (2012) de Oliveira for the Southern Africa treatment and resistance network (SATuRN): Primary drug resistance in South Africa: Data from 10 years of surveys. AIDS Res Hum Retroviruses 28: 558-565.

35. Baeten JM, Kahle E, Lingappa JR, Coombs RW, Delany-Moretlwe S, et al. (2011) Genital HIV-1 RNA predicts risk of heterosexual HIV-1 transmission. Sci Transl Med 3: 77.

36. Celum C, Wald A, Hughes J (2008) Effect of aciclovir on HIV-1 acquisition in herpes simplex virus 2 seropositive women and men who have sex with men: A randomised, double-blind, placebo-controlled trial. Lancet 371: 2109-2019.

37. Watson-Jones D, Weiss HA, Rusizoka M (2008) Effect of herpes simplex suppression on incidence of HIV among women in Tanzania. N Engl J Med 358: 1560-1571.

38. Rebbapragada A, Wachihi C, Pettengell C, Sunderji S, Huibner S, et al. (2007) Negative mucosal synergy between Herpes simplex type 2 and HIV in the female genital tract. AIDS 21: 589-598.

39. Nagot N, Ouedraogo A, Defer MC, Vallo R, Mayaud P, et al. (2007) Association between bacterial vaginosis and herpes simplex virus type-2 infection: Implications for HIV acquisition studies. Sex Transm Infect 83: 365-368.