HIV viral load suppression in male and female sex workers enrolled in the Nairobi Sex Worker Outreach Programme (SWOP)

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Background

Antiretroviral therapy

- Significantly decreases HIV-related morbidity and mortality.
- Prevents HIV transmission by suppressing viral load.
- Treatment as Prevention (TasP) is an effective, evidence-based strategy to reduce HIV transmission.
- Requires regular access to HIV testing, treatment initiation, and adherence to antiretroviral treatment (ART).
- Limited published data on the treatment cascade in sex workers.
- Difficult to evaluate the impact of TasP on HIV transmission associated with sex work.

Key populations

- HIV incidence is **3X** and **16X** higher in female sex workers (FSW) and male sex workers (MSW) respectively compared to the Kenyan general population.
- Modelling studies suggest that reducing HIV in sex workers will have an impact at the population level.
- Ongoing and targeted HIV prevention in FSW and MSW will be critical to reduce transmission at the population level.
- Evidence suggests that HIV epidemics do not operate in silos but, are linked in complex ways which can increase overall HIV prevalence.
- Understanding how epidemics are linked and drive transmission within and between key populations can inform intervention strategies.

Study objectives

- **Objective 1:** measure HIV viral load suppression in both FSW and MSW accessing SWOP, Nairobi.
- **Objective 2:** examine correlates of HIV viral load suppression in HIV positive FSW and MSW accessing SWOP, Nairobi.
- **Objective 3:** examine HIV transmission networks and correlates of HIV transmission clusters in HIV positive FSW and MSW accessing SWOP, Nairobi.
- The Sex Worker Outreach Program (SWOP) is a large PEPFAR-funded HIV prevention and treatment program in Nairobi, Kenya implemented by a collaboration between the Universities of Manitoba and Nairobi for the past 12 years. Over 33,000 FSW and 2,500 MSW are currently enrolled in the program.

Methods

Bio-behavioural surveys

- All HIV positive FSW and MSW attending SWOP were consecutively sampled between February 2016 and October 2018.
- Sociodemographic, sexual behavior, and clinical variables were captured using a structured questionnaire.
- Biological specimens were collected as part of the routine HIV treatment program at SWOP, Nairobi.

HIV viral load sequencing

- Plasma HIV viral load measured using the Abbott RealTime HIV-1 assay according to the manufacturer's instructions (Winnipeg, MB).
- A portion of the HIV *pol* gene was sequenced using an in-house HIV drug resistance mutation genotyping assay on an Illumina MiSeq platform (Winnipeg, MB).
- Next generation sequencing data was analyzed using the automated analysis pipeline HyDRA Web.
- This approach is currently being used to determine strain and drug resistance patterns in Canada by the National HIV and Retrovirology Laboratory (Public Health Agency of Canada).

Cluster and statistical analysis

- HIV sequences were aligned, visually inspected, and manually edited as required using Geneious Prime software.
- Phylogenetic analysis was done using maximum likelihood trees assembled under the best-fitting nucleotide substitution model, as implemented in IQ-TREE v1.2.3 and the reliability of the tree topologies was evaluated using bootstrap re-sampling.
- Phylogenetic clusters were identified using a patristic distance of ≤0.02 nucleotide substitutions/site.
- Comparison of HIV viral load suppression or phylogenetic clustering and questionnaire data assessed using logistic regression in SPSS v25.

Results

Table 1. Baseline characteristics of FSW attending SWOP, Nairobi stratified by viral load.

	Detectable VL (n=142)	Undetectable VL (n=378)	p-value
Mean age (years)	32.9	34.9	0.07
Mean duration of sex work (years)	6.0	6.5	0.68
Condom use (always)			
Regular partners	26.8% (n=11)	32.7% (n=47)	0.57
Casual partners	63.8% (n=44)	70.7% (n=140)	0.29
At last sex	77.9% (n=53)	76.5% (n=153)	0.87
Other STIs	65.2% (n=45)	67.0% (n=134)	0.88

Table 2. Baseline characteristics of FSW attending SWOP stratified by clustering status.

	Clustered (n=67)	Non-clustered (n=58)	p-value
Mean age (years)	46.0	42.5	0.05
Mean duration of sex work (years)	5.0	3.0	0.15
Condom use (always)			
Regular partners	75.0% (n=9)	65.9% (n=29)	0.47
Casual partners	33.3% (n=3)	26.7% (n=8)	0.29
At last sex	83.3% (n=10)	77.3 % (n=34)	0.81
Detectable viral load	33.3% (n=5)	31.5% (n=17)	0.86

Figure 1. Viral load suppression among FSW and MSW attending SWOP, Nairobi.

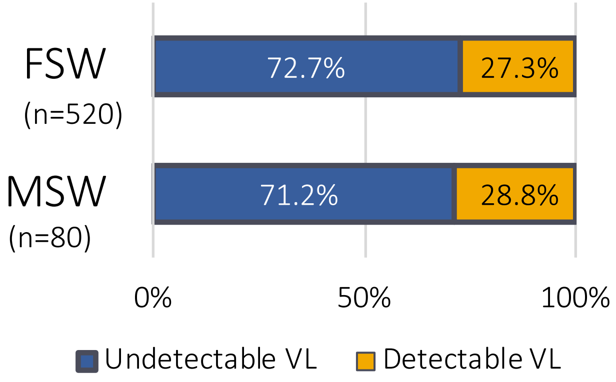

Figure 2. Phylogenetic clusters inferred using patristic distance between HIV sequences measured on phylogenetic trees.

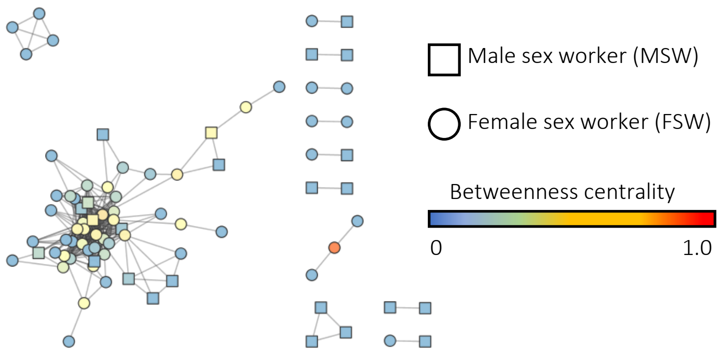

Table 3. Correlates of viral load suppression in FSW attending SWOP, Nairobi.

	OR (95% CI)	p-value
Age (>35 years)	1.50 (0.48– 4.73)	0.49
Duration of sex work (> 6 years)	1.26 (0.40 – 4.03)	0.69
Condom use (always)		
Regular partners	1.32 (0.61 – 2.86)	0.48
Casual partners	1.37 (0.77 – 2.45)	0.28
At last sex	0.92 (0.48 – 1.78)	0.81
Other STIs	1.08 (0.61 – 1.93)	0.79

Table 4. Correlates of phylogenetic clustering in FSW attending SWOP, Nairobi.

	OR (95% CI)	p-value
Age (>35 years)	0.52 (0.17 – 1.59)	0.25
Duration of sex work (>6 years)	0.40 (0.13 – 1.20)	0.10
Condom use (always)		
Regular partners	2.19 (0.52 – 9.27)	0.29
Casual partners	0.67 (0.21 – 2.11)	0.50
At last sex	0.52 (0.14 – 2.00)	0.35
Other STIs	0.84 (0.28 – 2.52)	0.76

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Background

Conclusion

- A significant proportion of FSW and MSW accessing antiretroviral therapy showed evidence of HIV viral load suppression.
- Viral load suppression in FSW and MSW is comparable to the general population in Kenya (~75%).
- Over one third of F/MSW HIV sequences were linked to at least one other individual in the phylogenetic analysis suggesting a significant overlap between FSW and MSW transmission networks.
- Understanding how FSW and MSW epidemics are interlinked remains poorly understood. Future studies involving different approaches such as spatial epidemiology, social network analysis, and ethnography may help us further understand transmission networks.
- Expanding biological specimen collection is likely required to determine correlates of HIV viral load suppression and phylogenetic clustering.
- As antiretroviral therapy expands in key populations, initiatives to effectively promote adherence may also be critical

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