Nearly half of participants (48.4%) were sexually inactive during last one year and 76.4% stated decrease or complete loss of sexual desire following the diagnosis. Diminished sexual desires showed significant association with ageing. Among sexually active women 92.5% had one sexual partner for last one year and 69.4% of sexually active women used condom at last coitus. Significant low condom usage seen among women with detectable viral load. None were found positive for Gonorrhea and Trichomoniasis. Prevalence of infectious syphilis was 0.3%.

Conclusion Approximately half of WLHIV reported being sexually inactive despite satisfactory treatment outcomes and existence of a long term relationship. Findings demonstrate high condom use at last coitus, whilst low condom usage among women with detectable viral load need evaluation.

P206 DOES THE PERFORMANCE AND OPERATIONAL SUPERIORITY OF POINT OF CARE TEST MAKE IT THE INVESTIGATION OF CHOICE IN CONFIRMING SYPHILIS?

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10.1136/sextrans-2021-sti.295

Background According to World Health Organization, 6 million cases of syphilis occur every year, and low-income countries bear a 90% burden of the disease. Serological tests for syphilis form the mainstay of diagnosis for syphilis. Unlike various specific Treponemal tests, Rapid Immunochromatographic Test, also called the point-of-care test (POCT) for syphilis, does not require expert training or equipment. We evaluated the performance of POCT against other specific Treponemal tests for confirming the diagnosis of syphilis.

Methods Retrospectively data was analyzed of samples from the year 2017 to 2020 at Apex Regional STD centre, Safdarjung Hospital, New Delhi, which were tested by all the three treponemal test for syphilis, namely Treponema Pallidum Hemagglutination (TPHA), fluorescent treponemal antibody absorption test (FTA-ABS) and POCT. Sensitivity, Specificity, Positive Predictive Value (PPV), Negative Predictive Value (NPV), Diagnostic Accuracy of POCT, and TPHA were evaluated against the gold standard FTA-ABS.

Result A total of 599 samples were evaluated, of which 61.76% were positive by FTABS. Upon analysis, the sensitivity of POCT was 91.08% (95%CI: 87.70%-93.78%) and TPHA was 91.89% (95%CI: 88.63%-94.46%), specificity of POCT was 89.08% (95%CI: 84.31%-92.81%) and TPHA was 87.34% (95%CI: 82.32%-91.35%), PPV of POCT was 93.09% (95%CI: 89.97%-95.48%) and TPHA was 92.14% (95%CI: 88.91%-94.67%), NPV of POCT was 86.08% (95%CI: 81%-90.22%) and TPHA was 86.96% (95%CI: 81.91-91.02%) and Diagnostic accuracy of POCT was 90.32% and TPHA was 90.15%.

Conclusion Owing to its operational superiority and higher specificity, POCT can replace TPHA for confirming the diagnosis of syphilis. POCT is affordable, equipment-free, has room temperature storage, and yields results within 15 minutes, enabling same-day testing and treatment. It can be used in a limited resource setting, community setup, or even self-testing. Wider patient reach will help improve patient identification and treatment, thereby strengthening STI prevention and control programmes.

P207 EVALUATION OF OXFORD NANOPORE MINION SEQUENCING TO PREDICT ANTIMICROBIAL RESISTANCE PROFILES IN CLINICAL N. GONORRHOEA STRAINS

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10.1136/sextrans-2021-sti.296

Background Antimicrobial resistance (AMR) in *N. gonorrhoeae* (NG) is a big concern for public health and has an impact on treatment efficiency. Whole genome sequencing (WGS) of clinical strains can be used to predict AMR profiles based on detection of known resistance-associated mutations (RAM) and AMR gene acquisition. While Illumina short read sequencing gives low error rates, third-generation sequencing with Oxford Nanopore Technologies (ONT) has the advantage of generating long reads in real-time. We aimed to evaluate the ability of ONT sequencing to predict AMR in NG.

Methods WGS was performed on one azithromycin resistant and four ceftriaxone resistant clinical NG strains using ONT (MinION R9.4 flowcell) and Illumina (MiSEQ) sequencing platforms. Assemblies were obtained from: Illumina data (by SPAdes), ONT data (by Flye) and a hybrid assembly of both ONT and Illumina data (by Unicycler). Moreover, we evaluated four different polishing strategies (based on rebase, racon and/or medaka) after Flye. Completeness of the assemblies were visually checked with bandage. AMR profile prediction based on RAM detection and AMR gene acquisition were obtained by using pathogenwatch and compared with phenotypic antimicrobial susceptibility testing.

Results Hybrid and ONT assemblies showed a complete, closed chromosome, while Illumina assemblies were not able to resolve genome structures. Pathogenwatch could predict AMR profiles (except for CRO) correctly on Illumina and hybrid assemblies, and detected RAM were concordant in both assemblies. RAM detection on ONT assemblies was inconsistent among the different polishing strategies. Moreover, fewer RAMs were detected which resulted in missed resistance in the predicted AMR profiles.

Conclusion Here, we demonstrate that ONT sequencing reveals the genomic structure of NG isolates, but high error rates leads to it missing RAMs in the consensus assembly. Polishing strategies of MinION based assemblies can reduce the proportion of RAMs missed but remain inferior to Illumina based assemblies.

P208 EXPLORING THE DATA-SHARING ECOSYSTEM IN HIV CARE: HEALTHCARE PROFESSIONALS' BELIEFS AND PRACTICES

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10.1136/sextrans-2021-sti.297

Background Understanding data-sharing in HIV care is timely given the shift to remote consultations during COVID-19. We describe the 'data-sharing ecosystem' in HIV care by analysing