genital tract disease, screening for this bacterium should be considered, particularly with a surgical procedure such as termination of pregnancy, although the lack of a commercial test is problematic.

O3-S6.03 THE DIAGNOSIS OF LYMPHOGRANULOMA VENEREUM AT ONE'S FINGERTIPS

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Background Outbreaks of Lymphogranuloma venereum (LGV) in sexual networks of men who have sex with men (MSM) are reported in several countries in Europe. Although accurate laboratory diagnosis is required to provide adequate patient management, the laboratory identification of LGV can be problematic.
Objective To establish a fast and reliable testing algorithm for the identification of *Chlamydia trachomatis* L serovars.
Methods Previously, anal specimens from MSM suspected to be positive for *C trachomatis* were tested with a testing algorithm using commercial molecular amplification assays. Confirmed *C trachomatis* samples were then analysed in batches by RFLP to identify the L serovars. From September 2010 onwards, the Abbott CT/NG Real Time PCR has been used for the detection of *C trachomatis* in biological specimens collected at or referred to the ITM for Chlamydial infection diagnosis. Furthermore, confirmation of *C trachomatis* and identification of the L serovar types are performed with an in-house Real Time PCR assay. This assay uses DNA extract obtained with the Abbott assay. The selection of the primers and test procedure is based on the publication by Chen et al. and includes two specific probes for the detection of the L and the non L serovars.
Results Out of a total of 940 samples tested with the new methods, we detected 58 (6.2%) positive samples for *C trachomatis* and of those 12 (20.7%) were L serovars. Eight were detected in specimens collected from the anus, two in urethral specimens, one in urine, and one in a vaginal specimen. All non vaginal specimens were collected from men. With the Abbott CT/NG Real Time PCR for screening and the in house RT PCR assay for confirmation, we were able to confirm positive results for *C trachomatis* and to distinguish the L serovar from the non L serovar types within 2 days after specimen reception. In addition the in house RT PCR assay was more sensitive, more discriminative and at least 4 times cheaper compared to the RFLP method.
Conclusion The detection of L serovar of *C trachomatis* can be done on a routine basis at a very acceptable cost and test around time. The L serovar types may be more frequent in Belgium then initially thought, they are present in various biological specimens and possibly in women.

Abstract O3-S6.03 Table 1 LGVV Testing

Year	specimens tested*	L serovar	non L serovar	not typable
2011 January	196	4	11	0
2010 Sept-Dec	744	8	35	0
2010 Jan-Aug	23	14	9	0
2009	23	17	5	1
2008	13	11†	1	1
2007	19	13	5	1
2006	14	7	4	3
2005	6	2	1	3
2004	11	8	2	1

*Until September 2010 only male anal specimens or rectal biopsies were tested except for 2008 when 2 specimens from penile ulcers were tested.
†Two penile ulcer specimens.

O3-S6.04 MULTI-SITE SCREENING FOR LYMPHOGRANULOMA VENEREUM (LGV) IN THE USA

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Background Lymphogranuloma venereum is a clinical condition caused by infection with one of the *Chlamydia trachomatis* (CT) L serovars. Proper diagnosis of LGV is critical as the treatment varies significantly from antibiotic therapy utilised for other CT infections. LGV has re-emerged in Europe as an important sexually transmitted infection (STI), particularly in men who have sex with men (MSM), due to an outbreak in the Netherlands. LGV surveillance data for the USA is lacking as LGV screening is not routinely performed, even in high risk populations. This study presents LGV surveillance data from multiple sites in the USA.
Methods 1671 rectal samples from African-American MSM participating in a study of the HIV Prevention Trials Network (HPTN 061) BROTHERS Project, were collected from six different cities: Los Angeles and San Francisco CA, Atlanta, GA, Boston MA, Washington D.C., New York, NY; and tested for CT by Aptima Combo 2 (Gen-Probe). Additionally, 127 samples from men from Baltimore, MD who reported anal sex or were symptomatic for CT, and had rectal swabs positive for CT by Combo 2 were also included. All samples were screened for LGV utilising a previously verified LGV specific real-time PCR to determine if the samples were positive for any one of the CT L serovars.
Results Of the 1671 HPTN 061 samples, 112 (6.75%) were positive for CT and 102 of these have been screened thus far for LGV; none were LGV+. Of 127 CT+ samples from Baltimore, two were LGV+. Thus, of 229 CT+ rectal samples, only 2 (0.87%), tested positive for LGV by real-time PCR.
Conclusions Less than 1% of the CT positive samples obtained from rectal swabs from MSM in the US tested positive for LGV. The samples utilised for this study were from a population presumably at high risk for acquisition of LGV, as all samples tested were from men who had either tested positive for CT, reported anal sex, or were symptomatic for CT infection. The prevalence for LGV in this study was quite low, while the non LGV CT prevalence was high in African American MSM from the six cities. Concomitant STDs are thought to drive the disproportionate HIV epidemic among African American MSM and the low prevalence of LGV in this study is of interest. LGV has re-emerged as an important STI in Europe, however this data suggests that it has either not re-emerged in the U.S. or has re-emerged in a population that is not being screened.

O3-S6.05 PERCEPTIONS ON POINT-OF-CARE TESTS FOR SEXUALLY TRANSMITTED INFECTIONS-disconnect between frontline clinicians and professionals in industry

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Background Some recently developed or available sexually transmitted infection (STI) point-of-care tests (POCTs) are not very accurate and are not feasible for use in clinical settings. We conducted a study to determine if a gap exists between STI clinicians/academic experts and industry professionals regarding perceptions of the ideal types and characteristics of STI POCTs.
Methods Our online survey design informed by a large-scale focus group study among STI professionals contained sections on

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demographics; barriers of use for available STI POCTs; characteristics of an ideal POCT, including prioritising pathogens for targets; and building your own POCT". Practicing clinicians and academic experts from two venues, STI-related international conference attendees and U.S. STD clinic clinicians, were invited to participate in the clinician survey. Professionals from industry in the STI diagnostic field were invited to participate in the industry survey. χ^2 test and conditional logistical regression were used for data analysis.

Results Clinician survey participants (n=218) identified "the time frame required" (39.9%), "complexity" (31.2%), and "interruption of work flow" (30.3%) as the top three barriers making it difficult to use STI POCTs, while the industry survey participants (n=107) identified "complexity" (65.4%), "unreliability" (53.3%), and "difficulty in reading results" (34.6%) as the top three barriers. Significant differences in barriers named in the two surveys included "complexity", "the time frame required", "laboratory driven", "difficulty in reading results", and "unreliability". Participants from both surveys ranked *C trachomatis* as the top priority organism chosen for a new POCT (clinician: 62%, industry: 39%, $p<0.05$), followed by a test that would diagnose early seroconversion for HIV (clinician: 14%, industry: 32%, $p<0.05$). Sensitivity was always the most important attribute to be considered for a new STI POCT by both participant groups. Participants of the clinician group chose cost as the second priority attribute, while those of the industry group chose specificity as the second priority.

Conclusions We identified differences in the perceptions regarding barriers and ideal attributes for STI POCTs between frontline clinical providers and industry personnel. Tailored training is warranted to inform scientists, biomedical engineers, and other industry experts about characteristics that clinicians desire for STI POCTs.

O3-S6.06 SELF-COLLECTION VS PHYSICIAN-COLLECTION FOR THE DETECTION OF *CHLAMYDIA TRACHOMATIS*, *NEISSERIA GONORRHOEAE*, *TRICHOMONAS VAGINALIS* AND *MYCOPLASMA GENITALIUM*

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Background To determine the efficacy of self-collection for primary screening of an array of sexually transmitted infections.

Methods A cross-sectional baseline analysis was conducted on a cohort of 300 female sex workers (FSW) within an outpatient clinic from a suburban/slum area of Nairobi, from December 2009 to June 2010. APTIMA transcription-mediated amplification (TMA) assays (Gen-Probe Incorporated) were used for the detection of *Chlamydia trachomatis* (CT), *Neisseria gonorrhoeae* (GC), *Trichomonas vaginalis* (Trich) and *Mycoplasma genitalium* (MGen) infections and, were analysed in San Diego, California. The APTIMA COMBO 2 assay (AC2) was used for CT/GC, the APTIMA *Trichomonas vaginalis* assay for Trich, and an APTIMA *Mycoplasma genitalium* research assay for Mgen. FSW conducted a self-collected sample in privacy, based on standardised instructions, and then underwent a pelvic exam to obtain a physician-collected sample.

Results A total of 299 FSW (mean age of 30) participated, of which 15% were HIV-seropositive. MGen was the most common infection (12.7% in physician; 20.7% in self-collection), followed by Trich (7.7%; 9.7%), CT (4.3%; 5.4%), and GC (2.7%; 3.3%). For all STIs examined, the self-collected samples detected more positive cases than the physician-collected samples. No self-collected sample missed an infection that was picked by the physician sample. κ for agreement between self-collected and physician-collected samples were high for CT: 0.89, GC: 0.89 and Trich: 0.87, and slightly lower for MGen: 0.73. Using physician sampling as the gold-standard, the sensitivity of self-collection was 100% for all STIs. The specificity for self-collection was high for CT, GC, and Trich (99.0%, 99.3% and 97.8% respectively) and slightly lower for MGen (91.6%).

Conclusion A single self-collected sample appeared to perform with comparable sensitivity and specificity to that of physician-collected sampling for the detection of *Chlamydia trachomatis, Neisseria gonorrhoeae, Trichomonas vaginalis* and *Mycoplasma genitalium*.

Basic sciences oral session 1—Genomics, replication and pathogenesis

O4-S1.01 RAPID ARRAY-BASED MULTILOCUS GENOTYPING OF *CHLAMYDIA TRACHOMATIS*: THE EASY AND ECONOMICAL ALTERNATIVE

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Background Genotyping of*Chlamydia trachomatis* (C.) is an important technique to understand its epidemiology. Methods such as DNA sequencing of the ompA gene or multilocus sequence typing (MLST), either offer limited epidemiological resolution, or are laborious and expensive, or both. Here we present a microarray-based method for genotyping of*C trachomatis*.

Methods The database for our high-resolution MLST system (http://mlstdb.bmc.uu.se/) was used to design a multilocus typing (MLT) DNA microarray based on the ArrayStrip format (Alere Technologies, Jena, Germany). In total, the present MLT array version includes 210 different oligonucleotide probes covering the discriminatory variation in the highly variable, but stable, MLST target regions (hctB, CT058, CT144, CT172 and pbpB), as well as 61 probes for ompA. Validation of the array was done by examining 80 clinical C. trachomtis specimens from unselected adolescents and compare with results from MLST and ompA-based serotyping.

Results Successful typing was achieved for 78 (97%) of the specimens. Processing of the obtained hybridisation patterns resulted in 17 different MLT array groups, whereas sequence-based examination led to 19 MLST genotypes and seven ompA genotypes. Thus, the MLT microarray assay provided 2.4 times higher resolution than ompA and separated the commonly predominating ompA E/Bour genotype into seven genotypes. The MLT array showed 100% specificity. Compared to MLST analysis, the equipment needed for the MLT array is about 75% cheaper, consumables are 50% cheaper, analysis can be completed within one working day, instead of 3–4 days, and data analysis is easily conducted in high troughput conditions using up to 96 wells, while the practical operations are easy-to-handle and do not require specially trained personnel.

Conclusion This novel MLT array is a promising alternative for high resolution and high throughput typing of C. trachomatis and will facilitate molecular epidemiology studies of chlamydia infections.

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