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A82

Sex Transm Infect
Year specimens tested* L serovar non L serovar not typable

Table 1 LGV Testing

<table>
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<th>Year</th>
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<th>non L serovar</th>
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*Until September 2010 only male anal specimens or rectal biopsies were tested.
†Two penile ulcer specimens.

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 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 than initially thought, they are present in various biological specimens and possibly in women.

Yu-Hsiang Hsieh, C Gaydos, T Hogan, O Uy, J Jackman, Mary Jett-Goheen, A Rompalo. Johns Hopkins University, Baltimore, USA

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

Perceptions on Point-of-Care Tests for Sexually Transmitted Infections—disconnect between frontline clinicians and professionals in industry
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. χ² test and conditional logistical regression were used for data analysis.

Results Clinician survey participants (n=218) identified “the time frame required” (59.9%), “complexity” (51.2%), and “interruption of work flow” (50.3%) as the top three barriers making it difficult to use STI POCTs, while the industry survey participants (n=107) identified “complexity” (65.4%), “unreliability” (55.3%), and “difficulty in reading results” (54.6%) 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: 59%, 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.

Self-collection vs physician-collection for the detection of Chlamydia trachomatis, Neisseria gonorrhoeae, Trichomonas vaginalis and Mycoplasma genitalium

03-S6.06

04-S1.01 RAPID ARRAY-BASED MULTILOCUS GENOTYPING OF CHLAMYDIA TRACHOMATIS: THE EASY AND ECONOMICAL ALTERNATIVE
doi:10.1136/sextrans-2011-050109.139

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.mgc.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. trachomatis 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 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.

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.

Basic sciences oral session 1—Genomics, replication and pathogenesis

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