

P07.10 EVALUATION OF THE NEW BD MAX GC REAL TIME PCR ASSAY, ANALYTICALLY AND AS A SUPPLEMENTARY TEST TO THE BD PROBETEC GC QX AMPLIFIED DNA ASSAY, FOR MOLECULAR DETECTION OF *NEISSERIA GONORRHOEAE*

¹D Golparian*, ²S Boräng, ¹M Sundqvist, ¹M Unemo. ¹WHO Collaborating Centre for Gonorrhoea and Other Sexually Transmitted Infections, Swedish Reference Laboratory for Pathogenic Neisseria, Department of Laboratory Medicine, Microbiology, Faculty of Medicine and Health, Örebro University, Örebro, Sweden; ²Department of Clinical Microbiology, Karolinska University Hospital, Huddinge, Sweden

10.1136/sextrans-2015-052270.326

Introduction The BD ProbeTec GC Qx Amplified DNA assay (Becton, Dickinson and Company) is used on the BD Viper System to detect *Neisseria gonorrhoeae*. However, suboptimal specificity and cross-reaction with commensal *Neisseria* species have been described. Recently, the BD Max GC real time (rt) PCR assay was developed for the BD Max System (BD) as a supplementary test.

Methods We evaluated the performance of the new BD Max GC rt PCR assay by examining clinical specimens positive in the BD ProbeTec GC Qx Amplified DNA assay during July–October 2014 among 23815 screening or clinical patients (14846 females and 8969 males) as well as samples spiked with isolates of gonococci (n = 189), non-gonococcal *Neisseria* species (n = 261) and other closely related bacteria (n = 10).

Results Of 23815 patients tested with the BD ProbeTec GC Qx Amplified DNA assay, 85 (0.6%) females and 259 (2.9%) males were positive. Of these 344 positive specimens, 322 were tested with BD Max GC rt PCR assay. Sixty-nine (21%) of these samples were negative in BD Max GC rt PCR assay, a gonococcal dual target PCR and in the APTIMA Combo 2 (Hologic). These 69 specimens were obtained from pharynx (50% of all screening positive pharyngeal specimens), urine (33%), vagina (11.4%), rectum (4.3%), and cervix (1.4%). In the analytical evaluation of the BD Max GC rt PCR assay, all gonococcal isolates were positive and all but one (*N. cinerea*) of the non-gonococcal isolates (99.4%) were negative. The *N. cinerea* isolate also cross-reacted in the BD ProbeTec GC Qx Amplified DNA assay.

Conclusion The BD ProbeTec GC Qx Amplified DNA assay had a suboptimal specificity for both urogenital and extragenital clinical specimens. The new BD Max GC rt PCR assay showed a high clinical and analytical sensitivity and specificity, and might also be used for initial detection of *N. gonorrhoeae*.

Disclosure of interest statement We are grateful to BD Diagnostics for providing the BD Max GC real time PCR tests. The present work was funded by grants from the Örebro County Council Research Committee and the Foundation for Medical Research at Örebro University Hospital, Sweden.

P07.11 WHOLE GENOME SEQUENCING CHARACTERISATION OF A UNIQUE *NEISSERIA* STRAIN GENERATING A POSITIVE RESULT WITH THE COBAS® CT/NG TEST

C Honisch*, S Cayabyab Hibbard, R Mehta, H Phan, S Sunkara, J Osiecki, M Lewinski, C Fillmore. Roche Molecular Systems, Inc., Pleasanton, CA, USA

10.1136/sextrans-2015-052270.327

Introduction *Neisseria gonorrhoeae* (NG) cause sexually transmitted bacterial infections. The Roche cobas® CT/NG Test is a qualitative Nucleic Acid Amplification test (NAAT) utilising a dual-target approach to detect sequences within the direct repeat

(DR-9) region of the NG genome. To date, clinical performance data show excellent sensitivity and specificity for urogenital specimens. The test is validated for endocervical swabs, vaginal swabs and urine specimens.

Methods One clinical case report¹ describes a positive test result for an oropharyngeal swab, an off-label specimen type for the cobas® CT/NG Test. This interesting *Neisseria* sample was subject to analysis as part of Roche's Global Surveillance Program. The isolate was tested by culture, phenotyping, whole cell MALDI-TOF MS and molecular methods such as 16S rDNA based typing and whole genome sequencing.

Results Whole genome sequencing resulted in a complete genome assembly supporting phylogenetic analysis. Sequencing data assembled into a 2,882,113bp contig and genome closure, which identified the sample as a *Neisseria* commensal species clustering in the same clade with both *N. sicca* and *N. macacae*.

One partial assay specific DR-9 target region was identified within the genome of this commensal strain in the context of a phage like motif, which can facilitate genomic exchange of DNA fragments between *N. gonorrhoeae* and commensal strains. BLAST searches for the prophage/DR9 genetic signature of this newly characterised *Neisseria* strain revealed no matches to sequences in the public domain, suggesting that this strain is rare.

Based on the sequence information of the prophage/DR9 genetic signature oropharyngeal swab specimens determined to be positive by the cobas® CT/NG Test are currently being evaluated for the presence of this sequence motif.

Conclusion The cobas® CT/NG Test on the cobas 4800 system is a reliable molecular method for detection of Chlamydia and Gonorrhoeae from genital specimens.

Disclosure of interest Authors of the abstract are employees of Roche Molecular Systems.

REFERENCE

- 1 Upton A, Bromhead C, Whiley DM. *Neisseria gonorrhoeae* false-positive result obtained from a pharyngeal swab by using the Roche cobas 4800 CT/NG assay in New Zealand in 2012. *J Clin Microbiol.* 2013;**51**:1609–10

P07.12 FACTORS INFLUENCING THE DETECTION OF *NEISSERIA GONORRHOEAE* FROM THE TONSILS AND POSTERIOR OROPHARYNX

^{1,2}M Bissessor*, ^{3,4}DM Whiley, ¹DM Lee, ¹AF Snow, ^{1,5}CK Fairley, ^{1,5}CS Bradshaw, ²JS Hocking, ^{6,7}M Lahra, ¹J Peel, ^{1,2}MY Chen. ¹Melbourne Sexual Health Centre, Alfred Health, Melbourne, Victoria, Australia; ²Melbourne School of Population and Global Health, University of Melbourne, Melbourne, Victoria, Australia; ³The University of Queensland, St Lucia, Queensland 4072, Australia; ⁴Queensland Paediatric Infectious Diseases Laboratory, Queensland Children's Medical Research Institute, The University of Queensland; ⁵Central Clinical School, Monash University, Melbourne, Victoria, Australia; ⁶WHO Collaborating Centre for Sexually Transmitted Diseases, SEALS Microbiology, The Prince of Wales Hospital, Randwick, New South Wales 2031, Australia; ⁷University of New South Wales, Kensington, New South Wales 2052, Australia

10.1136/sextrans-2015-052270.328

Background Limited data exists on the specific anatomical areas within the pharynx from which *Neisseria gonorrhoeae* can be detected. We examined factors influencing the detection of gonorrhoea from the pharynx.

Method Men who had sex with men (MSM) diagnosed with pharyngeal gonorrhoea by culture were recalled for repeat swabbing 7 days later: firstly from both tonsils then, using separate swabs, from the posterior oropharynx. These were tested for *N. gonorrhoeae* using culture and real-time PCR targeting the

gonococcal porA pseudogene and multi-copy opa genes. Cycle threshold (Ct) values obtained were used as semi-quantitative measures of gonococcal DNA. Sampling adequacy was assessed using a real-time PCR for human endogenous retrovirus 3 (ERV3).

Results 100 MSM with culture positive pharyngeal gonorrhoea were included. Isolation rates by culture from the tonsils and posterior oropharynx were 62% and 52% respectively ($p = 0.041$). PCR was significantly more sensitive than culture at both the tonsils (84% vs. 62%; $p < 0.001$) and oropharynx (81% vs. 52%; $p < 0.001$). Culture positivity was greater with higher gonococcal DNA loads at both the tonsils ($p = 0.001$) and oropharynx ($p < 0.001$). At the oropharynx, higher ERV3 DNA load was associated with improved gonococcal detection using culture ($p = 0.013$) as well as PCR ($p = 0.045$). At the tonsils, higher ERV3 DNA load was associated with improved gonococcal detection by PCR ($p = 0.040$).

Conclusion *Neisseria gonorrhoeae* can be cultured from the tonsils as well as the posterior oropharynx with greater isolation rates where gonococcal loads are higher. While PCR is substantially more sensitive than culture at each site, like culture, PCR is dependent on the adequacy of sampling.

Disclosure of interest statement None to disclose.

P07.13 DETECTION OF *TREPONEMA PALLIDUM* DNA FROM WHOLE BLOOD AND EARLOBE SPECIMENS IN PATIENTS FROM TWO STI CLINICS IN LIMA, PERU

¹JY Chow*, ²JA Flores, ²SK Vargas, ²SR Leon, ^{1,2}KA Konda, ¹JD Klausner, ²CF Caceres. ¹Division of Infectious Diseases, Division of Infectious Diseases, School of Medicine, University of California, Los Angeles, CA, USA; ²Unit of Health, Sexuality and Human Development, and Laboratory of Sexual Health, Universidad Peruana Cayetano Heredia, Lima, Peru

10.1136/sextrans-2015-052270.329

Background Prior studies have reported PCR detection of *Treponema pallidum* DNA from whole blood and earlobe scrapings. Factors affecting efficiency such as PCR target gene and clinical stage of syphilis have been studied. We aimed to determine other factors associated with detection of *T. pallidum* DNA from whole blood and earlobe samples.

Methods Data were obtained from baseline samples collected for a prospective cohort study of 401 men who have sex with men (MSM) and transgender women (TW) in Lima, Peru. Participants were assessed for HIV using rapid HIV testing (Alere Determine, USA), a combined Antigen/Antibody HIV EIA, and Western blot confirmation (Genscreen ULTRA HIV Ag-Ab and Genetic Systems HIV-1 Western Blot, Bio Rad, USA). Syphilis infection was assessed with RPR (BD Macro-Vue, USA) and TPPA (Fujirebio, Japan). Whole blood samples and earlobe capillary blood was collected from patients with a positive RPR and TPPA. DNA extraction was performed using the QIAamp mini kit (Qiagen, Valencia, CA), and samples were then concentrated. Ujchowsing specific primers for the TpN47 gene, an aliquot of the DNA sample was amplified using conventional PCR for participants with high RPR titers ($\geq 1:16$). Positivity was determined by visual detection of PCR product on 1% agarose gel.

Results 56 participants had RPR titer $\geq 1:16$ (1:16 ($n = 18$), 1:32 ($n = 16$), 1:64 ($n = 17$), 1:128 ($n = 3$), and 1:256 ($n = 2$)). A total of 7 (12.5%) participants had *T. pallidum* DNA detected from whole blood, and 6 (10.7%) from earlobe capillary blood

(10 participants total). Of these 10 participants, 5 were HIV positive, and 5 were HIV negative.

Conclusion Our relatively low efficiency of detection from both whole blood and earlobe samples suggest that neither HIV status nor high RPR titer ($\geq 1:16$) seem to predict high likelihood of DNA detection. Further study is ongoing to determine if these or other characteristics are associated with positive detection of *T. pallidum* DNA.

Disclosure of interest statement The Picasso study is funded by a grant from the United States NIAID and was implemented by the Universidad Peruana Cayetano Heredia in collaboration with the University of California, Los Angeles. The molecular part of the study was implemented under the supervision of the University of Washington. No pharmaceutical grants were received during the development of this study.

P07.14 APTIMA TV NAAT TEST PERFORMANCE IN GUM CLINICS AND PRIMARY CARE IN THE UK

¹J Nicholls*, ²P Muir, ²P North, ²R Ferguson, ³M May, ³K Turner, ³J Madeod, ^{1,3}P Horner. ¹Bristol Sexual Health Centre, University Hospitals Bristol NHS Trust, Bristol, UK; ²Public Health Laboratory Bristol, Public Health England, Bristol, UK; ³School of Social and Community Medicine, University of Bristol, Bristol, UK

10.1136/sextrans-2015-052270.330

Introduction The Aptima TV NAAT for the detection of *Trichomonas vaginalis* (TV) is ~100% sensitive compared to wet mount microscopy (50%) or culture (75%). Asymptomatic women attending genitourinary medicine (GUM) clinics and patients in primary care are often not tested for TV, as the prevalence and sensitivity of current tests is assumed to be too low for testing to be cost effective.

Our aim was to determine how many additional cases were identified with the new test and whether self-taken and clinician-taken vaginal swabs are of equivalent sensitivity in symptomatic GUM patients.

Methods Patients were tested using the Aptima TV NAAT alongside existing testing methods.

Results The positivity of TV determined by TV NAAT was 4.8% (26/543) and 1.8% (28/1593) in women with and without symptoms attending GUM and 2.7% (95/3512) and 1.1% (41/3593) respectively in primary care.

TV NAAT significantly outperformed our existing testing methods. In a subset of 491 GUM patients in whom all tests were performed, 14/23 (61%) TV NAAT positive patients were identified on wet prep or culture ($p = 0.004$). In a subset of 2930 primary care patients in whom all tests were performed, 19/74 (26%) TV NAAT positive patients were identified on wet prep or culture ($p < 0.0001$). These results may reflect deterioration of specimens in transport to the laboratory.

Self-taken vaginal swabs were equivalent in sensitivity to clinician taken swabs; of the 26 patients who tested positive on either NAAT test, 25 tested positive on self-taken swab and 21 tested positive on clinician taken swab ($p = 0.51$).

Conclusion Testing women attending GUM clinics and in primary care with the Aptima TV NAAT test will identify additional cases and should replace conventional microbiological testing methods if found to be cost-effective.

Disclosure of interest statement Hologic provided the tests for the Aptima TV NAAT research study and have sponsored the authors to present this data at ISSTD.