

In China, *Chlamydia trachomatis* infections are endemic in the general population, but most infections are found in specific risk groups, such as female sex workers. The most prevalent *C. trachomatis* genovar strains, as defined by *ompA* genotyping, were described to be E, D, and F, which are also common in high risk groups in other parts of the world. We wondered whether by using high resolution multilocus sequence typing (MLST) we could distinguish distinct new CT strains in China

In this study we investigated Chinese strains from 101 heterosexual visitors of the sexually transmitted infections (STI) clinic in Nanjing using MLST. These strains were compared with 256 typed strains from heterosexual visitors of the STI clinic in Amsterdam, the Netherlands. Epidemiological data were obtained from structured questionnaires.

Full MLST data were obtained for 90 samples from 58 men and 32 women from Nanjing, showing 34 sequence types. These types were dispersed over 5 *C. trachomatis* clusters in a minimum spanning tree. When combining MLST data from the Chinese samples with the Dutch samples, distinct new clusters for Nanjing appeared, but some *Chlamydia* strains clustered with and thus were identical to those from Amsterdam. More than half of the Nanjing participants paid or received money for sex in the previous 6 months. None of the patient characteristics was related to a specific *Chlamydia* cluster. High resolution typing revealed both distinct and shared *C. trachomatis* strains in China. These shared strains proved to be highly prevalent among heterosexuals in all countries investigated so far, using this MLST typing. Geographical variation in circulating *C. trachomatis* strains could not have been detected using *ompA* genotyping only.

P3.258 INVESTIGATING THE EPIDEMIOLOGY OF REPEAT CHLAMYDIA TRACHOMATIS DETECTION AFTER TREATMENT USING CHLAMYDIA TRACHOMATIS OMP A GENOTYPING

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Background Detection of *Chlamydia trachomatis* (CT) infection within months of initial diagnosis and treatment is a common occurrence. Origins of such infection (persistence vs. reinfection from an untreated or a new partner) are complex. CT strains can be differentiated by complete nucleotide sequence analysis of the *ompA* gene, encoding an antigenically diverse surface protein outer membrane protein A (OmpA). We are evaluating urogenital CT OmpA genotypes in an ongoing prospective CT natural history study in order to investigate the epidemiology of repeat CT detection after treatment.

Methods CT-infected subjects are prospectively enrolled, treated with azithromycin, and return for a 6-month follow-up visit for repeat CT testing using the Gen-Probe APTIMA Combo 2 (Gen-Probe, Inc., San Diego, CA). Urogenital specimens are collected at enrollment and follow-up, from which CT strains are genotyped by *ompA* amplification and sequencing.

Results Enrollment visit genotypes have been determined for 145 subjects to date (91% female, 93% African American). CT infection was detected at follow-up in 39 (27%). Enrollment genotype distribution did not significantly differ in those without versus with repeat CT detection at follow-up (major genotypes: D/Da 25%,23%; E 22%,28%; F 13%,15%; I/1a 17%,15%; J/Ja 12%,13%). Of 35 subjects with CT strains genotyped from both enrollment and follow-up visits, 7 (20%) had the same CT strain at both visits versus 28 (80%) with a different strain at follow-up. Sexual activity post-treatment was reported in 32 subjects with strains genotyped at both visits; a new sexual partner was reported more often in subjects with discordant vs. concordant strains (52% vs. 14%, $p = 0.1$).

Conclusion Baseline CT Omp A genotype did not predict repeat CT detection. Most repeat CT infection detections were new infections with a different CT strain. Genotyping will be a useful tool in understanding the origins of repeat CT infection detection after treatment.

P3.259 SIMILAR CHLAMYDIA TRACHOMATIS BACTERIAL LOAD IN PATIENT SAMPLES FROM STI-CLINIC AND POPULATION-BASED SCREENING

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Introduction *Chlamydia trachomatis* (CT) load is suggested to be higher in symptomatic patients. This may have implications for screening policies in target groups that differ in their percentage of symptomatic patients. Here, we hypothesise that population-based screening yields lower CT loads as it is thought to include mainly asymptomatic patients. The objective of this study was to compare the CT load between 2 cohorts of CT positive patients (1) those attending a sexually transmitted infection (STI)-clinic and (2) those participating in the Dutch population-based screening (CSI), thereby taking into account symptoms as well as other determinants relevant for bacterial load.

Methods The CT load from 1286 CT-positive participants from the CSI-cohort (59.8%; 562 women) and STI-clinic in South Limburg (40.2%; 312 women) was determined using real-time qPCR. CT load was based on the copy number of the major outer-membrane protein (MOMP) gene normalised per copy number of eukaryotic cells (HLA gene).

Results The overall mean logarithmic bacterial load was 1.50 MOMP/HLA for women and 1.15 MOMP/HLA for men. For both sexes there was no independent association between cohort type and mean logarithmic CT load (women, $p = 0.86$; men $p = 0.22$). Symptoms were independently associated with load. Load was higher in women reporting dysuria (1.65 MOMP/HLA) than in women without dysuria (1.46 MOMP/HLA) ($p = 0.027$). For men, load was higher when reporting frequent urination (1.56 MOMP/HLA) than without this symptom (1.10 MOMP/HLA), ($p = 0.015$). Contrary to the expectation, these symptoms were reported in the CSI cohort more often than in the STI clinic cohort (women: 26.8 and 13.6%; men 16.5 and 7.3%). None of the other determinants were found to be associated with load.

Conclusion Our results indicate a similar bacterial *C. trachomatis* load in the general population and in a high-risk population, highlighting the relevance of population-based CT-screening.

P3.260 DIFFERENCE IN DISTRIBUTION OF CHLAMYDIA TRACHOMATIS GENOTYPES AMONG DIFFERENT PROVINCES: A PILOT STUDY FROM FOUR PROVINCES IN CHINA

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The objective of this study was to assess the distribution of *Chlamydia trachomatis* (*C. trachomatis*) genovars in male sexually transmitted disease (STD) clinic patients from 1 province in eastern China (Jiangsu) and 3 provinces in southern China (Guangdong, Guangxi, and Hainan). Urine specimens ($n = 140$) were collected

from 46 public STD clinics in the 4 provinces. Specimens that tested positive for *C. trachomatis* by polymerase chain reaction were genotyped for the infecting *C. trachomatis* strain by amplifying and sequencing the genovar-specific *ompA* gene, which encodes the chlamydial major outer membrane protein. Nine *C. trachomatis* genovars were identified from 129 specimens; they consisted of the F (25.6%, n = 33), E (17.1%, n = 22), J (16.3%, n = 21), D (15.5%, n = 20), G (11.6%, n = 15), K (5.4%, n = 7), H (3.9%, n = 5), I (1.6%, n = 2), and B (0.8%, n = 1) genovars. Nine genovars were found in specimens from Guangxi province, 6 were found in specimens from each of Guangdong and Hainan provinces, but only 5 were found in specimens from Jiangsu province. Significant differences were observed in *C. trachomatis* genovar distributions between different provinces: G/Ga was absent among male STD clinic patients (MSPs) from the eastern province of Jiangsu (Fisher exact test = 0.036), while being prevalent in the 3 southern provinces.

P3.261 GLOBAL MULTILOCUS SEQUENCE TYPE (MLST) ANALYSIS OF CHLAMYDIA TRACHOMATIS STRAINS FROM 16 COUNTRIES

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Background The *Chlamydia trachomatis* MLST database was established in 2007 and is based on five target regions (non-housekeeping genes) and the conventional *ompA* gene. It enables worldwide epidemiological analyses.

Methods Samples were included from 11 studies focusing on specific risk groups and with different study objectives. Geographical distribution of MLST profiles was carried out and eBURST analysis identified genetic founders.

Results A total of 414 MLST profiles were recognised from 2087 entries. Polymorphism of target regions was reflected in varying numbers of alleles; *hctB* 89, CT058 51, CT144 30, CT172 41, *pbpB* 35. With addition of 49 *ompA* gene variants 459 profiles exist.

There were 16 countries from which samples originated, the majority coming from the Netherlands 39%, Sweden 16% and Norway 12%, but also samples from countries in North and South America, Africa and other European countries. Overall 605 (29%) of the database samples originated from men having sex with men (MSM) while the remaining samples were assumed to be from heterosexuals.

Singletons or small clusters emerged from 377 of the MLST profiles that were found 1–9 times while 31 profiles were found 10–43 times each. There were 8 profiles that predominated and were each found between 83 and 140 times and constituted large clusters that comprised 868 samples (41.6%). Four of the predominating profiles were strongly associated with MSM, with 96–100% of the samples coming from MSM. In the other four large clusters heterosexuals comprised > 90% of the samples. eBURST analysis identified 3 of the 8 predominating profiles as founders, and another 3 as subgroup founders. The genetic diversity was much lower in the MSM clusters compared to clusters in heterosexuals.

Conclusions Worldwide a few *C. trachomatis* MLST profiles predominate. Different MLST profiles predominate among MSM and heterosexuals.

P3.262 COMPARISON OF URINE SAMPLES AND PENILE SWABS IN THE DETECTION OF HUMAN PAPILLOMA VIRUS IN MEN USING THE SPF₁₀ LINE PROBE ASSAY

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Background Penile swab sampling is the gold standard when testing for human papilloma virus (HPV) in men. Urine could provide a more convenient sampling material. Therefore we compared the detection and typing of HPV in urine samples and penile swabs using a highly sensitive method.

Methods First void urine and self-obtained penile swabs were collected from 120 men visiting a Sexually Transmitted Infections (STI) clinic in South Limburg, The Netherlands. When exclusion criteria were met, the results of 111 men (mean age 29.4 years) were analysed. Broad-spectrum HPV DNA amplification and genotyping were performed using SPF₁₀-DEIA-LiPA₂₅ system (Labo Bio-Medical Products, Rijswijk, The Netherlands). There are 12 high risk HPV types (hrHPV), 5 possible hrHPV types and 8 low risk HPV types (lrHPV) detectable by SPF₁₀-LiPA₂₅.

Results HPV DNA was found in 75 (67.6%) men. In 73 men HPV DNA was detected in the penile swab or both samples and in two men HPV DNA was detected only in the urine sample. Sixty-six paired samples were concordant in being HPV positive (n = 30) or negative (n = 36). Eleven of the 30 matching samples were concordant in their genotypes, fourteen pairs were comparable (≥ 1 genotype identical) and five pairs were discordant in genotypes. Three of these discordant and one comparable urine sample contained (possible) high risk types which were not found in the swab. Furthermore, the two positive urines with a negative swab contained (possible) high risk types as well.

Conclusion Urine samples are not comparable to penile swabs in the detection of HPV in men. However, in the urine sample of six men high risk types were found that could not be detected in the penile swab alone. This could be an indication of an additional value of the urine sample aside the penile swab in the detection of HPV in men.

P3.263 DO MEN HARBOUR THE SAME STRAIN OF GONOCOCCUS AT MULTIPLE ANATOMICAL SITES?

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Background All *N. gonorrhoeae* clinical isolates in Scotland are routinely typed by *Neisseria gonorrhoeae* multi-antigen sequence typing (NG-MAST). The frequency with which individuals harboured the same *N. gonorrhoeae* strain at > 1 anatomical site concurrently was examined.

Methods Episodes of gonorrhoea between 2004 and January 2013 comprising typed isolates from two or more anatomical sites of the same male individual submitted within a one-month period were analysed for similarity.

Results 410 episodes of gonorrhoea were identified with > 1 site cultured. The table shows differences in sequence type (ST) within episodes. Forty episodes with three cultures are included in all three pairwise combinations. Overall 91.2% of episodes had identical STs at all sites.

Where STs differed at only one allele, the sequences were compared using CLUSTALW. Thirteen of 14 alleles compared were at the *porB* locus. Nine pairs were 99.8% similar, representing a difference of 1 nucleotide. The remaining pairs showed 88.4%, 98.2%, 97.8%, 96.9% and 75.1% (*tbpB*) similarity.