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 54 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.

**Conclusion** Baseline CT OmpA 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.

**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 = 0.26; men p = 0.22). Symptoms were independently associated with load. Load was higher in women without 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.

**Background** Detection of Chlamydia trachomatis (CT) infection within months of initial diagnosis and treatment is a common occurrence. Origins of such infection (persistance 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 gene, encoding an antigenically diverse surface protein outer membrane protein A (OmpA).

**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 mainly consist of 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 = 0.26; men p = 0.22). Symptoms were independently associated with load. Load was higher in women without 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.
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 = 0.056), while being prevalent in the 3 southern provinces.

**Poster presentations**

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


**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 specific risk groups and with different study objectives. Geographical distributions between different provinces. 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 577 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 predominated. Different MLST profiles predominated 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** All *N. gonorrhoea* clinical isolates in Scotland are routinely typed by Neisseria gonorrhoea multi-antigen sequence typing (NG-MAST). The frequency with which individuals harboured the same *N. gonorrhoea* 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% (3bp) similarity.