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 multi-locus 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.

INVESTIGATING THE EPIDEMIOLOGY OF REPEAT *CHLAMYDIA TRACHOMATIS* DETECTION AFTER TREATMENT USING *CHLAMYDIA TRACHOMATIS* OMP A GENOTYPING

R Kapil, M L Hwang, C G Press, E W Hook, **W M Geisler**. *University of Alabama at Birmingham, Birmingham, AL, United States*

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/Ia 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.

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

[1,2]**A Dirks**, [1]A A T P Brink, [3]A Speksnijder, [1,2]N H T M Dukers-Muijrers, [1]P F G Wolffs, [1,2]C J P A Hoebe. *[1]Department of Medical Microbiology, Maastricht University Medical Center, Maastricht, The Netherlands; [2]Department of Sexual Health, Infectious Diseases and Environmental Health, Public Health Service South Limburg, Geleen, The Netherlands; [3]Public Health Laboratory, Cluster Infectious Diseases, Public Health Service Amsterdam, Amsterdam, The Netherlands*

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.

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

Y Han, Y Yin, M Shi, M Zhong, S Chen, Z Xiang, N Jiang, X Chen. *National Center for STD Control & Chinese Academy of Medical Sciences &, Nanjing, China*

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