

P3.239 HIGH-RESOLUTION MULTILOCUS SEQUENCE TYPING OF UROGENITAL *CHLAMYDIA TRACHOMATIS* IN STD CLINIC OUTPATIENTS IN TWO CHINESE PROVINCES

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Introduction: *Chlamydia trachomatis* infection is the most common bacterial sexually transmitted disease (STD) in the world. Multi-locus sequence typing (MLST) is a nucleotide sequence based approach for unambiguously characterising isolates of bacteria and other organisms via the internet, and has been used to monitor the molecular epidemiology of pathogenic bacteria and also to help understand their evolution and population biology. To enrich genetic background information on *C. trachomatis* in the MLST database and to deepen the current knowledge of the molecular characteristics of *C. trachomatis* strains circulating in China.

Methods Ninety-nine *C. trachomatis*-infected patients and 16 follow-up patients were recruited from selected STD clinics in Jiangsu Province and Guangxi Zhuang Autonomous Region, from whom cervical swabs and demographic data were collected. *C. trachomatis* type was determined by MLST analysis. Chlamydia sequence types from different areas were compared by using Bio-Numerics 7 to generate a minimum spanning tree.

Results Six out of the 16 follow-up samples tested positive for *C. Trachomatis* DNA. Of 105 Chlamydia-positive samples, 90 (85.71%) were available for MLST analysis, by which seven *ompA* genovars and 26 MLST types were determined. Significant differences in genovar distribution were not observed between *C. trachomatis* strains from Jiangsu and Guangxi, but noted between Chinese and Italian strains. Among the six Chlamydia-positive follow-up samples, three were identified as Chlamydia re-infections, while the other three failed to yield an MLST result.

Conclusion The prevalent STs of *C. trachomatis* in China were different from those in Italy. Half of Chlamydia-positive follow-up samples (3/6) were identified as re-infections; hence, follow-up Chlamydia infected patients deserve more attention of clinicians.

P3.240 PREVALENCE AND GENOTYPE DISTRIBUTION OF *CHLAMYDIA TRACHOMATIS* IN URINE AMONG MALES ATTENDING STD CLINICS IN GUANGDONG PROVINCE, CHINA, 2016

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Introduction Chlamydia is the most common sexually transmitted disease worldwide. Many studies have been evaluated the prevalence of *Chlamydia trachomatis* (CT) infection while very rare studies assessed the genotype distribution in urine among males attending sexually transmitted diseases (STD)

clinics (MSCs) in China. This study aimed to investigate the prevalence and molecular epidemiology of CT infection by urine samples among MSCs from different geographic areas of Guangdong province, China.

Methods A cross-sectional study was performed among MSCs from ten HIV surveillance sites of Guangdong province, China. CT DNA in male urines were extracted and detected by using the Roche cobas 4800 CT/NG. The *ompA* genes were amplified by nested polymerase chain reaction and sequenced. Urine leukocyte esterase test were performed.

Results Of the 1926 urine specimens, 1903 urines were successfully validated for detection of CT. Of the 1903 samples, one hundred and sixty-three (8.6%, 95% CI 8.2% to 9.0%) were found to be positive for CT. One hundred and thirty CT positive specimens were successfully genotyped by nested PCR, resulting in eight genotypes. The most prevalent genotypes were D, E, F, and J with proportions of 20.8%, 20.0%, 17.7%, 16.9%, respectively. There was no significant difference between age, geographic area, leukocyte esterase test and genotype distribution.

Conclusion There was a high prevalence of CT infection among males attending STD clinics in eastern area of Guangdong province, China. Promoting detection and molecular epidemiology research are needed for effective and comprehensive prevention and control programs.

P3.241 CLINICAL AND CEREBROSPINAL FLUID (CSF) CHARACTERISTICS OF HOSPITALISED PATIENTS FOR NEUROSYPHILIS (NS) TREATMENT AT A UNIVERSITY HOSPITAL OF THE STATE OF SÃO PAULO FROM 2010 TO 2015

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Introduction Syphilis is a systemic sexually transmitted infection caused by *Treponema pallidum*. NS can occur in any of its phases. Coinfection with HIV interferes with the clinical course of NS, leading to atypical diagnostic features. The aim of this study is to describe clinical and laboratory characteristics of inpatients treated for NS and to compare HIV-coinfected (HIV+) with HIV seronegative (HIV-) subjects.

Methods Retrospective analysis of medical records of patients hospitalised for NS treatment at HCFMUSP (2010–2015) with reactive serum treponemal test and abnormal CSF analysis. Clinical and laboratory findings were compared between HIV+ and HIV- patients.

Results In our cohort of 47 patients with NS, 31 (66%) were HIV+. Median (M) age was 35 (Interquartile-IQR: 30–46) in the HIV+ group and 48 (IQR: 40–58) among HIV- patients. Half of participants reported previous syphilis treatment. Serum VDRL was reactive in 44 patients. Mean time from symptoms onset to diagnosis was 30 days (IQR: 1–180). 23 patients were symptomatic: 5 neuropsychiatric disorders, 2 stroke, 11 ocular signs; 1 seizures and 4 brain stem/cranial nerve disorders. Among symptomatic individuals, 14 (61%) were HIV+. In the HIV+ group the M CD4 count was 326 cel/mm³ (IQR: 204–546). CSF analysis was performed in 45 patients and yielded -M (IQR) values for HIV+ and HIV-