Short Communication

Difference in Distribution of Chlamydia trachomatis Genotypes among Different Provinces: a Pilot Study from Four Provinces in China

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SUMMARY: The objective of this study was to assess the distribution of Chlamydia 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%), E (17.1%), J (16.3%), D (15.5%), G (11.6%), K (5.4%), H (3.9%), I (1.6%), and B (0.8%) 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. Genovar G/Ga was shown to be endemic among male patients in southern China.

Urogenital Chlamydia trachomatis infection is one of the most prevalent sexually transmitted infections (STIs) worldwide. The World Health Organization (WHO) estimates the global incidence of new cases of C. trachomatis infection to be approximately 92 million; disease is asymptomatic in approximately 50% of men and 70% of women (1). In recent years, China has experienced widespread increases in the incidence of sexually transmitted diseases (STDs), including genital C. trachomatis infection, through various forms of sexual contact (2). A population-based survey conducted in China showed that the overall prevalence of C. trachomatis infection was 2.1% in the general population (3).

It has been well established that this infection can lead to serious complications, particularly of the reproductive system, including pelvic inflammatory disease, ectopic pregnancy, tubal infertility, and epididymitis. C. trachomatis infection may also increase the risk of cervical cancer (4) and human immunodeficiency virus acquisition and transmission (5). To enhance the clinic care of infected patients and improve the prevention and control of C. trachomatis infection, molecular typing based on polymerase chain reaction (PCR) amplification and sequencing has been increasingly used to assess genotype distribution, which may contribute to a better understanding of its acquisition and transmission. There have been several molecular epidemiological studies on the genotype distribution of C. trachomatis among patients attending STD clinics in other countries, but in China it has been investigated only among male STD clinic patients (MSPs) in Guangdong province (6,7). The present study investigated the distribution of C. trachomatis genovars in public STD clinics across diverse areas in eastern and southern China.

From July 2009 to September 2010, men who attended STD clinics seeking STD care were enrolled in this study. The study included MSPs from Guangxi province (cities of Wuzhou and Hezhou), Guangdong province (cities of Jiangmen and Maoming), Hainan province (cities of Qionghai and Sanya), and Jiangsu province (Yangzhou and Changzhou). Detailed information on the recruitment of MSPs who participated in this study has been described previously (Fig. 1) (8). All participants were invited to provide first-void urine specimens. This study was approved by the Medical Ethics Committee of the Institute of Dermatology, the Chinese Academy of Medical Sciences & Peking Union Medical College, Nanjing, China.

The urine specimens were evaluated for C. trachomatis using the Roche Amplicor CT/NG PCR assay (Amplicor CT/NG; Roche Molecular Systems, Branchburg, N.J., USA), according to the manufacturer’s instructions. Initial genomic DNA extraction and C. trachomatis genotyping of the ompA gene were performed as described previously (9), with a minor modification of the nested PCR: aliquots of 4 μL of extracted genomic DNA and the first PCR product were used as DNA templates for the first and the second PCRs, respectively. The amplification products of the nested PCR were purified and sequenced at BGI Bio, Co. (Shanghai, China). All PCR products were sequenced bidirectionally. The sequences of the ompA gene were edited, aligned, and analyzed using DNAStar software for Windows (version 5.0; DNAStar, Inc., Madison, Wis., USA).

Data were analyzed with SPSS for Windows (version 11.0; SPSS Inc., Chicago, Ill., USA). Differences in C. trachomatis genotype distributions between different
provinces were determined using the chi-square or Fisher exact test, assuming a threshold level of significance of 0.05.

There were 140 MSPs infected with *C. trachomatis* among the 2,041 attendees (7). The *ompA* gene was successfully amplified by the nested PCR in 129 specimens (129/140, 92.1%). Two samples had ambiguous sequences considered to be a result of mixed infection with different *C. trachomatis* genotypes. In the 129 specimens, 9 *C. trachomatis* genotypes were identified; the most prevalent were F (25.6%, *n* = 33), E (17.1%, *n* = 22), and J/Ja (16.3%, *n* = 21). Other genotypes identified were D/Da (15.5%, *n* = 20), G/Ga (11.6%, *n* = 15), K (5.4%, *n* = 7), H (3.9%, *n* = 5), I/Ia (1.6%, *n* = 2), and B (0.8%, *n* = 1). Nine genovars were found in specimens from MSPs from Guangxi province, 6 genovars were found in specimens from MSPs from Guangdong and Hainan provinces, while only 5 were found in specimens from MSPs from Jiangsu province (Fig. 2).

Significant differences were observed in *C. trachomatis* genovar distributions between different provinces: G/Ga was absent among MSPs from the eastern province of Jiangsu (Fisher exact test = 0.036), while being prevalent in the 3 southern provinces. Meanwhile, genovar H was absent among participants from Guangdong and Jiangsu provinces (Fisher exact test = 0.011).

In this pilot study, more genovars were found in the 3 southern provinces (6–9 genovars) than in the eastern Jiangsu province (5 genovars). The prevalence of *C. trachomatis* infection was also shown to be higher in the 3 southern provinces (7.4%) than in Jiangsu province (5.9%) (8). Southern China has close social and economic ties with Southeast Asian nations; similar STD
epidemics have been described for these regions (10). It has been reported that 70% of men and 18% of women who attended STD clinics in southern China had had sex with non-regular sex partners in the previous 6 months and that the prevalence of unprotected sex among those subjects was more than 70% (11). The high level of diversity and broad distribution of C. trachomatis genovars among MSPs from southern China, as found in this study, might be due to the prevalence of unprotected sexual activity. Such activity could lead to long-term prevalence of C. trachomatis infection in the population through widespread transmission from untreated infected subjects to susceptible individuals.

Overall, the most prevalent genotypes detected in this study were F (25.6%), E (17.1%), and J (16.3%). This C. trachomatis genovar distribution pattern is similar to the patterns that have been reported among male patients in Guangdong province (6,7) and Taiwan (12), female sex workers in southern China (13), prostitutes and non-prostitutes in Thailand (14) as well as female patients in Japan (15). These genovars may be the most prevalent circulating in Asia (14,15), and possibly the world (16).

In this study, genovar G/Ga was found to be endemic among male patients from southern China, which is consistent with the C. trachomatis genovar distribution patterns found in populations of men who have sex with men (MSM) in China (6), Australia (17), and the Netherlands (18). An earlier study has shown that polymorphisms of the open reading frames of the ompA gene were strongly associated with rectal tropism in serovar G isolates (19). Among the C. trachomatis-infected MSPs participating in this study, only one self-reported having had sex with men. In MSM, the rectum is often the only site infected with C. trachomatis, and concurrent urogenital tract infection is not always present (20); as for urogenital infections, most rectal C. trachomatis infections remain asymptomatic (21). This important feature should be taken into account when establishing programs for surveillance and screening for C. trachomatis infections among MSM in different areas. In future studies, anal swabs should be collected from male patients who seek care at STI clinics in order to thoroughly screen for C. trachomatis and to monitor its prevalence, especially in southern China.

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Conflict of interest None to declare.

REFERENCES


