Chlamydia trachomatis Serovars among Strains Isolated from Members of Rural Indigenous Communities and Urban Populations in Australia

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We genotyped Chlamydia trachomatis strains from 45 women or men living in either a rural indigenous community or in urban heterosexual communities. We found six different C. trachomatis serovars: E (n = 22; 48.9%), F (n = 10; 22.2%), J/Ja (n = 5; 11.1%), D/Da (n = 4; 8.9%), G (n = 3; 6.7%), and K (n = 1; 2.2%). The distribution of C. trachomatis serovars among members of the indigenous rural and the urban Australian communities appears similar to that in other Western countries.

The high prevalence of Chlamydia trachomatis urogenital infections among indigenous populations and urban young adults in Australia, 7.5% and 5.6%, respectively, is an important health concern in this country (8). While numerous studies have addressed the epidemiology of C. trachomatis in Australia, very little is known about the distribution of C. trachomatis serovars. One of these studies characterized the C. trachomatis serovars in eye swab samples from people living in remote Australian communities (7). Among the C. trachomatis serovars A, B, and C, which are usually associated with trachoma, only serovar C (87%) and serovar Ba (15%) were found in conjunctival samples from 31 patients. A second study addressed the distribution of C. trachomatis serovars in urogenital specimens collected from 39 men who visited male-only saunas in Melbourne, Victoria (4). This study found serovars D/Da (53.8%), G (25.6%), J/Ja (10.2%), B/Ba (2.6%), E (2.6%), F (2.6%), and H (2.6%). The relatively high prevalence of serovars D/Da and G in this population was different from the overall distribution of C. trachomatis serovars in most populations around the world, in which serovars E, D/Da, and F share the highest prevalence (6). Lister et al. (4) extended their study by investigating the distribution of C. trachomatis serovars in 42 women from the same city and found serovars E (40%), F (19%), G (17%), J/Ja (10%), D/Da (7%), and K (7%) (5). This distribution pattern was similar to the worldwide distribution of C. trachomatis serovars except for the relatively low prevalence of serovar D/Da.

Studying the distribution of C. trachomatis serovars among different populations is important as it enables better understanding of the epidemiology and transmission of and susceptibility to C. trachomatis infection. The objective of our study was to investigate the distribution of C. trachomatis serovars among members of rural indigenous communities and urban populations in Australia.

Urine specimens were collected from 45 women and men positive for C. trachomatis living in either a rural indigenous community (n = 32) or in urban heterosexual communities (n = 13). Of the 13 urban-based specimens, collected in the city of Brisbane, 3 were from nonindigenous females, 2 from indigenous females, and 7 from nonindigenous males (indigenous classification was based on individuals’ self-identification as descendants of the original inhabitants of Australia); 1 specimen was collected from a homeless young person, but no gender was recorded. Of the 32 specimens from members of a rural indigenous community of approximately 3,000 people located 300 km from Brisbane, 26 were from females and 6 from males. Currently, C. trachomatis serovars are identified by using genotyping methods, such as restriction fragment length polymorphism or DNA sequencing of the major outer membrane protein (MOMP) gene (ompA) (2). In our study, we amplified the MOMP gene from urine specimens, which are a convenient and reliable source for both diagnosis and genotyping of C. trachomatis strains (1, 2), using a nested PCR procedure as previously described (1). Briefly, the urine specimens, which were stored at −20°C until processing, were prepared for nested PCR by using a modified HighPure PCR template preparation kit (Roche Molecular Biochemicals). A DNA fragment comprising the entire ompA gene was amplified and sequenced by using a CEQ dye terminator quick start kit (Beckman Coulter) (Table 1). To determine the serovars, we used the neighbor-joining phylogenetic program provided in the GeneStudio package using ompA sequences specific for each serovar as references (GeneStudio, Inc.).

The C. trachomatis strains are conventionally classified into 15 serovars, A through K, L1, L2, and L3, which were identified and defined by using polyclonal antibodies. Additional serovariants (e.g., Ba, Da, Ia, and Ja) have been identified by using monoclonal antibodies specific for MOMP. The MOMP amino acid variations responsible for the serological specificity of these serovariants have not been well defined, and the merit of classifying these variants as distinct evolutionary lineages (i.e., distinct serovars) is not clear. Therefore, no attempt to identify these serovariants was made in our study. Also, the distribution of serovars in studies that used different types of urogenital specimens collected from the same region is usually similar, which indirectly suggests that there are no significant differences.
We found six different C. trachomatis serovars among the specimens collected from 45 study participants: E (n = 22; 48.9%), F (n = 10; 22.2%), JJa (n = 5; 11.1%), D/Da (n = 4; 8.9%), G (n = 3; 6.7%), and K (n = 1; 2.2%) (Table 2). Similar to findings in other regions of the world, E and F were the predominant serovars. However, serovar D/Da was found at a lower prevalence. Also, the serovar I/Ia, which was found at a relatively high prevalence in some regions of the world, particularly in the United States (6), appears absent in our study populations, as well as in the other Australian populations that have been studied (4, 5, 7). There were no significant differences in the distribution of serovars between men and women in our study populations.

Notably, 18 (56.25%) of the 32 patients from the rural indigenous community were infected with serovar E, followed by serovars F (n = 5; 15.6%) and JJa (n = 5; 15.6%). Overall, only four (8.9%) patients in our study population were infected with serovar D/Da, similar to the results of the study of women with urogenital infections in Melbourne, Australia (5). This relatively low prevalence of serovar D/Da compared to its worldwide presence is in sharp contrast with the results of the Melbourne study on men who have sex with men (MSM), in which D/Da (53.8%) was the dominant serovar (4). This MSM study also found a relatively high prevalence (25.6%) of serovar G. The results of the study of women in Melbourne, as well as our results on the general distribution of serovars in Australia, indirectly suggest that the high prevalence of serovar D/Da and G among MSM in Melbourne was due to a local outbreak in male-only saunas. However, previous studies on the distribution of C. trachomatis serovars among MSM in Seattle, and Rotterdam, these results indicate a preferential transmission or tropism for these serovars among MSM.

In summary, the distribution of C. trachomatis serovars among members of the indigenous rural and the urban communities in Australia appears similar to that in other Western countries. However, there is a need for larger-scale investigations in both the general population and specific populations with strong transmission links in order to fully assess the epidemiology of C. trachomatis serovars.

REFERENCES


