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Published in:
Emerging Infectious Diseases

DOI:
10.3201/eid1611.100379

Citation for published version (APA):

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Download date: 04 Nov 2018
Typing of Lymphogranuloma Venereum Chlamydia trachomatis Strains

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We analyzed by multilocus sequence typing 77 lymphogranuloma venereum Chlamydia trachomatis strains from men who have sex with men in Europe and the United States. Specimens from an outbreak in 2003 in Europe were monoclonal. In contrast, several strains were in the United States in the 1980s, including a variant from Europe.

Lymphogranuloma venereum (LGV) is a sexually transmitted disease caused by Chlamydia trachomatis serovars L1, L2, and L3. This disease is endemic to parts of Africa, Latin America, and Asia but only occurred sporadically in Europe before 2003, at which time an outbreak of LGV occurred in the Netherlands among men who have sex with men (MSM) (1). Since then, a large number of LGV cases have been reported among MSM in Europe, North America, and Australia. Although the inguinal form (formation of buboes) is more common in heterosexual LGV patients, in the current epidemic among MSM, anal infections have been diagnosed in most LGV cases.

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The Study

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We analyzed by multilocus sequence typing 77 lymphogranuloma venereum Chlamydia trachomatis strains from men who have sex with men in Europe and the United States. Specimens from an outbreak in 2003 in Europe were monoclonal. In contrast, several strains were in the United States in the 1980s, including a variant from Europe.

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All except 1 of the 50 specimens from Europe had an ompA genotype identical to the L2b reference strain L2b/
UCH-1/proctitis (AM884177.1). The nonidentical specimen came from Spain and had a previously unpublished single C→T point mutation in variable segment 2 at position 517 when compared with L2b/UCH-1/proctitis. This sequence of this specimen has been deposited in GenBank (accession no. GQ413955). All 50 specimens from Europe shared an identical MLST genotype (Table). The 5 specimens from the contemporary United States had the same ompA and MLST genotype as specimens from Europe (Table).

The 22 specimens from San Francisco were separated into 3 ompA genotypes and 5 MLST genotypes (Table). Six specimens had an ompA genotype identical to the L2 reference strain L2/434/Bu, and 7 had a novel genotype that differed from the L1 reference strain L1/440 by 9 point mutations. The remaining 9 specimens had an ompA genotype identical those of specimens from Europe and L2b reference strain L2b/UCH-1/proctitis. Three of these 9 specimens had MLST genotypes of strains from Europe, and the other 6 had a novel 108-nt deletion in the hctB gene region. This hctB variant has not been found in other specimens of C. trachomatis serovars A–L3 and is unique in the MLST database (http://mlstdb.bmc.uu.se/), which contains genetic profiles for 496 specimens (February 2010).

Conclusions

We aimed to deduce the nature and origin of the LGV outbreak among MSM in Europe. Because of the conserved nature of Chlamydia spp. genomes, high-resolution genotyping, rather than following evolutionary changes over long periods as with conventional MLST systems, was essential for investigating this outbreak. We found that the high-resolution MLST system described by Klint et al. (6) was most suitable for the current study.

LGV specimens from MSM in Europe in this study were monoclonal for ompA and the 5 highly variable regions. This finding suggests a single source of origin for the LGV outbreak among MSM in Europe. One specimen in this study contained a novel, single, point mutation in ompA. In 373 contemporary LGV cases in MSM in the United Kingdom, the L2b ompA variant comprised >90% of the specimens, and the remaining 35 specimens belonged to 4 novel sequence variants, each differing from the L2b variant by a single point mutation (10). These single point mutations might have occurred recently, and their presence is less likely to indicate a separate source of origin.

LGV specimens from MSM in the 1980s in San Francisco showed genetic variation in ompA and the 5 highly variable gene regions. MLST analysis showed that 6 of the 9 specimens from San Francisco that had the L2b ompA variant were genetically different from the strain in Europe; the remaining 3 specimens had an MLST profile identical to that of the variant from Europe. Genetic variation among LGV specimens from San Francisco supports the idea that LGV is endemic in MSM in the United States, a finding that has been reported (11).

In contrast, the epidemiologic pattern and genetic characterization of LGV in several countries in Europe indicate that the L2b type has disseminated across Europe in recent years. In Sweden, 3 LGV cases that produced clinical signs were detected in 2004 and 2005 (12). In a survey of 81% of patients with C. trachomatis infection detected among high risk MSM in Stockholm, no additional LGV cases were detected (12), and a total of 15 LGV cases were detected in 2007. If one considers the highly internationalized network of sexual contacts among MSM (13), the L2b variant may have been imported to Europe from the United States. A
limitation of our study is that it does not include old LGV strains from Europe. However, after widespread investigations, we believe that no such strains are available.

Our study shows that the MLST system of Klint et al. (6) is suitable for epidemiologic analysis of C. trachomatis transmission, as indicated by our ability to differentiate the L2b ompA variant found in San Francisco into 2 strains. Investigation of additional LGV specimens from the United States and regions to which LGV is endemic with the MLST system could help determine a more detailed epidemiologic picture of the LGV outbreak in 2003 among MSM.

Acknowledgments

We thank Maria Blomqvist, Estrella Caballero, Vroni Girbinger, Thomas Morin, and Jolein Pleijster for assistance with laboratory work.

This study was supported by local funds from Uppsala University Hospital and was part of a collaboration with the European EpiGenChlamydia Consortium (www.EpiGenChlamydia.eu) (14), which is supported by the European Commission within the Sixth Framework Programme through contract LSHG-CT-2007-037637.

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References


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