**In silico** comparison serotyping and genotyping methods for *Chlamydia trachomatis*

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**Summary**

Knowing prevalent sexually transmitted bacterial infections, we can mention *Chlamydia trachomatis* as one of the most important. For the purpose of the study, the genotyping methods have some advances being more precise, compared to immunotyping. In this context, the present study aims to compare phenotypic and genotypic methods for subspecies identification of *Chlamydia trachomatis* in term of discriminatory power and concordance. For analysis, a data table of *Chlamydia trachomatis* isolates with identified serovars/genovars and sequence types (ST) was used. Also considered were clonal relationships of sequence types (ST), defined with minimum spanning tree using BURST algorithms. In line with the aim of this study, concordance between typing methods were calculated using Simpson index and adjusted Rand and Wallace coefficients. Results are in context with the methods used for purpose of the study.

**Introduction**

*Chlamydia trachomatis* is a cause of the most prevalent sexually transmitted bacterial infection worldwide, with 89 million cases annually (Gaydos et al., 2004; Pannekoek, 2008; Roca, 2007). From studies, three variants of Chlamydia trachomatis have been identified: trachoma (serotypes A–C). Also it is known there are two sexually transmitted pathovars, respectively serotypes D–K and lymphogranuloma venereum (LGV). (Abdelsamed, 2013; Nicholas et al, 2008). A new variant of the genital tract *Chlamydia trachomatis* emerged relatively recently in Sweden. The new variant of *C. trachomatis* escaped routine diagnostic tests because it carries a plasmid with a deletion (Seth-Smith et al, 2009). This deletion included the targets used by the commercial diagnostic systems. This new nVCT is clonal (serovar/genovar E) and it spread rapidly throughout Sweden, undiagnosed by clinical test systems (several commercial diagnostic nucleic acid amplification tests). Supplementary to this, and knowing results of studies, the degree of spread may indicate an increased biological fitness of nVCT (Unemo et al, 2010). Using antibacterial control measures, *C. trachomatis* infections have been increasing. Moreover, infection with *C. trachomatis* is regarded as a serious public health problem, with a high impact on socioeconomic aspects and there is a known association with the disease and younger, sexually active people (Cevenini, 2008; Nunes et al, 2013). For prevention of such sexually transmitted diseases, it is best to use screening methods, for personal
protection (Bébéar et al, 2009; Fisher, 1993). In this context, chlamydiae are both human and animal pathogens, dangerous to public health (Griffiths, 2005; Gupta, 2006).

As a cause for enlarged types of bacterial infections, C. trachomatis is responsible for both asymptomatic and wide spectrum clinically significant diseases (Corsaro, 2003; Corsaro, 2004, Manavi, 2006).

Based on serological typing using antibodies against the major outer-membrane protein (MOMP) there are 19 prototypic serovars of C. trachomatis. Compared to immunotyping, the genotyping methods have some advantages in terms of being more precise, sensitive and specific for the typing of C. trachomatis (Borges, 2012; Molano, 2004).

As mentioned above, and following earlier studies, the aims of the present study were to compare phenotypic and genotypic methods for subspecies identification of C. trachomatis in terms of discriminatory power and concordance.

Materials and methods

A data table of C. trachomatis isolates, with identified serovars/genovars and sequence types (ST), was used for analysis (see: http://pubmlst.org/). Clonal relationships of ST were defined with minimum spanning tree using BURST algorithms (MLVAcompare (Ridom GmbH)). Diversity and concordance between typing methods were calculated using Simpson index and adjusted Rand and Wallace coefficients (see: http://www.comparingpartitions.info).

Results and discussions

There were 3691 strains of C. trachomatis contained in the data table. For 3,242 isolates, serovar/genovar information was determined. Sequence type based on 7 loci multilocus sequence typing (MLST) Chlamydiales scheme and 5 loci MLST Uppsala University scheme, were identified for 512 and 3277 isolates respectively. Discriminant power of each typing method and concordance are presented in Table 1.

Table 1. Resolution ability and concordance between serotyping (MOMP)/genotyping (ompA gene) and MLST methods.

<table>
<thead>
<tr>
<th>Typing method</th>
<th># Different types</th>
<th>Simpson index (95% CI)</th>
<th>Adjusted Rand's coefficient</th>
</tr>
</thead>
<tbody>
<tr>
<td>Serovar/genovar (n=3242)</td>
<td>27</td>
<td>0.822 [0.814 - 0.831]</td>
<td></td>
</tr>
<tr>
<td>MLST (Uppsala) (n=3277)</td>
<td>519</td>
<td>0.974 [0.972 - 0.976]</td>
<td>0.171 (n=3104)</td>
</tr>
<tr>
<td>MLST (Chlamydiales) (n=512)</td>
<td>58</td>
<td>0.903 [0.893 - 0.914]</td>
<td>0.609 (n=49)</td>
</tr>
</tbody>
</table>

Adjusted Wallace coefficients were 0.096 for W1(serovar/genovar -> MLST (Uppsala)) and 0.793 for W2 (MLST (Uppsala) -> serovar/genovar). In the case with serovar/genovar and MLST (Chlamydiales) the W1 was 0.758, and W2 was 0.508.

Clonal complexes (CC) of MLST and their characteristics including pairwise agreement between CC and serovars/genovars are presented in Figure 1.
Conclusions

Our results showed the higher level of discriminatory power of MLST in comparison with serotyping. The highest resolution ability (97.4%) had Uppsala scheme MLST using 5 loci. In spite of a weak-to-moderate degree of global congruence between serovars/genovars and sequence types (adj.Rand in Table 1) there was greater concordance for clonal complexes with more than 90% successive prediction using serovars/genovars (W1 coefficients in figure1). Interestingly, MLST typing method demonstrated clonal population structure of Chlamydia trachomatis. The study shows the diagnostic power of computer-aided assessment of serious bacterial infections.

References


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