Chlamydia Trachomatis omp1 Genotypic Diversity and Concordance with Sexual Network Data

Teresa Cabral,1 Ann M. Jolly,2,a and John L. Wylie1,2

1Department of Medical Microbiology, University of Manitoba, and 2Cadham Provincial Laboratory, Manitoba Health, Winnipeg, Manitoba, and 3Department of Epidemiology and Community Medicine, University of Ottawa and the Bureau of HIV/AIDS, Sexually Transmitted Disease, and Tuberculosis, Laboratory Centre for Disease Control, Ottawa, Ontario, Canada

Sexual and social network analysis have been proposed as novel sexually transmitted disease control and research tools. Here, the concordance between chlamydia genotype data and a large sexual network constructed from routinely collected contact tracing data was examined. A sexual network was constructed for Manitoba, Canada, from province-wide contact tracing data. Positive chlamydia specimens from the same time period were collected and genotyped by omp1 DNA sequencing. A high degree of concordance was found between transmission events, on the basis of molecular data, and proposed transmission events, on the basis of sexual network data. Discordant results appeared to occur when a portion of the network contained potential core group members or in areas where contact tracing is difficult to carry out. The agreement between the molecular and epidemiologic data suggests that the use of routine contact tracing data is a valid approach for the construction of sexual networks.

Sexually transmitted diseases (STDs) continue to exact a tremendous health and economic toll on society. To decrease the incidence, prevalence, and costs of chlamydial infections, many jurisdictions have introduced screening programs. These programs, however, may have reached their point of maximal effectiveness, because incidence rates in many jurisdictions have leveled off in the past few years and have begun increasing again. This phenomenon suggests that new methodologies and new approaches to STD control may be necessary to regain the downward trend in STD incidence.

Sexual network analysis has been proposed as a valuable tool in understanding the epidemiology of STDs [1–3]. Application of network analysis reflects the growing realization, stemming from both empirical and modeling studies, that an individual’s risk of acquiring an STD is governed not only by his or her own behaviors, but by the infection status and behaviors of the people with whom they choose to interact [4–8]. Various methods are used for the collection of network data, including contact tracing, snowball sampling, and asking individuals to report on their partner’s behavior. Each has its own advantages and disadvantages and potential for biasing estimates of sexual network measures [9]. In many situations, contact tracing may be the preferred approach because it focuses on those most at risk of infection and its routine practice in many areas provides a ready data source [9]. We have previously demonstrated the ability to use routinely collected data of this type to conduct...
large scale analyses of STD epidemiology within the context of sexual networks [10].

Recently, several authors have suggested combining molecular epidemiology with network analysis to further increase our understanding of STD epidemiology [11, 12]. At a minimum, by combining these 2 independent approaches, molecular data would help to demonstrate whether a sexual partnership network constructed from epidemiologic data accurately reflects the underlying transmission network of individual strains of an STD through a population. Molecular data would therefore serve to verify the social data provided by interviewed case patients and also indicate where the data were inaccurate. To date, several studies in England have focused on the molecular epidemiology of Neisseria gonorrhoeae within networks [5, 11, 13], whereas similar studies on genital infections by Chlamydia trachomatis have been limited to pairs of sexual partners [14]. In general, the extent to which large networks constructed from contact tracing data reflect the transmission of individual strains of C. trachomatis remains unanswered.

In this study, we present an analysis linking C. trachomatis molecular genotyping data with sexual network data. The main objectives of the study were to examine the genotypic diversity of chlamydia in Manitoba, assess the agreement between sexual network data and molecular data, and analyze the factors associated with discrepancies between the 2 types of data. Because contact tracing data are currently the most readily available source of STD epidemiologic data for this and future studies and, as Ghani et al. [9] note, because they are routinely available in other areas, we chose this data type to construct the sexual network for comparison with our molecular data. Given the known shortcomings in contact tracing as a data source (e.g., potentially incomplete/inaccurate sexual histories), agreement between the contact tracing and molecular data would increase our confidence in the accuracy of sexual networks constructed from routinely collected data of this type.

METHODS

Study population and data collection. A detailed description of the data sources for the construction of the sexual network used in this paper have been published elsewhere [10]. In brief, all patients with chlamydia and gonorrhea in the province of Manitoba, Canada, are reported to the Manitoba Communicable Disease Control (MCDC) unit. Detailed demographic, laboratory, treatment, symptoms, and health-care provider information are recorded in a MCDC database. After the client interview, information on the names and location of sexual contacts are also added to the database. This provincial database provided the information necessary to construct the sexual network for the province.

The contents of the STD case and contact databases at the MCDC unit from November 1997 to May 1998 were used for this study. Additional case subjects from August 1997 to October 1997 were also included to facilitate the inclusion of contacts entered into the database after November 1997 but who were named by subjects prior to that time. Individuals who appeared >1 time in the database were considered to be the same person, based on an algorithm involving a comparison of first and last names, components of birth dates, and/or address [10].

Nominal information was removed from the database and replaced with unique numerical identifiers. PAJEK, a social network analysis program [15], was used to identify all individuals who were directly and indirectly connected through sexual contact. As per social network terminology, the term “component” is used to designate a group of persons with known direct or indirect sexual links to each other.

Specimen collection and DNA extraction. Cadham Provincial Laboratory (CPL; Winnipeg) conducts ~95% of the diagnostic testing for chlamydia in Manitoba. At the time of this study, the chlamydia diagnostic test in use at CPL was Chlamydiazyme (Abbott Laboratories). From November 1997 to May 1998, corresponding to the 6 of 9 months for which STD data were obtained from the MCDC Unit, the remainder of all chlamydia-positive Chlamydiazyme specimens identified at CPL were retained and frozen at ~20°C. Samples were removed from storage, as needed, and used for DNA extraction and nucleotide sequence analysis.

DNA extraction was carried out using QIAamp DNA minikits (Qiagen) according to manufacturer’s instructions. Fifty microliters of specimen was used for extraction. In some cases, urine, rather than Chlamydiazyme swab samples, were available for typing. In these subjects, 50 μL urine specimen was used and treated in an identical manner as for the Chlamydiazyme samples.

Polymerase chain reaction (PCR) amplification. PCR was

![Figure 1](image)

**Figure 1.** Summary of primers used for polymerase chain reaction amplification and DNA sequencing of VD1, VD2, and VD4 of the Chlamydia trachomatis omp1 gene. Primer position is shown in relation to omp1. The nucleotide sequence of the primers and their position within the omp1 DNA sequence is as follows: CT1, GCCGCTTGTAGTTCTGCTTCTCC (sense), 39–56; CT2, ATTACGTGAGGACGCTCTCAT (antisense), 1145–1167; CT3, TGACCTTGTTTTGCAGGTGTGTTT (sense), 199–216; CT4, CCCTCAAGATTATTTCTAGATTCTATTGT (antisense), 1048–1076; CT5, CTTGTCCTTCCT (antisense), 699–73; and CT7, CCTACATGAGATTTAGG (sense), 859–881.
used for amplification of \textit{omp1}, which encodes the major outer membrane protein, of \textit{C. trachomatis}. Primers are summarized in figure 1. Primers CT1, CT2, and CT3 have been described elsewhere [16]. Primers CT4 and CT7 are based on sequence data reported by Yuan et al. [7], and primer CT6 was based on sequences reported in GenBank (accession numbers AF063204 and AF0663213). Primers were obtained from the Regional DNA Synthesis Laboratory (University of Calgary, Calgary, Alberta). Primers for sequencing were purified by PAGE. Primers CT1 and CT2 were used for initial amplification of \textit{omp1}, whereas primers CT3 and CT4 were used for nested PCR.

The 100 \(\mu\)L PCR mixture contained 30 pmol of a given primer, 0.2 mM dNTPs, 10 \(\mu\)L DyNAzyme EXT optimized buffer (MJ Research), 1.5 mM MgCl\(_2\), and 2.5 U DyNAzyme EXT DNA polymerase (MJ Research). The initial PCR contained 5 \(\mu\)L of Chlamydiazyme extract (or extracted urine). Nested PCR was conducted with 0.5–2 \(\mu\)L of the initial PCR. PCR was conducted on a PTC-100 thermocycler (MJ Research). In the first round of PCR, samples were initially heated at 95\(^\circ\)C for 7 min, with 9 cycles of denaturation (95\(^\circ\)C for 1 min), annealing (60\(^\circ\)C for 1 min), and extension (72\(^\circ\)C for 1.5 min), followed by an additional 24 cycles with the annealing temperature reduced to 55\(^\circ\)C. The nested PCR used the same conditions, except the latter part of the program was increased to 30 cycles from 24.

PCR products were purified by ethanol precipitation. Fifty microliters of each PCR was added to 125 \(\mu\)L of 95\% ethanol and 5 \(\mu\)L of 3 \textit{M} sodium acetate (pH 4.6). The mixture was left at room temperature for 15 min, then centrifuged at 16,000 \(\text{g}\) for 20 min. The supernatants were removed, and the pellets were washed with 500 \(\mu\)L of 70\% ethanol and centrifuged at 16,000 \(\text{g}\) for 15 min. After removal of the supernatants, the pellets were dried at 95\(^\circ\)C for 1 min. Dried pellets were subsequently resuspended in 50 \(\mu\)L of distilled water and stored at −20\(^\circ\)C until used for nucleotide sequencing reactions.

\textbf{Nucleotide sequence analysis.} Sequencing reactions were carried out with purified PCR products by use of BigDye Terminators cycle sequencing kits (Applied Biosystems). Ten microliters of the sequencing reaction contained 1–3 ng of template, 1.6 pmol of primer, 2 \(\mu\)L of 5\(\times\) dilution buffer (Applied Biosystems), 2 \(\mu\)L of BigDye Terminators, and water to a final volume of 10 \(\mu\)L. DNA labeling was conducted using a Perkin-Elmer GeneAmp 9600 PCR system. Thermocycling conditions were 96\(^\circ\)C for 10 s, 50\(^\circ\)C for 5 s, and 60\(^\circ\)C for 4 min for 25 cycles. Labeled products underwent ethanol precipitation, as described above. The final purified DNA was resuspended in 15 \(\mu\)L of Template Suppression Reagent (Applied Biosystems) and denatured at 95\(^\circ\)C for 5 min. Prepared specimens were loaded on an ABI genetic analyzer 310 (Applied Biosystems). Each sequencing run used Performance Optimized Polymer 6, 1\(\times\) sequencing buffer, and 47 cm \(\times\) 50 \(\mu\)m capillary. Primers CT3 and CT7 were used for forward sequencing reactions, whereas CT4 and CT6 were used for sequencing in the reverse direction. Comparison of \textit{omp1} sequences was conducted with ALIGN PLUS (Scientific and Educational Software).

Traditional serotyping identifies distinct serovars of \textit{C. trachomatis} (designated A–L), on the basis of amino acid variability in the externally exposed, variable domains (VDs) of the major outer membrane protein (MOMP). Sequence analysis of the \textit{omp1} gene encoding the MOMP protein from each distinct serovar have identified the corresponding differences in the nucleotide sequence of the VDs of the gene [17]. Chlamydia genotypes based on sequence analysis are assigned by use of the same letter designation as that used for serovar status. We used the \textit{omp1} VD DNA sequences reported by Yuan et al. [17] as prototype strains. If DNA sequence variants were identified, they were assigned a subgenotype status by identifying the prototype sequence with the highest degree of homology and designating the isolate with a numerical subscript (e.g., \(D_1\), \(D_2\), and \(D_3\)). We used only the nucleotide sequences of VD1, VD2, and VD4 in this study for genotype assignment.

\textbf{Statistical analysis.} Information on individuals within each component (a subgroup of the network in which there is asignificant identified path from 1 person to every other person) was used to classify the overall nature of the components. Components were classified as coinfected if at least 1 person in a component was coinfected with chlamydia and gonorrhea. A component was classified as “aboriginal” if at least 1 person

\begin{table}[h!]
\centering
\caption{Chlamydia trachomatis genotypes identified in Manitoba, 1997–1998 (\(n = 359\)).}
\begin{tabular}{ll}
\hline
Genotype & No. of specimens \\
\hline
Ba1 & 2 \\
Ba2 & 9 \\
D & 73 \\
D1 & 37 \\
D2 & 2 \\
D3 & 1 \\
D4 & 1 \\
E & 93 \\
F & 41 \\
G & 4 \\
G1 & 10 \\
I1/H & 14 \\
J & 44 \\
J/C & 1 \\
K1 & 27 \\
\hline
\end{tabular}
\end{table}

\textbf{NOTE.} Two hundred ninety-seven specimens were used in the analysis of concordancy between molecular and epidemiologic data, and 50 specimens were used as part of the geographic analysis.
was of aboriginal descent (ethnicity information in our dataset permitted only this limited type of categorization; aboriginal classification was based on treaty status registry data). Components were classified as 1 partner, 2 partners, or 3 partners, on the basis of the largest number of sexual partners named by any case within the component. The variable "time interval" was the length of time between the earliest and latest diagnosis dates within components. Finally, component size was the number of individuals within a component. Since data on component size and time interval between the last and first diagnosis within each component were not normally distributed, differences between discordant and concordant components were evaluated using Kruskal-Wallis test for 2 groups, performed with Epi Info (version 6.04d; Centers for Disease Control and Prevention). Data on number of partners, aboriginal descent, and coinfection were all categorical, and differences were analyzed using \( \chi^2 \) tests or, in the case of coinfection and concordancy, an expected value was <5, Fisher's exact test was used.

**RESULTS**

**Genotypic diversity of chlamydia in Manitoba.** In total, we genotyped chlamydia specimens from 359 individuals. Of this total, 35 specimens were part of a random sample, 297 were entered in an analysis of concordancy between epidemiologic and molecular data, and 50 were part of a geographic analysis (individual analyses detailed below). The 3 subsets do not total 359 because some chlamydia specimens were entered in >1 analysis.

The frequency of each chlamydia genotype is shown in table 1. The nucleotide sequences of the variant genotypes identified are shown in figure 2. Prototype genotypes identified were D, E, F, G, and J. Variants of 3 of these prototypes were identified and designated D\(_1\), D\(_2\), D\(_3\), D\(_4\), G\(_1\), and J/C. Additional variant strains were identified for which the respective prototype strain was not identified in our study population. These variants were designated Ba\(_1\), Ba\(_2\), I\(_1\)/H, and K\(_1\). Variants I\(_1\)/H and J/C indicate omp1 sequences that are potentially the result of recombination events between omp1 sequences from 2 different chlamydia
Figure 3. Extent of concordancy for different sizes of components. Concordant components were those containing only 1 chlamydia genotype. Discordant components contained ≥2 chlamydia genotypes. The no. of components in each category is shown above the respective bar. The average no. of available specimens for components of size >8 was 3.9; size 7, 2.8; size 6, 2.3; size 5, 2.3; size 4, 2.1; size 3, 2.1. For size 2 components, only those with at least 2 available specimens were analyzed.

Concordancy between epidemiologic and molecular data.

We assessed the extent to which a given component, constructed from routinely collected contact tracing data, was concordant (containing only 1 chlamydia genotype) or discordant (containing ≥2 chlamydia genotypes). Concordancy between the sexual links, established by contact tracing, and the molecular data would be consistent with a component tracing the transmission route of a single type of chlamydia.

To establish a baseline for genotype diversity in the province, we first randomly selected 35 of our stored specimens for genotyping. Figure 3 illustrates the extent to which components were concordant with respect to chlamydia genotypes circulating within them. Overall, 86 (69.4%) of 124 components contained only 1 chlamydia genotype. Smaller components were more likely to show concordancy, ranging from 92.6% for components of 2 subjects to 24% for the largest components containing ≥8 subjects, such that discordant components were significantly larger than concordant ones (mean, 10.1 vs. 3.8 subjects, respectively; P < .001) (table 2).

For the 2 largest components with a relatively large number of specimens available for analysis, 2 types of discordant results were evident. Figure 4 shows component 23, with 82 subjects and 8 available specimens, and component 30, with 18 subjects and 7 available specimens. Although designated discordant, component 23 does appear to have largely captured the circulation pattern of 2 chlamydia genotypes, E and J. The former type appears to have been circulating largely in the northern Manitoba portion of this component and may have crossed a geographical bridge into (or out of) Winnipeg by way of one individual, whereas the J genotype was circulating in a subset of the Winnipeg individuals. In contrast, component 30, with 18 subjects, contains 4 different chlamydia genotypes with no clear pattern to their distribution within the component. In this case, the contact tracing data upon which this component was built appear to fall short of fully capturing the transmission routes of the chlamydia infecting these individuals.

Table 2. Univariate analysis of the variables associated with discordant genotyping results within components.

<table>
<thead>
<tr>
<th>Variable</th>
<th>Discordant components</th>
<th>Concordant components</th>
<th>P</th>
<th>OR (95% CI)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Coinfected</td>
<td>12</td>
<td>5</td>
<td>&lt;.001</td>
<td>7.5 (2.2–29.2)</td>
</tr>
<tr>
<td>Chlamydia infected</td>
<td>26</td>
<td>31</td>
<td>&lt;.001</td>
<td>5.0 (2.0–12.7)</td>
</tr>
<tr>
<td>Aboriginalb</td>
<td>28</td>
<td>31</td>
<td>&lt;.001</td>
<td>5.0 (2.0–12.7)</td>
</tr>
<tr>
<td>Nonaboriginal</td>
<td>10</td>
<td>55</td>
<td></td>
<td></td>
</tr>
<tr>
<td>No. of partnersc</td>
<td>≥3</td>
<td>22</td>
<td>.001</td>
<td>7.0 (1.7–40.5)</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>13</td>
<td>&lt;.01</td>
<td>3.7 (1.3–10.5)</td>
</tr>
<tr>
<td></td>
<td>1</td>
<td>3</td>
<td></td>
<td>4.0 (1.3–12.7)</td>
</tr>
<tr>
<td>Time interval, daysd</td>
<td>40.9</td>
<td>33.5</td>
<td>.99</td>
<td></td>
</tr>
<tr>
<td>Component sizea</td>
<td>10.1</td>
<td>3.8</td>
<td>&lt;.001</td>
<td></td>
</tr>
</tbody>
</table>

NOTE. Data are no. of subjects, unless otherwise noted. The P value for χ² analysis of partner number corresponds to the 2 × 3 table shown for the 3 levels of the variable. The odds ratio (OR) for this analysis corresponds to a comparison of the 1 partner category with that of the ≥3 partner category. CI, confidence interval.

a A component was classified as “coinfected” if at least 1 person in the component was infected with chlamydia and gonorrhea.

b A component was classified as “aboriginal” if at least 1 person was of aboriginal descent (ethnicity information in our dataset permitted only this limited type of categorization).

c Components were classified as 1 partner, 2 partners, or ≥3 partners, on the basis of the largest no. of sexual partners named by any case within the component.

d The time interval shown is the average no. of days between the earliest and latest diagnosis dates within concordant and discordant components.

“Component size” is the average number of individuals within concordant and discordant components.
We conducted a univariate analysis to determine whether there were any significant differences between concordant and discordant components. Five variables were analyzed on the basis of component size, coinfection, partner number, ethnicity, and dates of infection of the individuals within a given component (table 2). Discordant components were 5.0, 7.5, and 7.0 times more likely to contain an individual who was aboriginal, coinfected with gonorrhea and chlamydia, or who had named \( \geq 3 \) sex partners, respectively.

**Intercommunity patterns.** Geographic approaches have been presented as a possible means of targeting core groups for STD control programs [18–20]. Our previous analysis of large components in Manitoba suggested that geographical bridging via sexual contact may frequently connect STD core groups in different communities [10]. These latter results suggest that a coordinated approach spanning different geographic areas may be necessary when developing a targeted STD control program.

We conducted an analysis to determine the extent to which sexual contact between individuals living in different communities may contribute to successful bridge transmission of chlamydia. Of the components spanning \( >1 \) community, we determined which contained only 1 chlamydia genotype. In total, 55 components spanned \( \geq 2 \) geographically separated communities. For 34 of these 55 components, 50 specimens were available from the different communities represented within a given component. Of these 34 components, 20 (59%) were concordant across communities with respect to genotype. These data suggest that many of the geographic linkages identified by network analysis do reflect successful transmission.

We conducted a preliminary community analysis of genotype data to assess the genetic diversity of chlamydia present in small population centers. We analyzed all of the chlamydia specimens available in our stored collection from 7 towns and aboriginal reserves in Manitoba (50 specimens; table 3), ranging in population from 1212 to 15,145. The number of chlamydia genotypes varied from 4, in communities B and E (population, 8950 and 1212, respectively), to 5, in communities D and C (population, 2126 and 8039, respectively). These data suggest that chlamydia diversity in small communities is relatively high and that \( >1 \) chlamydia genotype simultaneously circulates in these small towns or reserves.

**DISCUSSION**

Manitoba is a Canadian province with a population of 1.14 million. The majority of the population (~660,000) lives in Winnipeg, the capital and only large urban center in the province. Most of the population outside Winnipeg lives in the southern portion of the province. At the time data were collected for this study, there were 61 aboriginal reserves in the province with 18 of these reserves accessible by air only. The sexual network we analyzed was based on routinely collected data for 4544 STD case subjects and contacts. In total, the network contained 1503 components, with the largest containing 82 people. Some initial analysis of this data has been published elsewhere [10, 21]. In the present report, we describe a linkage of chlamydia genotype data with sexual network data. To our knowledge, this is the first study to examine the molecular epidemiology of *C. trachomatis* within the context of large sexual networks.

In conducting this study, we generated a large collection of genotype data for chlamydia, consisting of 359 typed specimens. Fifteen distinct chlamydia types were identified; 5 types contained *omp1* VD sequences identical to the prototype serovar strains analyzed by Yuan et al. [17], and 10 were variants of these prototypes. A search in GenBank and the published literature indicated that none of the variants we observed is newly identified. Four of the variants were present in Manitoba 6 years prior to our study, when Yang et al. [16] conducted their molecular survey of chlamydia types in Manitoba (a fifth variant we identified, J/C, may match the C-like/J-like variant identified by Yang et al. [16]; however, we were unable to obtain sufficient nucleotide sequence data to confirm this possibility). An E and D variant type seen in 1992 was absent in our sample, whereas we identified 5 variants, D1, D2, D3, D4, and G1, that were not seen in 1992. Given the smaller sample size of Yang et al. [16], it is uncertain whether these latter 5 types of chlamydia have emerged in Manitoba since 1992 or if they were already present in low numbers at that time. Overall, this data suggests an endemic presence in Manitoba of several chlamydia genotypes, with little immigration of new strains and/or little occurrence of *omp1* nucleotide sequence variation in the province between the time points of the 2 studies.

We combined our network genotype data with sexual network data to observe the extent to which molecular typing data for *C. trachomatis* would agree with the proposed transmission routes within the sexual networks constructed from contact tracing data. The majority of the components containing individuals linked either directly or indirectly by sexual contact were concordant with respect to chlamydia type, which indicate that network analysis on the basis of routinely collected data frequently does reflect the transmission routes of individual chlamydia types. In addition, of the components that contained individuals from different geographic areas and for which specimens were available, 59% were concordant with respect to chlamydia type. These data indicate that, despite the vast physical distances involved, the geographic connections identified by network analysis do frequently reflect transmission events. Network analysis could therefore be used to identify the different areas in a region where it would be useful to coordinate STD control efforts.

Several factors were associated with the presence of \( \geq 2 \) ge-
Figure 4. Distribution of chlamydia genotypes within 2 of the largest components. Component 23 contains 82 people. Component 30 contains 18 people. For its size, component 23 had a limited number of specimens available, because many of the case subjects were diagnosed in the 3 month period preceding storage of chlamydia-positive Chlamydiazyme specimens. Black circles, Chlamydia-infected case subjects from which a chlamydia specimen was available for genotyping; gray circles, chlamydia-infected case subjects from which a specimen was not available; gray squares, gonorrhea-infected case subjects; black circles and gray squares or gray circles and gray squares, coinfected case subjects; gray rectangles, subjects with negative or unknown test results. Letters represent the chlamydia genotypes isolated from a given case subject.

Table 3. Genotypic diversity of Chlamydia trachomatis within specific geographic locales.

<table>
<thead>
<tr>
<th>Community</th>
<th>Population</th>
<th>Genotype</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>E</td>
<td>D</td>
</tr>
<tr>
<td>A</td>
<td>15,145</td>
<td>5</td>
</tr>
<tr>
<td>B</td>
<td>8950</td>
<td>2</td>
</tr>
<tr>
<td>C</td>
<td>8039</td>
<td>3</td>
</tr>
<tr>
<td>D</td>
<td>2126</td>
<td>3</td>
</tr>
<tr>
<td>E</td>
<td>1212</td>
<td>2</td>
</tr>
</tbody>
</table>

The association between multiple chlamydia types within a component and aboriginal status may reflect the difficulties associated with STD control in small communities. Some aboriginal communities in Manitoba are small, with populations of ≤1000. This characteristic is true of component 30 in figure 4, which is centered on a small, largely aboriginal, community in Manitoba. Given that the end result of effective contact tracing would be the tracking of individual chlamydia genotypes, the random dispersal of chlamydia types in this component suggests that either additional sexual connections have been missed or delays in locating individuals have created a temporal disconnection between the molecular and social data. Anonymity could be a concern in small, close-knit communities and individuals may, therefore, be reluctant to provide a complete list of their sex partners. Thus, components based on contact tracing from these communities would fail to fully capture the actual transmission pathways. Anonymity issues may also contribute to individuals not attending their local medical clinic but, instead, waiting until they have an opportunity to seek medical care in a larger urban center. Depending on the rate of sex partner change, these delays may ultimately result in spurious connections being identified with respect to degree of interconnectivity between those individuals [22].
the chlamydia genotypes actually present at the different time points. When a combination of molecular and social data reveals patterns of this type, it may indicate areas or circumstances in which STD control may not be meeting its goals.

Although geographic approaches to STD control have proven effective in lowering incidence rates [20], this approach does not incorporate the effects of connections between communities. A strict geographic approach focused on 1 area could result in an equilibrium being reached between local control efforts and reseeding of the targeted area by chlamydia from geographically remote, but socially continuous core groups in other areas. Our analysis of chlamydia types in small geographic centers in Manitoba (table 3) demonstrated that even relatively small population centers do not act as a focus of infection for a single chlamydia type. In combination with the extensive geographic connections revealed by network analysis (see map in Wylie and Jolly [10]), the picture that emerges of STD transmission is one of individual communities acting as staging points for the maintenance and transmission of multiple chlamydia types within the context of the larger sexual network in the area.

In summary, we identified considerable genetic diversity in the number of chlamydia genotypes circulating within Manitoba. Many of these chlamydia genotypes appear to have persisted in the province over ~6 year period. For the majority of components, genotypic data were concordant with epidemiologic data, suggesting that routinely collected contact tracing data is a valid means of constructing sexual networks. In some instances a lack of concordancy may reflect the identification of a core group or, alternatively, identify areas where STD control programs may need to be changed or modified.

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References


