Chlamydia Transmission: Concurrency, Reproduction Number, and the Epidemic Trajectory

John J. Potterat,[1] Helen Zimmerman-Rogers,[1] Stephen Q. Muth,[1] Richard B. Rothenberg,[2] David L. Green,[1] Jerry E. Taylor,[3] Mandy S. Bonney,[1] and Helen A. White[3]

To identify factors that influence individual and group transmission of *Chlamydia*, the authors conducted community-wide contact tracing of chlamydia cases in Colorado Springs, Colorado, from mid-1996 to mid-1997. Case patients identified persons with whom they had had contact during the 6 months preceding diagnosis; contacts were actively sought and offered DNA amplification testing. Sexual contact networks were used to identify "source cases" and "spread cases," permitting estimation of the basic reproduction number (R_0) for individuals and groups. Network and epidemiologic factors influencing R_0 were assessed using univariate and multivariate procedures. Of 1,309 case patients, 1,131 (86%) were interviewed, and 2,409 contacts were identified. The 1,131 interviewed cases yielded 623.9 computed spread cases, for an overall R_0 of 0.55. Few subgroups analyzed yielded a mean R_0 exceeding unity—an observation in keeping with routine surveillance information which suggests that chlamydia incidence is declining in Colorado Springs. Concurrency, a network measure of simultaneous partnerships, was the most powerful predictor of transmission. Direct estimation of basic reproduction numbers for chlamydia using contact tracing techniques is feasible and can produce useful data with which to prioritize control efforts, evaluate interventions, and gauge the place of chlamydia on the epidemic continuum. *Am J Epidemiol* 1999;150:1331-9.

chlamydia infections; *Chlamydia trachomatis*; communicable disease control; disease transmission; sexual partners; sexually transmitted diseases, bacterial

In an analysis of the dynamics of sexually transmitted disease (STD) epidemics, Wasserheit and Aral (1) proposed a classification of epidemic phases and of their determinants over time. They identified five phases in the spread of an STD: introduction, establishment, growth, maintenance, and decline. Each phase is characterized by a basic reproduction number (R_0) representing the average number of infected contacts generated by infected persons. This number is unity at endemic equilibrium; on average, cases are replaced 1:1 in the disease pool. A number below 1.0 signals declining incidence, and a number greater than 1.0 is associated with epidemic spread (2). This measure thus reflects a group's ability to sustain disease propagation, and the magnitude of the number reflects the intensity of transmission.

As Dietz (3) summarized in 1993 (3), the quantity R_0 has its origins in demography ("la reproductivité nette" (4)) and population ecology ("basic reproduction rate" (5)). It was first applied to directly transmitted infections independently in 1975 by Dietz ("basic reproduction number" (6)) and Hethcote ("infectious contact number" (7)). Diekmann et al., who used the term "reproduction ratio," defined the concept rigorously as "the expected number of secondary cases caused by one typical infected individual during its entire period of infectiousness, in a population consisting of susceptibles only" (8, p. 325). In practice, issues such as migration and immunity forbid strict adherence to this definition, but the concept has been nevertheless robust in its contribution to understanding infectious disease dynamics.

In principle, this basic reproduction number (the term we use here) should be estimable from individual-level data, that is, from observing the number of persons to whom an infected individual spreads the disease. In this context, the reproduction number can be an attribute of a person, a group, or a population. In STD settings, however, efforts to estimate reproduction

numbers have relied on the relation of R_0 to clinical parameters (duration of infectiousness, transmissibility, rate of new partner acquisition) rather than on contact data (9, 10). The prospect of successfully basing estimates directly on such data (that is, interviewing index cases and tracing their sexual partners) is thought to range from too difficult (11) to "almost never feasible" (12). This assessment springs from the well known difficulties attending the collection of sufficiently complete and reliable contact tracing data from STD patients. To our knowledge, only one community-wide, empirical estimate of reproduction numbers for an STD (gonorrhea) has been performed, but this estimate was limited to an analysis of male cases only (13).

The availability of community-wide data on a large proportion of *Chlamydia trachomatis* cases of both sexes and their contacts—collected to delineate infectious periods (14)—provided us with the opportunity to estimate individual reproduction numbers directly for chlamydial infection in Colorado Springs, Colorado. (The data used in the present study differ slightly from those presented in a previous report (14). These differences are accounted for by the arrival of late reports and by data corrections stemming from sexual network analyses, which revealed previously unnoticed case-contact connections—notably contacts that should have been named but were not.) In this study, we use these individual-level data to estimate subgroup and population reproduction numbers, and thus to position this community on the epidemic continuum defined by Wasserheit and Aral (1).

MATERIALS AND METHODS

Data collection methods and general results are described elsewhere (14). Briefly, case patients with genital chlamydia infection reported from all (public, private, and military) health care providers in the Colorado Springs Standard Metropolitan Statistical Area (1995 estimated population = 465,000 (50 percent male; 82 percent White, 8 percent Hispanic, 7 percent African-American, and 3 percent Other)) were offered contact tracing services by experienced civilian and military disease intervention specialists between July 1, 1996, and June 30, 1997. Disease intervention specialists interviewed index cases and actively sought named contacts. Index cases were asked to identify all contacts and their demographic attributes for the 180 days preceding treatment. If this interval yielded only a single contact, the notification was extended to identify a previous contact (if one existed). Contacts were tested for evidence of *C. trachomatis* infection using DNA amplification technology (LCx assay; Abbott Laboratories, Chicago, Illinois).

Source versus spread determination

The definitions and criteria for this study were based on those used in our previous report of reproduction numbers for gonorrhea (13). A "source contact" was a person from whom the index case presumptively acquired infection. This person was designated on the basis of multiple data sources (see below) and may or may not have been demonstrated to be positive for chlamydia. A "spread contact" was a person with laboratory-confirmed *C. trachomatis* infection whose first exposure to the index case occurred after that of the source contact. A "possible spread contact" was a person judged to have been exposed after the index case was assumed to be infectious but for whom laboratory confirmation was not available (because the contact was not located, or was treated without the benefit of testing, or refused examination). An "improbable spread contact" was a person judged to have been exposed after the index case was assumed to be infectious but for whom laboratory testing was negative for chlamydia. A "condom-use spread contact" was a person judged to have been exposed after the index case was assumed to be infectious but who reported 100 percent condom use with the index case. An "indeterminate contact" was a person for whom exposure information was missing or insufficiently complete to make a determination. An "extraneous contact" was a person whose last sexual exposure had occurred before the first sexual exposure between the index case and the source contact.

Although we have entered information on STD index cases and their contacts into relational microcomputer databases since 1994, chlamydia contact interviewing records for the study period were manually analyzed by three people: the two senior authors and one of six other (rotating) disease intervention specialists. Our STD relational databases were searched during manual case review. Whenever contacts of an index case could be demonstrably linked, by manual and computer-aided analyses, to the same sexual network as that of another index case, such case-contact records were merged into "lots" prior to assessment of the evidence. Multiple data sources were used to classify persons into one of the seven categories enumerated above. Data were gathered on reported dates of first and last sexual exposure, along with frequency, between the index case and his or her contact(s); reported condom use between index cases and their respective contacts; chlamydia test results, when available; dates of chlamydia treatment; dates of chlamydia diagnostic testing, if done; dates and duration of signs or symptoms associated with genitourinary infection; and self-reported history of antecedent chlamydia infection. Ancillary information was supplied by examination of informa-

tion in the "lots" or groupings of contacts. Because some of our chlamydia patients were coinfected with gonorrhea or exposed to gonorrhea, we reviewed associated gonorrhea interview records to assist in our "source versus spread" determinations. Assignment of contact status was predictably simpler for persons who were serially monogamous (the majority of interviewed persons (see "Results")).

Assigning values to each contact

To compensate for deficiencies in contact tracing outcomes, we assigned each category of contacts a value from 0.0 to 1.0 (13). These values are the probabilities that a member of the category was both infected and represented a contribution to spread of disease by the index case. Source and extraneous contacts were assigned a value of 0.0. A value of 1.0 was given to each spread contact. A possible spread contact, irrespective of gender, was assigned a value of 0.67 (meaning that the person represented 0.67 of a case), based on a published approximation of bidirectional chlamydia transmission probabilities (15). Improbable spread contacts were arbitrarily assigned a value of 0.1, to compensate for the chlamydia test's imperfect sensitivity. Condom-use spread contacts were assigned a value of 0.35 for male contacts and of 0.80 for female contacts. These estimates were based on a subset of 71 of our sexual contacts (43 men and 28 women) for whom the index case reported invariable condom use and for whom chlamydia test results were available. Fifteen of these men (35 percent) and 22 of these women (79 percent) had positive chlamydia tests. Last, the few indeterminate contacts were arbitrarily assigned a value of 0.33, an estimate approximately midway between "possible" and "improbable." The values for each index case's contacts were added to produce an individual reproduction number for each index case. Index cases were classified as transmitters if their R_0 exceeded 1.0, indicating that there was a source contact and the potential for at least one transmission thereafter. In one analysis, we also used a more stringent definition ($R_0 \geq 2.0$) for classification as a transmitter.

Subgroups

We examined univariate associations of chlamydia infection with a set of demographic, epidemiologic, and network variables that might bear a relation to the propensity to transmit disease (R_0). Residential stability was defined as duration of residence at one's present address (self-reported); it was categorized as low (duration $\leq$ 30 days), medium (30 days < duration < 365 days), and high (duration $\geq$ 365 days). We grouped

diagnosed cases into two categories per sex according to clinical presentation. Male cases were classified as urethrally symptomatic or asymptomatic (14). Women were classified as those with pelvic inflammatory disease and those without it. Previous chlamydia infection was based on self-report and on a search of our computerized STD surveillance records (1994–1997). Cases for which all contacts resided in the Colorado Springs metropolitan area were classified as endogenous; cases for which contacts included anyone residing outside of the metropolitan area were classified as exogenous. Index cases for which a contact was assessed as the source contact were classified as "source identified"; those for whom no contact could be assigned a source status were classified as "no source identified."

Routinely collected contact tracing information permitted delineation of two measures of network structure. First, we classified persons by their self-identified ethnicity as White (non-Hispanic), African-American, or Hispanic (regardless of other ethnic designations). Persons who shared the same ethnicity with all of their contacts were judged to have assortative (like-with-like) mixing with regard to ethnicity. Those with at least one contact of differing ethnicity were termed disassortative.

We assessed the concurrency of partnerships using the index case's first and last dates of sexual exposure with each contact. An index case with n contacts will have $n(n-1)/2$ pairs of contacts. Each possible pair of contacts for each index case was assessed to determine whether the index case had overlapping sexual exposure with those two people. A concurrency number was assigned to each index case that was equal to the number of concurrent pairs in that case's sexual network. Cases with more than one contact but no overlapping exposures were considered to be serially monogamous.

Analyses

We examined the R_0 associated with a number of groups defined by univariate characteristics. Since the R_0 is calculated as a sum of estimates for which the variances are unknown, we did not attempt formal statistical testing for this descriptive analysis. We used a number of these variables to construct an ordinary least squares regression model with R_0 as the dependent variable. We conducted a parallel analysis with logistic regression—using transmitter status ($R_0 \leq 2.0$) as a binary variable—to determine the odds ratios associated with important potential predictors of transmission. We used standard surveillance methods to calculate chlamydia occurrence in Colorado Springs in ecologic association with control efforts.

RESULTS

Characteristics of Index cases

During the study period, 1,309 cases (849 in females, 460 in males) of genital chlamydia infection in persons aged >12 years were reported to our health department. Among female cases, 52 percent were White, 26 percent African-American, 16 percent Hispanic, and 6 percent were of other ethnicity; the mean age was 20.7 years (standard deviation 4.9). Among male cases, 35 percent were White, 46 percent African-American, 16 percent Hispanic, and 3 percent Other; the mean age was 23.4 years (standard deviation 5.2). Eighty-six percent (1,131/1,309) of the case patients were interviewed for contacts; all nominated contacts were of the opposite sex (except for one man and one woman who each named a contact from each sex). There were no significant differences in the sex, age, or ethnic distribution of interviewed index cases compared with those not interviewed (14). Patients in the private sector were less likely to be interviewed (282/386) than those in the public (541/586) and military (308/337) sectors (χ^2 = 83; odds ratio = 4.23, 95 percent confidence interval 3.01, 5.95; $p < 0.001$ for private sector vs. public and military sectors combined).

Interviewed cases and their contacts

Persons with chlamydia came to the interview process as clinic volunteers (38.6 percent), as routine screenees (31.8 percent), and as contacts of interviewed cases (29.6 percent; among men, 55.6 percent were contacts). The 1,131 interviewed case patients named 2,409 contacts (2.1 contacts per interview). Of these, 701 (29 percent) were diagnosed with chlamydia; 359 (15 percent) were not infected; 40 (1.7 percent) were treated without being tested; 45 (1.9 percent) refused to participate; and 1,264 (52.5 percent) were either not locatable or not located. Of 2,402 contacts for whom information on frequency of exposure was available, 488 (20.3 percent) had one-time exposures, 565 (23.5 percent) had 2–5 exposures, and 1,349 (56.2 percent) had more than five sexual exposures. Twenty-four percent of the sexual partners of index cases were persons with addresses exogenous to the Colorado Springs area. As we reported previously (14), condom use was minimal, with less than 7 percent of all sexual exposures being protected by condoms.

Of 405 index case interviews in men, 87 men (21.5 percent) were shown to have failed to report all of their contacts—a conclusion based on reports by the men's female sexual contacts and/or on failure to identify a source contact. Using similar criteria, 84 (11.6 percent) of 726 interviews in women

were judged to lack complete contact information initially.

Chlamydia trends

Consistent reporting for chlamydia infection in public and military medical venues of the Colorado Springs Standard Metropolitan Statistical Area began in 1988, nearly 4 years before *C. trachomatis* infection became reportable in Colorado. Trends derived from these two sentinel sectors are presented in figure 1. During the 10-year period of observation, chlamydia rates per 100,000 population declined by one third.

Basic reproduction numbers for individuals, subgroups, and the population

From the data gathered in this study, it appears that 46.5 percent of those infected with chlamydia did not spread the disease (figure 2). An additional 21.3 percent had R_0's less than 1.0. At the other end of the spectrum, 5.4 percent of the population were active transmitters ($R_0 \geq 2.0$). The estimated overall reproduction number for the entire cohort was 0.55, substantially below the endemic maintenance level of 1.0 (table 1). The reproduction number did not exceed unity for any clinical group, though asymptomatic men closely approached it ($R_0 = 0.94$). Had all eligible contacts (those without a negative test, and removing the extraneous contacts ($n = 764$)) been assigned a spread value of 1.0, the overall R_0 would have been 0.68.

Reproduction numbers by subgroup

The range of reproduction numbers for groups of either sex according to various demographic, clinical, and epidemiologic characteristics was 0.05–2.29 (table 2). Other than for the two subgroups for which the reproduction number exceeded unity by definition (male and female transmitters), only a few approached or exceeded unity. Highest among these were cases of both sexes who had any concurrent contacts (1.36 for men, 1.18 for women). Women diagnosed with dual gonorrhea/chlamydia infection and male index cases with no identified source (who by definition—since no source was found—probably had more contacts than they revealed) had R_0's exceeding unity. The R_0 gradient of symptomatic men by reported duration of urethral symptoms revealed that a long duration of symptoms, like asymptomaticity, is associated with an R_0 close to unity. Disassortative mixing for chlamydia patients was a predictor of a relatively high R_0, as was suggested by previous data on gonorrhea patients in Colorado Springs (16).
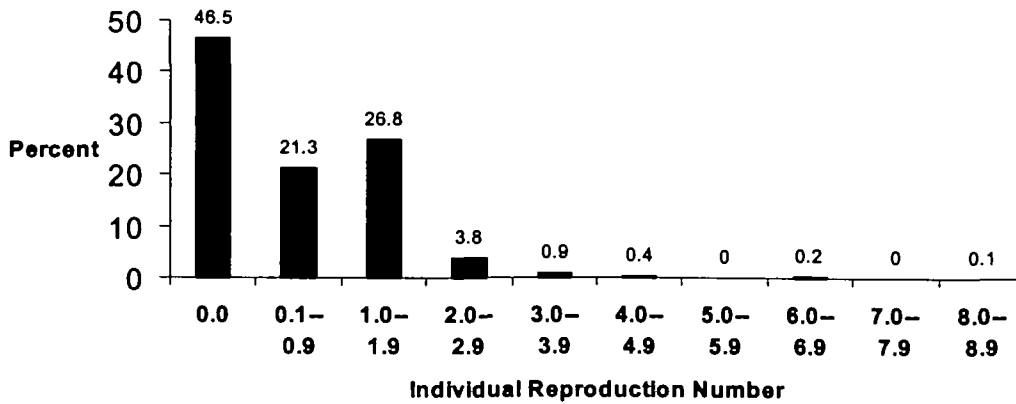
FIGURE 1. Frequency distribution of individual reproduction numbers (R_0) among *Chlamydia* index case patients interviewed during the study period, Colorado Springs, Colorado, 1996–1997.

Reproduction numbers for men were uniformly higher than those for women in all but two subgroups (persons with dual chlamydia-gonorrhea infection and persons of "other" ethnicity). Patients whose cases were diagnosed in the public and military sectors, particularly men, had notably higher R_0's than those whose cases emanated from private venues. Finally, men who reported a previous chlamydia infection had an R_0 approaching unity.

Combined influence of important factors

Using logistic regression, the presence of concurrent sexual contacts (compared with serial monogamy)

bore the strongest relation to transmitter status (that is, $R_0 \geq 1.0$) (adjusted odds ratio = 3.2; unadjusted odds ratio = 6.7) (table 3). Although, as expected, concurrency was highly correlated with number of sexual contacts (Pearson's $r = 0.66$; $p < 0.001$), the odds ratio for concurrency was twice as great as the odds ratio for the reported number of sexual contacts. An interaction reduced the odds ratio for concurrency, but it remained significant and higher than that for number of partners (see footnote in table 3). A public or military site for initial diagnosis also had significant influence on being a transmitter. A prior history of chlamydia was a somewhat weaker but still significant predictor. Being female and (for men) having symptoms were both
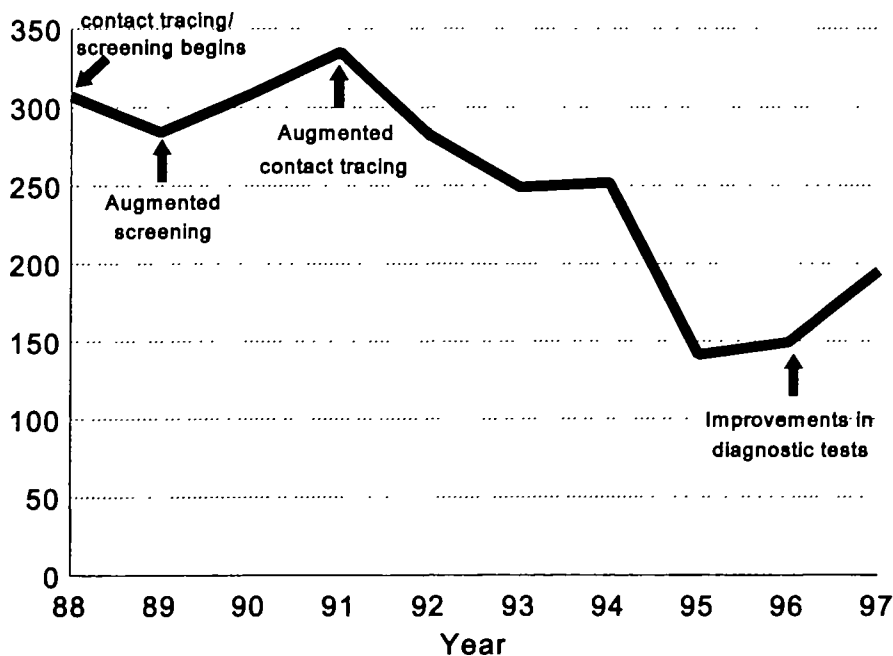
FIGURE 2. Reported numbers of public and military cases of *Chlamydia trachomatis* per 100,000 population in Colorado Springs, Colorado, 1988–1997. Private sector cases were excluded because of reporting artifacts.

TABLE 1. Distribution of patients with *Chlamydia trachomatis* by clinical category and by category of their respective sexual contacts, Colorado Springs, Colorado, July 1996–June 1997

Clinical group	Contact category*								R_0†
	Source	Spread	Possible spread	Improbable spread	Condom-use spread	In-determinate	Extraneous	Total	
Symptomatic men ($n = 229$)	206 (0)‡	79 (79.0)	46 (30.8)	33 (3.3)	11 (8.8)	0 (0.0)	125 (0)	(121.9)	0.53
Asymptomatic men ($n = 176$)	142 (0)	120 (120.0)	32 (21.4)	22 (2.2)	26 (20.8)	3 (1.0)	45 (0)	(165.4)	0.94
Women with pelvic inflammatory disease ($n = 187$)	177 (0)	38 (38.0)	51 (34.2)	39 (3.9)	9 (3.2)	1 (0.3)	86 (0)	(79.6)	0.43
Women without pelvic inflammatory disease ($n = 539$)	500 (0)	125 (125.0)	158 (105.9)	105 (10.5)	38 (13.3)	7 (2.3)	185 (0)	(257.0)	0.48
Total ($n = 1,131$)	1,025 (0)	362 (362.0)	287 (192.3)	199 (19.9)	84 (46.1)	11 (3.6)	441 (0)	(623.9)	0.55

* See "Materials and Methods" for definitions of the types of contacts. Values assigned to each contact type: source = 0; spread = 1.0; possible spread = 0.67; improbable spread = 0.1; condom-use spread (male to female) = 0.8; condom-use spread (female to male) = 0.35; indeterminate = 0.33; extraneous = 0.

† Reproduction number, estimated by dividing the total number of spread cases (in parentheses) by the number of index cases.

‡ Numbers in parentheses, computed value.

"protective" against transmitting the infection. With use of a more stringent definition of transmitter ($R_0 \geq 2.0$), there was some alteration in the size of the odds ratio, but the underlying pattern was not changed, except for the loss of significance of symptoms as a predictive factor. In a least squares multiple regression analysis, using the actual R_0 as the dependent variable, the six significant factors listed in table 3 accounted for 50 percent of the variance in the model. In this setting, dependent to some extent on the order in which variables are placed into the model, the number of contacts accounted for a greater proportion of the variance than did concurrency.

DISCUSSION

In this Colorado Springs study, the estimated overall reproduction number for genital chlamydia infection (0.55) was well below unity, in keeping with the observed decline in reported cases. The findings suggest that Colorado Springs was in the declining disease incidence phase on the Wasserheit-Aral scale (1) during the 1996–1997 study period. The observation of reproduction numbers below unity for nearly all subgroups studied further buttresses that conclusion. The lack of complete elimination of chlamydia from Colorado Springs is related to the fact that the city is not a closed population; importation of cases is suggested by the high proportion (nearly one quarter) of exogenous sexual partners. This result is in keeping with the mathematical modeling result of Stigum et al. (10), who stated that diseases for which $R_0 < 1$ for the

majority of the population are strongly affected by in-migration.

Separating true incidence changes from artifactual changes in chlamydia case reporting and detection practices is difficult. Vagaries stemming from changes in reporting requirements and compliance, in the intensity of public health interventions such as screening, in contact tracing, and in the implementation of superior testing technologies, as well as random variation, complicate the interpretation of chlamydia trends. This holds true for Colorado Springs, where focal contact tracing, initiated in 1988, was intensified starting in 1996; where targeted screening, initiated in mid-1987, was expanded in 1989; and where implementation of ligase chain reaction technology, initiated in mid-1996, was expanded a year later (figure 1). In any event, observed rates of chlamydia infection per 100,000 population in Colorado Springs declined by one third between 1988 and 1997. The association of this decrease with the empirically derived overall reproduction number of 0.55 for the 1996–1997 study period suggests that these two values are meaningfully related.

Our study used contact tracing data to arrive at direct estimates of chlamydia reproduction numbers in Colorado Springs. Such data are notorious for their incompleteness: Not all cases are enrolled; patients fail to report certain contacts; identified contacts may not be located or tested; and the infectious interval ("interview period") chosen may fail to capture "historical" contacts that are epidemiologically relevant (14). We attempted to compensate for such predictable shortcomings by enrolling a high proportion (86 percent) of

TABLE 2. Estimated reproduction numbers (R_0) for *Chlamydia* index cases, according to sex and various demographic, clinical, and epidemiologic characteristics, Colorado Springs, Colorado, July 1996–June 1997*

Characteristic	Men		Women	
	No.	R_0	No.	R_0
Source of report				
Public	244	0.76	297	0.64
Private	30	0.41	252	0.34
Military	131	0.68	177	0.35
Age (years)				
≤19	98	0.80	367	0.49
>19	307	0.68	359	0.44
Residential stability				
Low	26	0.91	43	0.62
Medium	178	0.63	309	0.41
High	130	0.84	254	0.42
Ethnicity				
White	143	0.56	374	0.46
African-American	186	0.82	188	0.45
Hispanic	62	0.78	122	0.42
Other	13	0.51	40	0.76
Disease history				
Previous *C. trachomatis*	52	0.96	175	0.41
No previous *C. trachomatis*	353	0.67	551	0.48
C. trachomatis only	359	0.70	682	0.43
Coinfected with *C. trachomatis* and *Neisseria gonorrhoeae*	46	0.77	44	1.05
Symptomaticity				
Asymptomatic	176	0.94		
≥2 weeks of symptoms	142	0.37		
2–3 weeks of symptoms	8	0.77		
>3 weeks of symptoms	27	0.96		
Unrecorded	52	0.71		
Concurrency				
Single partner	195	0.19	408	0.05
Serial partners	88	0.96	146	0.77
Concurrent partners	122	1.36	172	1.18
Mixing pattern				
Assortative	203	0.57	375	0.31
Disassortative	202	0.85	351	0.63
Location of contacts				
Endogenous	293	0.64	532	0.36
Exogenous	112	0.90	194	0.74
Source of infection				
Source identified	340	0.60	663	0.43
No source identified	65	1.26	63	0.85
Transmitter status				
Transmitter	57	2.29	86	2.05
Nontransmitter	348	0.45	640	0.25

* Categories represent the population of interviewed index cases (n = 1,131), except "residential stability" (n = 940 (83%)) and "ethnicity" (n = 1,128 (99.7%)).

TABLE 3. Results of a multiple logistic regression analysis comparing the relative effect of key variables on determining whether or not a person is a transmitter of *Chlamydia trachomatis* (R_0 > 1.0), Colorado Springs, Colorado, July 1996–June 1997

Variable	Odds ratio*	p value
Concurrent contacts	3.2	<0.001
Reported from a public or military source	1.9	<0.01
No. of contacts	1.6	<0.001
Prior history of *Chlamydia* infection	1.4	<0.01
Female sex	0.3	<0.001
Presence of symptoms (males)	0.4	<0.001
Age	1.0	NS†
Married	1.1	NS
African-American ethnicity	1.0	NS
Hispanic ethnicity	0.9	NS
Other ethnicity	1.5	NS

* Introducing a term for an interaction between concurrency (dichotomized to yes or no) and number of contacts reduced the odds ratio for concurrent contacts from 3.2 to 1.8 and the odds ratio for number of contacts from 1.6 to 1.5. The interaction term had an odds ratio of 1.5. Results similar to those described, with and without inclusion of the interaction term, were obtained when using "*Chlamydia* transmitter" ($R_0 \geq 2.0$) as the dependent variable (see text).

† NS, not significant.

our community's reported cases, by using sexual network analysis to add unidirectionally named contacts of cases that should have been named as partners, by using experienced contact tracers to locate reported contacts, and by using flexible infectious interval periods to capture presumably relevant contacts. Although half of reported contacts were not located for examination, the impact on the reliability of our findings is likely to have been modest. The central task in our analyses was to assign a role (e.g., source vs. spread) to each reported contact and then to reasonably estimate the probability of that contact's potentially contributing to disease spread, using the substantial amount of contextual information available. Although it is desirable, obtaining chlamydia test results for all relevant contacts is not crucial to the assignment of source-spread status. Though it was imperfect, our "committee" approach produced a consistent and reproducible classification. This experience challenges the belief that usable contact tracing data are too difficult to obtain.

From the available data, we could not determine the extent to which spontaneous clearance of *C. trachomatis* affected our findings. A recent study suggests that approximately one quarter of chlamydia-infected women, and perhaps one half of infected men, harbor transient (in terms of weeks) *C. trachomatis* infection (17). These transiently infected patients, potential spreaders, are likely to be negative upon testing should this testing occur months after presumed acquisition of infection. Thus, for our calculations, the assignment of 0.1 as a value for contacts classified as improbable spreaders may have been an underestimate. However, this potential underestimate may have been balanced by the likelihood that some persons classified as "possible spread" contacts were immune (18) and that the probability we used (0.67) for acquisition of infection was, for them, an overestimate.

The skewed female:male ratio in chlamydia index cases is customarily thought to reflect underdetection of cases in men. Such underdetection may be attributable to the infection's high rate of asymptomaticity in

men (15, 19), to the dearth of screening programs for men (14), and to the use of relatively insensitive (non-DNA amplification) tests. However, some proportion of "missing" male cases may be related to the higher estimated rate of spontaneous clearance of *C. trachomatis* in infected men compared with infected women (17). Should data from the recent study of spontaneous clearance (17) be confirmed with larger numbers of patients, a ratio approaching parity between the sexes would not be expected.

In these data, concurrency of sexual partnerships played a major role in chlamydia transmission. Several definitions of concurrency are available; we used the one that emerges easily from contact tracing information: overlapping periods of sexual activity. In fact, this is potential concurrency, since documentation of true concurrency would require the exact dating of sexual episodes and demonstration that an encounter with one contact was followed by an encounter with a second contact, and then a reencounter with the first. Our measure of concurrency was thus a surrogate. Since we used the number of overlapping pairs in an index case's sexual network, the measure may also have been confounded by the number of sexual contacts. However, the analysis revealed that the effect of concurrency was not confounded by number of contacts, and suggests that the number of contacts is actually less important than the type of interaction with them. Our other network measure—the type of mixing by ethnicity—demonstrated that disassortative mixing appears to play a more important role in chlamydia transmission than assortative mixing, though the effect was not strong in this population.

The phenomenon of concurrency, or simultaneous contacts, is actually a simple example of a network "microstructure" (sometimes referred to as a "cycle"). These are groupings of individuals who are intensely interconnected in ways that can be formally described (20). We have proposed the importance of microstructures for maintaining disease transmission (21–23), but we suspect that the analytic approach used here would not work as well in network and epidemiologic settings that are dominated by high-order microstructures (23). For example, Rothenberg et al. were unable to delineate source-spread relationships in a network of syphilis patients and their contacts with multiple interconnections and multiple overlapping sexual exposure dates (22). In such settings, people may have overlapping exposures to several other persons who are infected. Although the method of assigning source and spread may be problematic in such settings, the importance of network structures in disease propagation is reinforced.

In conclusion, this attempt to estimate reproduction numbers using extensive contact tracing data is a

workable way of tracking community disease transmission in the face of reporting and detection artifacts. It remains to be shown whether sampling from available chlamydia cases can yield estimates as reliable as those derived from using virtually the entire available cohort. In either case, however, such data may prove useful in prioritizing contact tracing efforts, in evaluating interventions, in dampening the temptation to claim credit for incidence changes when such changes may be more demonstrably attributable to changing sexual activity, and in selecting phase-appropriate intervention strategies.

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