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Genotype-specific Concordance of *Chlamydia trachomatis* Genital Infection within Heterosexual Partnerships

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Abstract

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Conflict of interest For the remaining authors none were declared.

Background—Sexual transmission rates of *Chlamydia trachomatis (Ct)* cannot be measured directly; however, the study of concordance of *Ct* infection in sexual partnerships (dyads) can help to illuminate factors influencing *Ct* transmission.

Methods—Heterosexual men and women with *Ct* infection and their sex partners were enrolled and partner-specific coital and behavioral data collected for the prior 30 days. Microbiological data included *Ct* culture, nucleic acid amplification testing (NAAT), quantitative *Ct* polymerase chain reaction (qPCR), and *ompA* genotyping. We measured *Ct* concordance in dyads, and factors (correlates) associated with concordance.

Results—121 women and 125 men formed 128 dyads. Overall, 72.9% of male partners of NAAT-positive women and 68.6% of female partners of NAAT-positive men were *Ct*-infected. Concordance was more common in dyads with culture-positive members (78.6% of male partners, 77% of female partners). Partners of women and men who were NAAT-positive only had lower concordance (33.3%, 46.4%, respectively). Women in concordant dyads had significantly higher median endocervical qPCR values (3,032) compared with CT-infected women in discordant dyads (1,013 IFU DNA equivalents per ml), $p<0.01$. Among 54 *Ct*-concordant dyads with *ompA* genotype data for both members, 96.2% had identical genotypes.

Conclusions—Higher organism load appears associated with concordance among women. Same-genotype **c**hlamydial concordance was high in sexual partnerships. No behavioral factors were sufficiently discriminating to guide partner services activities. Findings may help model coitus-specific transmission probabilities.

Keywords

Chlamydia trachomatis; concordance; transmission; sexual partnerships

INTRODUCTION

Chlamydia trachomatis (Ct) is the most common cause of bacterial sexually transmitted infections (STI), with 1.4 million cases reported in the U.S. in 2014 [1] and more than twice that number estimated to occur each year. *Ct* infection is associated with an increased risk of pelvic inflammatory disease, ectopic pregnancy and tubal infertility [2] but infection is usually asymptomatic and many cases are detected only by screening. *Ct* case rates have risen over the past decade [1], likely as a result of increased screening and widespread use of sensitive nucleic acid amplification tests (NAATs); however, population prevalence has decreased during the same period [3]. These seemingly contradictory observations may be related to the use of NAATs that detect infections with a lower organism-load than can be detected by culture or other non-amplified methods. If people with NAAT-positive, but culture negative infections (NAAT-only infections) pose a lower risk of transmission to their sex partners, incidence could increase at the same time population prevalence decreases.

Concordance studies of STI examine the extent to which sex partners are infected with the same STI (concordance); partnerships wherein only one member is infected are considered discordant. Robust predictors of *Ct* concordance in sex partnerships could be useful for prioritizing provider-led partner notification, an effective but resource-intensive intervention that involves eliciting the names and contact details for the sex partner(s) of a person with an

STI in order to notify them of their exposure and ensure testing and treatment. Because of the vast numbers of diagnosed chlamydial infections, provider-led partner notification is not widely used to identify sex partners of *Ct*-infected persons. Data from concordance studies with detailed coital and behavioral information specific to the sexual partnership could also be used to estimate the probability of *Ct* transmission per coital act.

Past *Ct* concordance studies have been limited by: small sample sizes, index cases of a single sex, diagnostic tests of low sensitivity, a limited number of specimen types, incomplete information regarding frequency, timing, and partner-specificity of coitus, and lack of biomarkers to establish that the strain in each infection-concordant partnership is the same [4-9, 31s-34s]. We conducted a multi-center sexual partnership study in Boston and Indianapolis to: examine biologic and behavioral correlates of *Ct* infection concordance using laboratory and data collection methods designed to overcome many of the limitations of previous concordance studies. We also sought to establish how often *ompA* genotypes were identical within a partnership and determine if partners of NAAT-positive, culture-negative participants were less likely to be infected than the partners of culture-positive participants.

MATERIALS AND METHODS

Study population and study design

Participants were 14-24 year old heterosexual males and females infected with *Ct* and their opposite-sex, sex partners. The study was a cross-sectional design consisting of a single visit for each member of a partnership (referred to as a dyad). Participants were recruited between April 10, 2000 and September 29, 2003, at adolescent and sexually transmitted infection (STI) clinics in Boston, Massachusetts and Indianapolis, Indiana. The first dyad member to enroll was required to have a working knowledge of English and stated willingness to name all sex partners. Potential participants were excluded from enrollment if they had: taken antibiotics in the past 30 days, a known immunosuppressive condition, a clinic visit necessitated by sexual assault, evidence of an emotional or mental health crisis, or had previously enrolled in the study.

Study personnel interviewed enrollees found to be *Ct*–infected to elicit the names and locating information for sex partners during the 30 days before enrollment. Sex partners were sought for evaluation and treatment; they were subject to the same inclusion criteria as the first enrolled dyad member, and the same exclusion criteria, (with the exception that previous enrollment was permitted) and were offered study enrollment if they were age 14 or older.

Unit of analysis

The unit of analysis for this study was a sexual dyad that had at least one member infected with *Ct*. A study participant with multiple enrolled sex partners could contribute to more than one dyad.

Data collection

Participants completed an enrollment questionnaire that collected basic demographics and a reproductive and sexual history. Study personnel used a standard script to administer sexual event-specific calendar interviews concerning sexual and other behaviors and events in the 30 days before study enrollment, using a modification of the calendar-event method [10] previously applied to adolescent sexual behavior [11]. For each day, the interviewer ascertained the number of episodes of intercourse and recorded the initials of the sex partner for each coital event. Information was collected on coital event-specific behaviors including condom, spermicide use, and drug use in the two hours before sex.

Physical examination and specimen collection and testing

All participants were interviewed and had a detailed genital examination. Samples were obtained from each participant for detection of *Ct* (males: urethral swabs for both culture and NAAT, urine for NAAT; females: endocervical and urethral swabs for both culture and NAAT, and vaginal and urine specimens for NAAT), *Neisseria gonorrhoeae* (male urethral, and female endocervical swabs for culture), *Trichomonas vaginalis* (male urethral swabs and urine, and female vaginal swabs for NAAT), and bacterial vaginosis (BV) (high vaginal swabs).

Laboratory methods

NAATs—*Ct* was detected by polymerase chain reaction (PCR) (Amplicor, Roche Diagnostics) in Indianapolis, and by transcription-mediated amplification (TMA) (APTIMA, Gen-Probe) in Boston. *T. vaginalis* was detected using a modification of the Amplicor assay that included primers and probes specific for *T. vaginalis* [12].

Quantitative PCR for *Chlamydia trachomatis*—The number of Ct organisms in endocervical, and male urethral specimens (in IFU DNA equivalents per ml (IFUde), defined as the amount of Ct DNA obtained from a preparation containing one culturable organism (IFU) of strain ATCC VR-346 serovar F) were measured by quantitative asymmetric PCR (qPCR) using primers, CTR70 (5’ biotinylated, 25 picomoles) and CTR71 (1.25 picomoles) and a touchdown protocol that used annealing temperatures (62°C to 52°C) with 2.5 mM MgCl2 [13,14]. Amplicons were measured by colorimetric capture-probe ELISA type assay [15]. Four tenfold dilution controls (5,000 IFUde to 5 IFUde) and a negative control were placed in each run and their colorimetric values utilized to translate the values from positive Ct specimens into IFUde [15].

STI cultures—Cell culture for *Ct* was performed using procedures established in the Indianapolis and Boston laboratories at the time of the study [16,17]; Specimens for culture of *N. gonorrhoeae* were inoculated onto modified Thayer-Martin medium; isolation and identification were done according to standard laboratory procedures.

***CtompA* genotyping—**DNA sequencing of PCR-amplified *ompA* from clinical samples was performed according to the methods of Stothard et al. [18,19]. PCR products were evaluated by a reverse dot blot to identify the presence of multiple serovars (eg, D and F) in study samples with the limitations that the procedure cannot distinguish between strains with

nucleotide polymorphisms (e.g., D and D6) and serovars I/Ia, and J/Ja that cross-react [20]. Sequences were not obtained on samples when two serovars were identified; therefore, strain identification for mixed infections was at the level of serovar, not genotype. We defined prototype and variant strains as previously described [18]

Other tests—Gram stains of high vaginal secretions were assessed for BV defined by a Nugent score of 4-6 with clue cells present, or by a Nugent score ≥ 7 [21].

Human subjects approval

Study participants were administered informed consent, and compensated $20-$25 for their time, and inconvenience. The study was approved by the Institutional Review Boards (IRBs) at: Indiana University School of Medicine, (Indianapolis, Indiana), Boston Medical Center and Boston Children's Hospital (Boston, Massachusetts), and the Centers for Disease Control and Prevention (Atlanta Georgia). The study was conducted in accordance with the ethical standards of the participating institutions' IRBs, and in accordance with the standards of the Helsinki Declaration of 1975, as revised in 2000.

Data analysis

Definitions—We defined sexual dyads as a heterosexual sexual partnership wherein at least one member was *Ct*-infected. Participants who had any specimen test positive for *Ct* by any diagnostic test were considered infected.

Dyads with two *Ct*-infected members were considered concordant. Dyad members with incomplete test results were not excluded from *Ct*-concordancy analyses; however, they were excluded from analyses of the chlamydial *ompA* genotypes in concordant dyads, as were dyads in which infecting *Ct* detected in both members of a dyad were not both genotyped or when a dyad member had mixed *Ct* serovar infection (n=4).

Drug use before intercourse was defined as use of alcohol, marijuana, or other illicit drugs in the 2 hours before having sex. Men who reported discharge, dysuria, genital rash or itching or testicular pain, and women who reported vaginal discharge, dysuria, genital rash or itching or lower abdominal pain were considered to have had symptoms at the time of sex. Reported condom use was categorized as "100%" if a dyad member reported using a condom for every coital event with the other dyad member.

Partner-specific measures and outcomes: To examine the association between sexual behaviors and concordance, we only considered sexual events between enrolled dyad members. If dyad members enrolled on different days the analytic dataset included observations from each dyad member's full 30 day recall period (even if they had fewer than 30 days in common during their respective recall periods).

Characteristics associated with concordance: We assessed characteristics associated with concordance using simple logistic regression models with generalized estimating equations (GEE) to account for correlations among dyads that shared a member. The strength of univariate associations were assessed by calculating odds ratios (OR); the GEE sandwich estimate for the standard errors was used to calculate 95% confidence intervals.

To explore male factors that could be associated with having a Ct-infected female partner, we examined the association between the characteristics of *Ct*-infected males in concordant dyads using a comparison group of discordant dyads with *Ct*-infected males and uninfected females. To examine female factors associated with having an infected male partner, we compared the characteristics of females in concordant dyads to the characteristics of females in discordant dyads wherein the female was infected, but the male was not.

To explore male factors that could be associated with male susceptibility to Ct infection, we compared the characteristics of males in Ct-concordant dyads to those of males in discordant dyads wherein the female was infected but the male was not. Likewise, to examine female characteristics that could be associated with female susceptibility to Ct infection we compared the characteristics of females in concordant dyads to the characteristics of females in discordant dyads wherein the male was infected but the female was not. Log transformed qPCR values were used to calculate ORs measuring the association qPCR values and concordance.

RESULTS

Characteristics of study participants

Characteristics of the study population are presented in Table 1. A total of 121 women and 125 men were enrolled, forming 128 dyads. Of these, 108 dyads were comprised of unique male and female members, and 20 dyads shared members (3 men contributed 2 dyads, and 7 women contributed 2 dyads.)

Characteristics of dyads

In more than a third of dyads, both members enrolled on the same day (35.2%, 45/128); 31.3% members (40/128) enrolled within 1-7 days, 19.5% (25/128) within 8-14 days, and 14.1% (18/128) within 15-30 days of each other. Among the 128 dyads, 122 (95%) included female members with complete test results for all 6 C*t* tests performed in women, and 127 (99%) included male dyad members with complete test results for all 3 tests performed in men.

Quantitative PCR results for members of sexual dyads

Quantitative PCR results were available for 85.4% (82/96) of Ct-infected female dyad members; the median endocervical qPCR value was 2,405 IFUde/ml among culture positive women (n=75) and 752 IFUde/ml among women who were positive by NAAT-only (n=7) (p=0.29). Urethral qPCR results were available for 85.3% (87/102) of Ct-infected male dyad members; the median male urethral qPCR result among culture-positive male dyad members (n=70) was 659 IFUde/ml, compared with 301 IFUde/ml among NAAT-only positive male dyad members (n=17) (p=0.0017).

ompA genotyping of chlamydial infection

We genotyped 166/185 (90%) of *Ct*-positive participants with specimens available (Table 2). We identified 15 variants, 10 that have not been previously reported in the literature. E and F strains were the most common in both sites. Ia strains were common in Indianapolis but not

seen in Boston. There were four participants with mixed infection; each of the four was a member of a different concordant dyad.

Concordance, and genotype-specific concordance

Overall, 54.7% (70/128) of dyads were concordant for Ct infection. Among 96 female dyad members with *Ct* infection (any test positive at any site), 84 were culture-positive (all 84 were also NAAT-positive), and 12 were culture negative, but NAAT-positive (Figure). Among 96 dyads with female members who were NAAT-positive (with or without a positive culture), overall concordance of *Ct*-infection was 72.9% (70/96). In dyads with female members positive by both culture and NAAT, concordance was 78.6% (66/84); among the 51 of these concordant dyads tested, 49 (96.1%) had identical genotypes. In dyads with culture-negative, NAAT-positive women, concordance was 33.3% (4/12) and the two concordant dyads tested had identical genotypes.

Among 102 male dyad members with *Ct* infection, all were NAAT-positive; 74 had culture-positive urethral swabs, and 28 had culture-negative urethral swabs, but NAAT-positive, urethral swabs or urine specimens (Figure). Concordance of *Ct*-infection was 68.6% (70/102) overall. In dyads with *Ct*-culture-positive male members, concordance was 77.0% (57/74). Among the 46 concordant dyads with Ct genotyping data available for both members, 95.7% (44/46) had identical genotypes. Concordance was 46.4% (13/28) in dyads with culture-negative, NAAT-positive male members, and 100% of the 7 concordant dyads with genotype information had identical genotypes.

Overall, the same genotype was detected in 96.2% (51/53) of concordant dyads with genotype results available.

Factors associated with concordance

Based on high genotype identity (96%) among *Ct* concordant partnerships tested, we included all *Ct*-concordant dyads in this analysis. No male or female demographic or behavioral characteristic was significantly associated with concordance (Table 3). Concordance for infection was lower in dyads with infected men who reported 100% condom use (52.2% versus 73.3%, OR 0.40, p=0.062) and in dyads with men who reported spermicide use (53.9% versus 70.6%, OR 0.49, p=0.23), and was higher in dyads with infected men who reported a greater frequency of coital events with the female dyad member (median of 10 coital events among concordant dyads versus 6.7 among discordant dyads, OR 1.04, p=0.072, or a 4% increase in concordance with each additional coital event).

Some biologic findings were associated with concordance (Table 4). In partnerships with a *Ct*-infected man, concordance was less likely if the man was NAAT positive-only (*Ct* culture negative) compared with those *Ct* culture positive (46.4% versus 77.1%, OR 0.26, p=0.0048). Similarly, in partnerships with a *Ct*-infected woman, concordance was less likely if the woman was NAAT-positive but *Ct* culture-negative (33.3% versus 77.2%, OR 0.15, p=0.0042). Both *Ct*-infected men and women in concordant dyads had higher median qPCR values (male urethral, 656, and female endocervical, 3,032) compared to *Ct*-infected men and -infected women in discordant dyads (male urethral, 372, female endocervical, 1013),

however, the association of higher qPCR values with concordance was statistically significant only among women (p=0.0067). Concurrent infection with other STI pathogens was not significantly associated with concordance for chlamydial infection.

DISCUSSION

In the largest *Ct* concordance study conducted to date, we observed high rates of concordance for *Ct* infection among the sex partners of *Ct* NAAT-positive men and women (72.9% of male partners, and 68.6% of female partners), rates comparable to those observed in other partnership studies that used NAAT [5-9]. We found even higher concordance in sexual dyads with culture-positive members (78.6% of male partners and 77.0% of female partners).

We also found that sexual dyads with a NAAT-only positive member were less likely to be concordant, similar to findings reported by two smaller studies [5,8]. We hypothesize that the lower rate of concordance among partners of NAAT-only positive participants (both men and women) is related to lower organism load. The lower median qPCR result among NAAT-positive only versus culture-positive male and female dyad members supports this idea, as does the finding that the odds of concordance was significantly lower in dyads with an infected female member who had a lower organism load. Our findings differ from those of Gomes et al [22] who reported no difference in the median Ct load measured by qPCR performed on urine specimens from men and women in concordant (n=12), and discordant (n=28) sexual partnerships. It is also possible that non-viable Ct DNA was detected in NAAT-only positive dyad members.

We did not identify any behavioral characteristics significantly associated with a lower probability of having a chlamydial infected partner. Taken together with the non-negligible (43%) concordance rate we found in dyads with NAAT-only positive members, these data confirm that the partners of persons with NAAT-diagnosed Ct should always be presumed *Ct*-infected and efforts made to ensure partner treatment. Partner management strategies such as expedited partner therapy, whereby the patient is asked to deliver medication or a prescription for medication to their sex partner without an intervening medical evaluation, are efficacious and far less resource intensive than traditional partner services, and should be utilized when appropriate [35s].

Almost all (96%) the concordant dyads with genotype results had identical genotypes. This suggests transmission within the dyad, although certain genotypes (E, F, Ia) common in the population could have occurred through sexual contact with a different partner. Multilocus sequence typing performed on a subset of 28 dyads from this study where both members had identical *ompA* genotypes; also demonstrated identical strain types [23]. Although not definitive, these additional data support transmission within dyads. In addition, the trends we found for higher rates of concordance among men reporting lower rates of condom, and spermicide use supports this hypothesis; however, transmission cannot be shown definitively in a cross sectional study in which not all sex partners are enrolled.

Concordance studies such as ours have been examined for evidence to support the concept of protective immunity to *Ct* infection [18]. The high rates of concordance that we observed do not suggest protective immunity and are comparable to the measured concordance of *N. gonorrhoeae*, an infection that confers little protective immunity because of extensive antigenic variation [5,24]. Furthermore we found no difference in concordance by age or history of past *Ct* infection; if previous infection were to provide even partial immunity, lower concordance would have been expected in dyads with older members or a history of past infection.

Robust estimates of the per coital act transmission probability of *Ct* can be used to understand the risks of re-infection after successful treatment of index cases, and to model the requirements for successful control measures. Investigators have used measures of concordance of infection within sexual partnerships to estimate Ct transmission rates per coital act, but these estimates have relied upon assumptions about coital frequency [25,36s]. Our data could be used to model transmission probabilities and could result in improved estimates because we collected partner-specific coital frequency data.

This study has a number of limitations. By definition, a cross-sectional concordance study cannot demonstrate transmission; in a concordant dyad it is not possible to show which partner is the source of infection, and in a discordant dyad it is not possible to know if the Ct-negative partner is truly uninfected, as our analysis assumed, or incubating infection, or has just cleared a Ct infection. Given the cross-sectional nature of our study, our quantitative culture and qPCR results are from single point in time, and it is not possible to know if organism burden was increasing, decreasing or remaining stable at the time the specimens were collected, nor whether the organism load we measured was similar to that to which the dyad member had been exposed. Dyads were restricted to heterosexual sex-partners that we located and enrolled, and it is possible that sex partners who were not enrolled differed from those who did, possibly affecting true concordance, however, the majority (89%) of study enrollees reported only 1 partner in the 30 days before enrollment so any bias resulting from excluding additional partners was likely minimal. Dyad members with incomplete test results could have been misclassified as uninfected, resulting in an underestimate of concordance, however, there were few such instances, so any impact was likely minimal. This might have resulted in misclassification, such that we have over- or under-estimated the association between organism load and concordance. We used *ompA* genotyping, a standard biomarker, to assign genotype; while not as informative as multilocus strain typing or whole genome sequencing, *ompA* genotype identity nevertheless establishes the plausibility of transmission within the partnership. Testing of multiple anatomic sites and specimen types may have increased the likelihood of positive tests but NAATs are highly specific and the populations studied were at high-risk for STDs, which together would have minimized false-positive results. Although dyad members who enrolled on different days would have had fewer than 30 days of overlap in their recall periods, we analyzed all of the sexual events reported by each dyad member with the other member in their respective 30 day recall periods, which may have resulted in some misclassification. We did not measure markers of mucosal or systemic immunity, which may influence susceptibility to acquisition of infection. We used culture to detect GC; if GC NAATs had been used a different association between GC infection and Ct concordance may have been observed. Finally, while none of

the behavioral factors we examined were associated with significantly higher, or lower odds of concordance, we had limited power to detect significant associations for all the variables we examined.

In summary, we found high concordance rates of *Ct* infection in sexual dyads. Concordance studies cannot be interpreted as a proxy for transmission studies, however, our genotyping data suggested that concordance represented sexual transmission within dyads, and the qPCR data suggest that female dyad members with high organism loads may be more likely to transmit. Despite having examined numerous behavioral and microbiologic factors likely to influence concordance, we did not find any that indicated a way to prioritize partner notification, underscoring the need for effective and efficient strategies to identify and treat all sex partners exposed to *Ct*.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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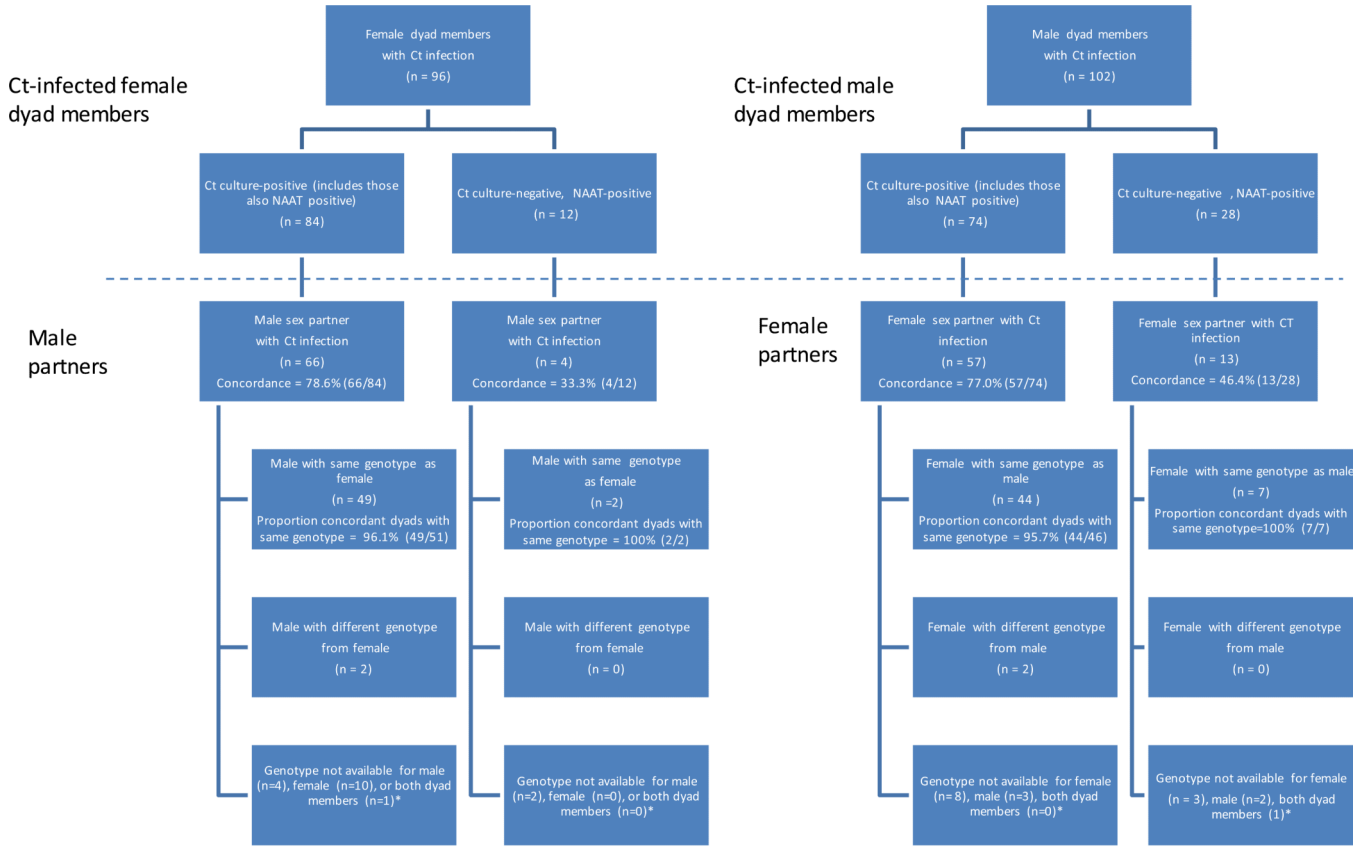
Short Summary

We found high rates of same-genotype *Chlamydia trachomatis* infection in heterosexual partnerships; among women, higher chlamydial organism load was associated with chlamydial infection among their male partners.



*Includes dyads wherein one member had a mixed infection

Figure.

Chlamydia trachomatis infection among participants in 128 dyads enrolled in a cross-sectional study of chlamydial concordance in Boston, and Indianapolis, 2000-2003. Figure on left displays dyads with an infected female and their male sex partners. Figure on right displays dyads with an infected male and their female sex partners. Individual boxes for sex partners include overall infection concordance and the proportion of concordant dyads with identical *ompA* genotype.

Table 1

Enrollment characteristics of males and females contributing to 128 sexual dyads enrolled in a cross-sectional study of chlamydial concordance in Boston and Indianapolis, during 2000-2003

	Males		Females	
Characteristic	**n**	***(%)***	**n**	***(%)***
Total	125		121	
Age, years, median (range)	21.1 [15.1, 38.7]		19.8 [14.4, 40.2]	
Race/ethnicity				
White non-Hispanic	12	*(9.6)*	24	*(19.8)*
Black non-Hispanic	93	*(74.4)*	77	*(63.6)*
Hispanic	10	*(8.0)*	12	*(9.9)*
Other	10	*(8.0)*	8	*(6.6)*
Site enrolled				
STD clinic	78	*(62.4)*	77	*(63.6)*
Adolescent clinic	47	*(37.6)*	44	*(36.4)*
Lifetime number of sex partners, median (range)	14 [1, 230]		7 [1, 50]	
Sex partners past 60 days,(number)				
1	76	*(60.8)*	90	*(74.4)*
2-5	47	*(37.6)*	31	*(25.6)*
6-10	1	*(0.8)*	0	*(0)*
>10	1	*(0.8)*	0	*(0)*
>1 sex partner, past 30 days	19	*(15.2)*	8	*(6.6)*
Coital frequency, past 30 days, median (range)[b]	7 [1, 62]		8 [1, 65]	
STI history				
Chlamydia	36	*(29.5)*	56	*(46.3)*
Gonorrhea	28	*(22.8)*	31	*(25.6)*
Trichomoniasis	6	*(4.8)*	18	*(14.9)*
Syphilis	2	*(1.6)*	1	*(0.8)*
STI at enrollment				
Chlamydia	99	*(79.2)*	86	*(71.1)*
Gonorrhea	12	*(9.6)*	13	*(10.7)*
Trichomoniasis	6	*(4.8)*	27	*(22.3)*
Current oral contraceptive use	--	--	40	*(33.1)*

[a] Measures frequency of coitus with any partner; not limited to coitus with an enrolled dyad member

Table 2

ompA genotypes identified among the members of 128 sexual dyads enrolled in a cross-sectional study of chlamydial concordance in Boston and Indianapolis, during 2000-2003

Genotype[a]	No. of Participants Boston	No. of Participants Indianapolis	Representative Strain[b]	GenBank Accession No.	Citation
D	0	6	B120	X62918	[26]
D1	0	2	IU-FW0353	FJ261929	[18]
D2	8	5	IU-FQ0213	FJ261926	[18]
D6	0	1	IU-TC0272ut	FJ261943.1	[Variant not previously described
D7	0	1	IU-FQ2468	FJ752554	[18]
D11	0	1	IU-TC0319ut	FJ261942.1	Variant not previously described
D12	0	2	IU-FW4101	FJ261933	[18]
D14	1	0	BT210182	FJ261952.1	Variant not previously described
E	19	40	UW5	X52557	[27]
E4	2	0	IU-TC0865ur	FJ261949.1	Variant not previously described
E5	0	1	IU-TC0426cx	FJ261946.1	Variant not previously described
E6	0	2	IU-TC0755ut	FJ261948.1	Variant not previously described
E7	4	0	BT210178	FJ261953.1	Variant not previously described
F	13	19	IC-Cal3	X52080	[28]
G	1	0	UW57	AF063199	[19]
G3	1	0	BT210142	FJ261954.1	Variant not previously described
H	0	2	UW4	X16007	[29]
Ia	0	13	IU-4168	AF063201	[19]
Ia1	1	1	IU-TC0018ut	FJ261940.1	Variant not previously described
J	2	5	UW36	AF063202	[19]
J4	2	0	BT110254ut	FJ261951.1	Variant not previously described
Ja1	2	0	IU-FW4076	FJ261932	[18]
K	0	5	UW31	AF056204	[19]
Mixed	0	4[c]			
Total	56	110			

[a] Genotypes identical to prototype strains shown as letters and variants thereof are numbered. Sequences of numbered variants E4, E5, E6 and E7 do not correspond to any numbered E variants previously described [30].

[b] Specific strains for which sequences are accessible in GenBank.

[c] Participants with mixed infections; all four were members of concordant dyads: (male, D6, female D/F; male E, female E/H; male, F/K, female, F; male, D/I, female, Ia).

Table 3

Univariate associations of demographic and behavioral factors with concordance for chlamydial infection in 128 sexual dyads enrolled in a cross-sectional study of chlamydial concordance in Boston and Indianapolis, during 2000-2003.

Characteristic	No. of dyads[a]	% dyads concordant for chlamydial infection	Odds Ratio[b]	95% Confidence Interval	p value
Dyads with an infected male member					
Male age, years (median)[c]	67	20.3 (concordant)	0.98	0.82, 1.16	0.78
	30	20.3 (discordant)			
Male reports 100% condom use					
Yes	23	52.2	0.40	0.15, 1.05	0.062
No	75	73.3			
Male reports drug use with sex					
Yes	32	75.0	1.64	0.60, 4.55	0.34
No	65	64.6			
Male had >1 sex partner (past 30 days)					
Yes	18	61.1	0.68	0.24, 1.92	0.46
No	80	70.0			
Male reports spermicide use					
Yes	13	53.9	0.49	0.15, 1.60	0.23
No	85	70.6			
Male report of coital frequency in past 30 days, number of events (mean)	67	10.0 (concordant)	1.04	1.0, 1.08	0.072
	31	6.7 (discordant)			
Female partner age, years (median)[c]	66	21.1 (concordant)	1.03	0.87, 1.22	0.73
	32	20.6 (discordant)			
Female report of lifetime sex partners, number (mean)	65	8.1 (concordant)	0.97	0.91, 1.03	0.30
	31	10.1 (discordant)			
Dyads with an infected female member					
Female age, years (median)[c]	66	21.1 (concordant)	1.12	0.93, 1.35	0.25
	26	20.2 (discordant)			
Female reports 100% condom use					
Yes	12	75.0	1.21	0.30, 4.85	0.79
No	80	71.3			

Characteristic	No. of dyads[a]	% dyads concordant for chlamydial infection	Odds Ratio[b]	95% Confidence Interval	p value
Female reports drug use with sex					
Yes	36	69.4	0.83	0.33, 2.10	0.70
No	56	73.2			
Female had >1 sex partner (past 30 days)					
Yes	7	74.1	3.82	0.78, 18.40	0.095
No	85	42.9			
Female report of spermicide use					
Yes	4	75.0	1.19	0.12, 11.89	0.88
No	88	71.6			
Female report of partner-specific frequency of coitus, (mean)	66	11.1 (concordant)	1.00	0.97, 1.04	0.97
	26	10.6 (discordant)			
Male partner age, years (median)[c]	67	20.3 (concordant)	1.09	0.91, 1.29	0.33
	25	19.8 (discordant)			
Male report of lifetime sex partners, number (mean)	66	21.0 (concordant)	0.99	0.98, 1.003	0.16
	24	31.5 (discordant)			

[a]The number of concordant, and total dyads varies slightly because data were missing for some dyad members.

[b]For continuous variables, the odds ratio represents the percent change in the odds of concordance observed with each unit change (e.g. one year of age) in the variable in question.

[c]Continuous variable.

Table 4

Univariate associations of biologic and clinical factors with concordance for chlamydial infection in 128 sexual dyads enrolled in a cross-sectional study of chlamydial concordance in Boston and Indianapolis, during 2000-2003.

Characteristic	No. of dyads[a]	% Dyads concordant for chlamydial infection	Odds Ratio[b]	95% Confidence Interval	p value
Dyads with an infected male member[c]					
Male Ct NAAT-positive, and culture negative					
Yes	28	46.4	0.26	0.10, 0.65	0.0048
No[d]	70	77.1			
Quantitative PCR (urethral, median value)[e]	72	655 (concordant)	1.2	0.94, 1.47	0.15
	27	372 (discordant)			
Male with *N. gonorrhoeae*					
Yes	12	75.0	1.50	0.28, 7.95	0.63
No	78	66.7			
Male with symptoms at time of sex					
Yes	33	66.7	0.88	0.36, 2.17	0.80
No	65	69.2			
Male history of chlamydial infection (self-reported)					
Yes	31	71.9	1.22	0.47, 1.38	0.69
No	64	67.7			
Female partner history of chlamydial infection (self-reported)					
Yes	46	63.0	0.71	0.31, 1.61	0.42
No	51	70.6			
Female partner cervical ectopy					
Yes	26	73.1	1.59	0.59, 4.17	0.36
No	68	63.2			
Female partner with *N. gonorrhoeae*					
Yes	10	100	*f*	*f*	*f*
No	81	61.7			
Female partner with *T. vaginalis*					
Yes	21	76.2	1.67	0.54, 5.00	0.37

Characteristic	No. of dyads[a]	% Dyads concordant for chlamydial infection	Odds Ratio[b]	95% Confidence Interval	p value
No	76	65.8			
Female partner with bacterial vaginosis					
Yes	51	70.6	1.35	0.57, 3.23	0.49
No	47	63.8			
Female partner on hormonal contraception					
Yes	19	59.9	0.60	0.22, 1.64	0.32
No	79	69.6			
Dyads with an infected female member					
Female Ct NAAT- positive and culture negative					
Yes	12	33.3	0.15	0.04, 0.55	0.0042
No[d]	79	77.2			
Quantitative PCR (endocervical, median value)[e]	64	3032 (concordant)	1.38	1.09, 1.73	0.0067
	24	1013 (discordant)			
Cervical ectopy					
Yes	24	79.2	1.75	0.58, 5.26	0.32
No	63	68.3			
Female with *N. gonorrhoeae*					
Yes	11	90.9	4.60	0.56, 38.0	0.16
No	73	68.5			
Female with *T. vaginalis*					
Yes	23	69.6	0.87	0.31, 2.43	0.79
No	69	72.5			
Female with bacterial vaginosis					
Yes	50	72.0	1.03	0.41, 2.56	0.95
No	42	71.4			
Female reported symptoms at time of sex					
Yes	42	73.8	1.21	0.49, 3.03	0.69
No	50	70.0			
Female history of chlamydial infection (self-reported)					
Yes	40	72.5	1.10	0.44, 2.78	0.84

Characteristic	No. of dyads[a]	% Dyads concordant for chlamydial infection	Odds Ratio[b]	95% Confidence Interval	p value
No	51	70.6			
Male partner history of chlamydial infection (self-reported)					
Yes	27	77.8	1.45	0.50, 4.18	0.50
No	65	70.8			
Male partner with *N. gonorrhoeae* infection					
Yes	10	90.0	3.81	0.45, 31.91	0.22
No	74	70.3			

[a] The total number of dyads varies slightly because data were missing for some variables

[b] For continuous variables, the odds ratio represents the percent change in the odds of concordance observed with each unit change (e.g. one year of age) in the variable in question.

[c] *Trichomonas vaginalis* infection in male dyad members could not be included in the model because of the small number of TV infections among males.

[d] Comparison group is dyads with culture-positive dyad member

[e] Quantitative PCR analyzed after a log transformation.

[f] The logistic regression model could not be fit for this variable because 100% of the dyads with a female partner with *Neisseria gonorrhoeae* infection were concordant, leaving the discordant comparison group to have a cell value of zero.