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Prevalence and Incidence of Zika Virus Infection Among Household Contacts of Patients With Zika Virus Disease, Puerto Rico, 2016–2017

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Abstract

Background.—Little is known about the prevalence or incidence of Zika virus (ZIKV) infection in settings affected by the 2015–2016 Zika pandemic and associated risk factors. We assessed these factors among household contacts of patients with ZIKV disease enrolled in a cohort study in Puerto Rico during 2016–2017.

Methods.—Household contacts of index case patients completed a questionnaire and gave specimens for real-time polymerase chain reaction (RT-PCR) and immunoglobulin M enzyme-linked immunosorbent assay testing to detect ZIKV infection. We measured the prevalence of ZIKV infection among contacts and associated individual and household factors, examined sexual transmission using a sexual-networks approach, and assessed incident infection among initially uninfected household contacts 2–4 months later.

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Supplementary Data

Supplementary materials are available at *The Journal of Infectious Diseases* online. Consisting of data provided by the authors to benefit the reader, the posted materials are not copyedited and are the sole responsibility of the authors, so questions or comments should be addressed to the corresponding author.

Results.—Of 366 contacts, 34.4% had evidence of ZIKV infection at enrollment, including 11.2% by RT-PCR. Having open doors and windows that were either screened (prevalence ratio [PR], 2.1 [95% confidence interval {CI}, 1.2–3.6]) or unscreened (PR, 2.5 [95% CI, 1.5–4.1]) was associated with increased prevalence. Sexual partners were more likely to both be RT-PCR positive relative to other relationships (odds ratio, 2.2 [95% CI, 1.1–4.5]). At follow-up, 6.1% of contacts had evidence of incident infection.

Conclusions.—This study identified sexual contact as a risk factor for ZIKV infection. Persons living with ZIKV-infected individuals should be a focus of public health efforts.

Keywords

Zika virus; arbovirus; household transmission; sexual transmission

Zika virus (ZIKV) is an emerging flavivirus transmitted predominantly via the bite of *Aedes* species mosquitoes [1], in Puerto Rico exclusively *Aedes aegypti*. ZIKV infection in humans may result in rash, fever, arthralgia, myalgia, and conjunctivitis, and infection has been linked to a spectrum of neurological sequelae in adults and in neonates born to infected mothers, most visibly microcephaly [2, 3]. During 2015–2017, an extensive ZIKV epidemic was documented throughout the Western hemisphere [2, 4]. In the United States and US territories, a total of 42 840 cases of ZIKV infection were reported, of which 36 273 (85%) were in the US territory of Puerto Rico and presumed to be due to local transmission [5, 6]. Of the 5663 cases reported from states, the large majority (95%) were travel associated.

Sexual transmission of ZIKV has been documented through case reports from returning travelers who have infected nontraveling partners via male–female, male–male, and female–male sex [7–9]. The biological plausibility of sexual transmission has been supported through detection of ZIKV nucleic acid in numerous compartments of male and female sexual fluids; however, infectious ZIKV and ZIKV nucleic acid persists in semen for substantially longer than in cervicovaginal fluids [7, 10, 11]. Modeling studies have assessed the overall contribution of sexual transmission in simulated ZIKV epidemics with *Aedes* mosquitoes, and though findings are inconsistent, they generally suggest the contribution is minor [12–16]. Such models are limited by the scarcity of data on individual-level absolute or relative risks for sexual transmission, which is crucial for informing guidelines and control strategies [17]. Some studies have ecologically examined these risks via biological sex ratios, but challenges persist in accounting for higher screening rates and likelihood of symptomatic infection among females [18, 19]. In the absence of well-controlled designs, such as longitudinal serodiscordant couples' studies, the risk of sexual transmission of ZIKV remains challenging to estimate empirically because partners are typically equivalently exposed to infection via mosquito bite [20].

Aside from sexual contact, household and individual risk factors for ZIKV infection among household contacts are incompletely understood. However, drawing from studies of dengue and chikungunya viruses, such factors may include age, biological sex, exposure to and protection from mosquitos, and household factors that are permissive to mosquito habitation such as lack of air conditioning and having open windows [1]. A recent household cluster investigation in Puerto Rico found that 31% of persons in participating households

within 100 m of ZIKV index case patients' households had laboratory evidence of recent ZIKV infection, with frequency of mosquito bites, having open doors and windows, and neighborhood presence of vacant homes being associated with increased likelihood of infection [19]. An earlier analogous investigation of chikungunya virus infection found that 30% of neighbors within 50 m of chikungunya virus index case patients' households had evidence of infection, with use of air conditioning being the main factor associated with decreased risk [21]. These studies provide insights into infection risk in areas with known transmission, but are less focused on specific factors associated with transmissions in households. Such houses may contain additional ZIKV-infected persons not presenting to care given high frequency of asymptomatic infection and other determinants of care-seeking [19, 22]. Additionally, household-focused analyses offer the opportunity to more finely explore risk factors such as sexual behaviors. Finally, only 1 report from a cluster or household studies of ZIKV infection has reported subsequent incidence after the initial visit [23].

In this analysis, we estimated the prevalence and incidence of ZIKV infection among household contacts of symptomatic persons who presented to care with ZIKV infection confirmed by real-time polymerase chain reaction (RT-PCR). Among these household contacts we evaluated the individual, sexual, and household factors associated with ZIKV infection.

METHODS

Study Design

The Zika Persistence (ZiPer) Study was a prospective cohort study conducted in Puerto Rico from May 2016 to July 2017 to understand the natural history of ZIKV infection. The full methods for the cohort are described elsewhere [24]. In brief, index case patients presented with history of fever, rash, conjunctivitis, or arthralgia to clinical sites in the municipalities of Ponce, San Juan, or Guayama, and tested positive for ZIKV infection by RT-PCR in serum or urine specimens [25]. At a subsequent study enrollment visit at home or the research clinic, index case patients completed a questionnaire and received additional diagnostic testing for ZIKV infection by Trioplex RT-PCR assay in specimens of serum, urine, saliva, and semen or vaginal fluids along with testing of serum by anti-ZIKV immunoglobulin M (IgM) antibody capture enzyme-linked immunosorbent assay (ELISA) [25, 26]. Concurrently, up to 5 household contacts were invited to enroll and complete an identical study visit. At this visit, educational pamphlets were distributed to enrolled households and all participants were counseled on repellent use and condoms to prevent transmission. Index case patients and RT-PCR–positive household contacts were prospectively followed and retested to assess the duration of detection of ZIKV RNA in body fluids. Household contacts who were RT-PCR negative but tested positive by IgM ELISA were considered to have had evidence of recent infection and were not prospectively followed. To detect incident ZIKV infections, starting in October 2016 household contacts negative by both RT-PCR and IgM ELISA at enrollment were revisited 2–4 months later. All participants provided written informed consent.

Questionnaire

The study questionnaire assessed participant demographics, employment locations, time spent outdoors, repellent use, nature of relationship to the index case patient (eg, intimate relationship, parent–child, nonfamilial), and sexual activity within the previous 7 days. Index case patients or their guardians completed a household-level section that assessed number of occupants, household income, presence and use of screens on windows and doors, presence of air conditioning, and use of personal protective measures such as repellent and mosquito coils.

Analysis

Individual-Level Prevalence—To measure the prevalence of ZIKV infection in household contacts, participants who tested positive by RT-PCR in any body fluid were defined as PCR positive. Individuals defined as PCR/IgM positive had evidence of ZIKV infection by RT-PCR or IgM ELISA. For these 2 combined outcomes, we estimated normal-approximation 95% confidence intervals (CIs) for the proportion.

We quantified the associations of being either PCR positive or PCR/IgM positive with the above individual-level and household-level factors using bivariate methods and χ^2 tests. Factors statistically significant at the $\alpha = .05$ level were entered together into a logistic regression model, with Wald *P* values and predictive margins prevalence ratios estimated [27]. Additional multilevel models to account for household-level clustering were not conducted due to the relatively few factors associated with prevalent infection.

Household-Level Prevalence—To quantify the prevalence of ZIKV infection collectively among the households of index case patients, we summed both outcomes within households and calculated the proportion of households with any or all contacts having prevalent ZIKV infection. The average frequency of prevalent ZIKV infection in houses was quantified, inclusive and exclusive of index case patients, using the mean intrahousehold prevalence, $\frac{\sum_{t=1}^{T}\left[\frac{I_t}{P_t}\right]}{T}$,, where T is the total households, P is the size of the *tth* household, and I is the number of prevalent infections in the *tth* household. The associations between each household-level factor and these household-level prevalence measures were assessed using the same methods as for individual-level prevalence. For mean household prevalence, comparisons were made with Student *t* test or linear models if factors had >2 levels.

Sexual Contact—Multiple methodologies allowed insight into the relationships between sexual contact and prevalent ZIKV infection. First, to understand sexual contact as a risk factor for household contacts, we examined the bivariate associations between prevalent ZIKV infection of household contacts and the questionnaire responses pertaining to sexual contact with index case patients, both overall and stratified by household contact demographics and recentness of sexual activity.

Recognizing that the above analysis is influenced by the partly arbitrary position of the index case patient within the household social structure, we examined all pairwise relationships within the network of household contacts. This approach potentially increases

statistical efficiency, while increasing the effective sample size, and thus power to identify the association between sexual contact and infection. Using the responses for each index case patient/household contact's relationship, participant demographics, and study contact records, we coded all pairwise relationships within households as sexual or nonsexual into an undirected, dyadic (pair-level) dataset [28].

Since each household had >1 prevalent ZIKV infection due to the index-sampling strategy, we sought to identify if additional ZIKV infections were likely to be found in sexual contacts. We then created dyadic-level outcomes of whether both dyad members had prevalent infection defined by RT-PCR or IgM ELISA, or not. Analyses thus assessed whether any 2 ZIKV infections in a household were associated with both persons being sexual contacts, which would support sexual transmission (Figure 1A), as opposed to being among 2 nonsexual contacts (Figure 1B). The association between prevalent infections and sexual contact was examined using odds ratios (ORs) bivariately and 2 approaches that controlled for household-level confounding. The first used generalized estimating equations (GEEs), controlling for repeated household measures with an exchangeable correlation structure [29]. The second approach was conditional logistic regression, matched on household.

Incidence—We measured cumulative incidence of ZIKV infections identified at the follow-up visit as the proportion PCR positive or PCR/IgM positive among initially PCR- and IgM-negative household contacts. These proportions were compared by era of study conduct (October–December 2016 vs January–June 2017) and sexual history of ZIKV-infected index case patients and household members at enrollment.

RESULTS

A total of 366 household contacts in 170 households of index case patients were enrolled in the ZiPer study (Table 1), representing 60% of 613 total contacts in these homes. An additional 51 households of index case patients who did not live alone had 0 household contacts enrolled (of 158 contacts), resulting in 47% of all potential contacts being enrolled. Among contacts, 61% were female, 48% were aged 18–49 years, and 45% lived in households with annual income <$10 000. Nearly 70% of persons did not work outside the home, and nearly as many spent some or all of the day outdoors. More than half of participants lived in households with open, unscreened windows, and 50% had any air conditioning in the home.

At enrollment, 41 of 366 (11% [95% CI, 8.3%–14.8%]) contacts were PCR positive in any fluid, with highest frequency of positivity in semen (7/46 [15.2%]), followed by serum (28/365 [7.7%]), urine (15/349 [4.3%]), saliva (5/345 [1.4%]), and vaginal fluid (1/132 [0.8%]). Forty PCR-positive contacts reported symptom data, of whom 12 (30%) were asymptomatic. Anti-ZIKV IgM antibody was detected in the serum of 112 of 362 (30.9% [95% CI, 26.3%–35.9%]) contacts, of whom 27 (24%) were currently PCR positive. Overall prevalence of ZIKV infection was 34.4% (95% CI, 29.7%–39.4%]; 126/366). Ten female contacts were pregnant, 3 of whom had evidence of infection: 1 (10%) was positive by both PCR and IgM, and 2 (20%) were PCR negative but IgM positive.

Levels of prevalent infection were comparable across all individual-level and most household-level factors (Table 1), with 3 exceptions. In a multivariable model, persons with windows and doors that remain unopened were least likely to have prevalent infection. Relative to them, persons with open but fully screened windows and doors were 2.1 (95% CI, 1.2–3.6) times as likely, and those with open and unscreened windows and doors 2.5 (95% CI, 1.5–4.1) times as likely, to have prevalent ZIKV infection. Persons living in homes that use antimosquito coils were 1.5 (95% CI, 1.1–1.9) times as likely to have prevalent ZIKV infection as those living in homes that did not use them.

At the household level, 49.4% of households contained a contact other than the index case patient with prevalent infection, including 21.2% with a PCR-positive contact. The mean intrahousehold prevalence of infection among participating contacts was 35.6% (95% CI, 29.3%–41.9%). In 40 households (23.5% [95% CI, 17.6%–30.3%]), all participating household contacts had prevalent infection. Inclusive of index case patients, the mean intrahousehold prevalence of ZIKV infection was 59.4%. Despite these estimated means, variation was substantial: After sorting the 84 households with at least 1 infected contact by the number of infected household contacts, 25 households (14.7%) contained 50% of all infected contacts. As earlier, the only factor associated with household-level prevalent infection was having open windows and doors and using mosquito coils (Supplementary Tables 1 and 2).

Adult sexual contacts of index case patients were 1.4 and 1.3 times more likely to be PCR positive and PCR/IgM positive, respectively, than nonsexual household contacts, although these associations were not statistically significant (Table 2). Sexual contacts >50 years of age and adults without sexual activity in the previous week were about twice as likely to have prevalent infection compared to their counterparts who were not sexual contacts of an index case patient. The network analysis included 732 dyads from all enrolled persons in the 170 households (Table 3). Although we found no significant association between sex partner dyads and being PCR/IgM positive, sex partner dyads were about twice as likely as other dyads to both be PCR positive (OR, 2.2 [95% CI, 1.1–4.5]; $P = .03$). This association was similar after controlling for household and community factors via matched and GEE logistic regression models.

We further examined the 11 sex-linked dyads who were both PCR positive to assess the likelihood of sexual transmission, focusing on temporality of symptom onset and fluid-specific detection, anchored to the onset date of the initial infection in the dyad (Supplementary Table 3). These details among 10 heterosexual and the study's only male–male couple (of 91 couples) generally supported the plausibility of male-to-female and male-to-male sexual transmissions.

Among 165 household contacts initially negative for ZIKV infection by RT-PCR and IgM ELISA, 2 (1.2% [95% CI, .2%–3.9%]) were PCR positive and 10 (6.1% [95% CI, 3.1%–10.5%]) were positive by PCR or IgM at follow-up visits that occurred a median of 63 days (interquartile range, 50–105 days) after enrollment (Table 4). Incidence was similar between both late 2016 and 2017. Both incident PCR-positive results occurred in sexual contacts of index case patients ($P = .02$, compared to all other groups), 1 in serum from a male and the

other in urine for a female. However, reported symptom onset dates of these contacts and the duration of shedding in their corresponding index case patient were not consistent with sexual transmission. An additional sexual contact of a household member who was PCR negative and IgM positive was IgM positive at follow-up, as were 7 other persons without sexual contact with ZIKV-positive persons.

DISCUSSION

In this study of ZIKV infection among household contacts of patients with ZIKV disease, about one-third of household contacts had evidence of ZIKV infection. As has been found in previous outbreak household contact studies of Zika and dengue, testing efforts focused on household members of diagnosed cases yielded additional diagnoses, including among females of reproductive age. The average prevalence among household contacts within households (36%) was similar to the overall study prevalence (34%), indicating clustering of infections in homes containing ZIKV patients. While the overall community-wide levels are likely lower than this, this high household ZIKV infection prevalence underscores the need for better control approaches for *Aedes aegypti* mosquitos [30]. Our finding of incident infections among contacts in the weeks following an index case patient's illness indicates ongoing household and/or community transmission. Rapid interventions targeted to households of ZIKV-infected individuals, and possibly their communities, may avert future infections.

Similar to earlier cluster studies of chikungunya, dengue, and ZIKV infections, we found that household factors, rather than individual ones, were most associated with individuals' infection risk [19, 21, 31]. Households in this study that reported always keeping windows and doors closed were least likely to have infected contacts, while only moderate protection was conferred when windows and doors were open but screened. A different ZIKV cluster investigation similarly found a protective effect of closed doors and windows [19]. We noted an inverse association between mosquito coils in the home and prevalence of ZIKV infection, which may be a marker of preexisting high levels of mosquitos in those homes in combination with low effectiveness of mosquito coils. Social determinants previously associated with arboviral prevalence such as household income were not associated with prevalence, which may have resulted from selection bias from sampling homes of ZIKV disease case patients.

In dyadic analyses, sexual contacts were twice as likely to have prevalent infection, suggesting elevated transmission risk associated with sex. The details of dual-PCR-positive cases add to the plausibility of sexual transmission, particularly for male-to-female and male-to-male transmission. We observed stronger linkages between sexual contact and prevalence as measured by RT-PCR rather than by IgM, likely because the relatively short duration of detection of viral RNA increases specificity of timing when infection may have occurred; however, this analysis also carries the limitation of decreased number of events to evaluate potential sexual transmissions.

Considering that only 13% of dyads in the sample were sexual, using standard attributable fraction formulae, these results are consistent with a recent model-based estimated of 5%

of transmissions attributed to sex in settings with mosquito transmission and a limited role for sexual transmission alone to sustain community-wide ZIKV epidemics [12, 14, 15]. These results may be interpreted per principles of the population attributable fraction: While for a given sexual couple the risk of ZIKV transmission via sex may be twice that of the background risk via mosquito bite, the relative risk is not high enough and the mode of sex is not common enough to account for a substantial portion of transmission in the population. Our results support Centers for Disease Control and Prevention, World Health Organization (WHO), and other clinical guidelines regarding the risks and prevention of sexual transmission of ZIKV, despite the low population-level risk [17, 32].

Although the relative transmission risk for male–male vs male–female sex remains undetermined, we note that the study's only male–male couple was among the 11 couples who were both PCR-positive. This finding is consistent with case reports among returning US travelers [8, 33], and suggests that men who have sex with men (MSM) may be at increased risk of infection, as occurs for other viral sexually transmitted infections. Whether this elevated risk is due to substantially longer viral shedding times in semen, increased infectiousness of semen, or to other differences in ZIKV transmission or susceptibility inherent to male–male sex, it remains to be determined whether ZIKV transmission can be sustained among MSM communities sexually [7, 16, 24].

This study contributes one of the first participant-level comparative estimates of sexual ZIKV transmission risk. Nonetheless, despite our study's statistical approach, causality remains difficult to demonstrate empirically in settings with the possibility of ongoing mosquito transmission. Our design has potential residual confounding due to sharing of sleeping quarters within homes, nonsexual behaviors of partners (eg, kissing), and other unmeasured but plausible risk factors. Because of the demonstrated need to separate these confounding factors, WHO has proposed a research agenda and possible study designs to fill gaps in understanding the role of sexual transmission [20].

Examination of the association with sexual contact by additional risk factors, available for the more simplistic index-based analyses, yielded several counterintuitive results. When analyzing according to degree of sexual activity in the week before enrollment, we observed an inverse association that is likely due to cessation of sexual activity owing to ZIKV symptoms and/or counseling by providers to abstain from sex. A more comprehensive retrospective sexual history covering the likely pre-infection period may have yielded clearer results. An apparent higher amount of prevalent infections among male sex partners of female index case patients, rather than the reverse, is likely due to both greater likelihood of care-seeking among females and increased duration of viral detection in the male reproductive tract, and does not inform the directionality of transmission [34]. In contrast, the detailed assessment for PCR-linked sex partners suggests a clearer picture of male-to-female transmission. An observed stronger association with sex for older persons may reflect faster reproductive tract clearance of ZIKV in younger persons, potentially attributable to more frequent ejaculations, as has been reported elsewhere [35].

Our study has additional limitations. Our sample of household contacts contained a majority of females (61%) due to a recruitment emphasis on male index case patients (to enable

estimation of duration of ZIKV shedding in semen), and a higher proportion of females reported being home during the day (30% overall; 26% male vs 38% female). Increased time spent at home may increase infection risk, possibly limiting the generalizability of prevalence findings. The 1- to 2-week lag between infection onset among index case patients and household study enrollment likely lowered estimates of ZIKV infection defined by RT-PCR among contacts. Last, follow-up of household contacts at only a single time point, possibly after the waning of an incident IgM or PCR signal and absent immunoglobulin G testing availability, may have limited incidence rate estimation.

In summary, this study found that household members of patients with ZIKV disease experience substantial infection risk, and suggests increased risk for sexual partners in an endemic setting. Such households are in need of additional medical and public health attention after an initial diagnosis, including recommendations regarding how to prevent sexual transmission, noting that household contacts may include pregnant women, among whom infections may lead to congenital Zika syndrome. We provide additional evidence that maintaining closed doors and windows can be effective in limiting mosquito-borne infections in homes. Although the Western hemisphere ZIKV outbreak receded during 2017 and 2018, these findings can inform public health guidance and interventions for future outbreaks.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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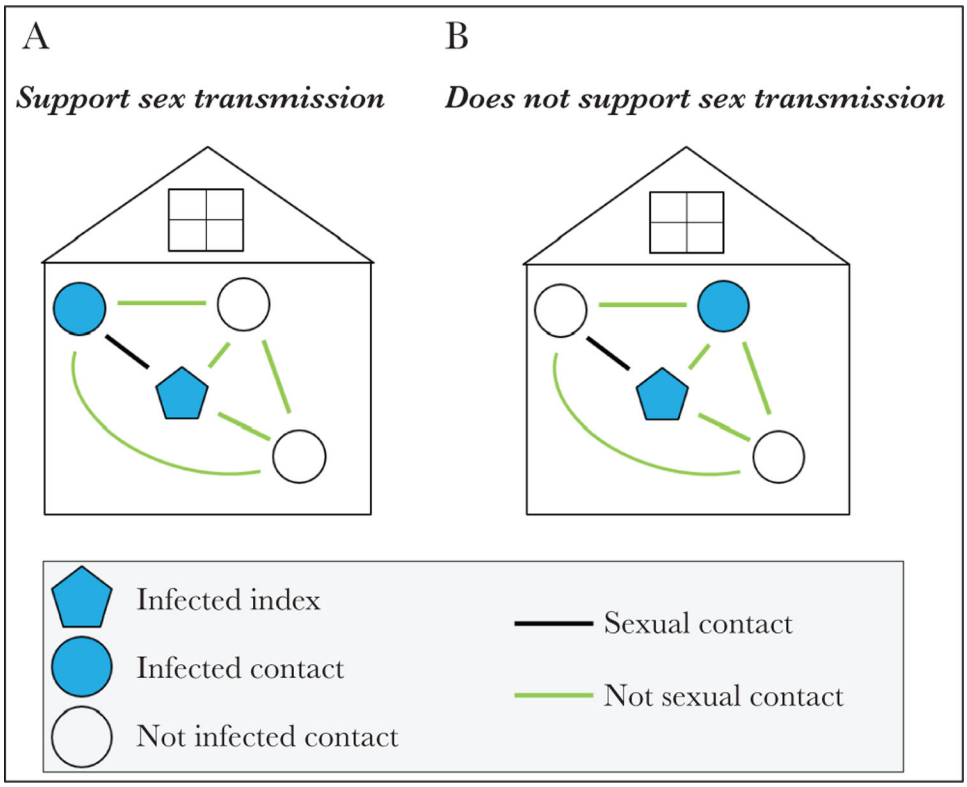

Figure 1.
Illustration of use of household dyadic data for inferring association between prevalence of Zika virus infection and sexual contact, Zika Persistence (ZiPer) study, Puerto Rico, 2016–2017.

Table 1.

Distribution of Household Contact Characteristics and Association With Prevalent Zika Virus Infection—Zika Persistence Study, Puerto Rico, 2016–2017

	Distribution		ZIKV Test Results					
			PCR Positive			PCR Positive or IgM Positive		
Characteristic	Column %	(No.)	Row %	(Pos)	Unadjusted *P* Value	Row %	(Pos)	Unadjusted *P* Value
Overall	…	(366)	11.2	(41)	…	34.4	(126)	…
Individual attributes								
Sex					.19			.75
Male	39.4	(144)	13.9	(20)		35.4	(51)	
Female	60.6	(222)	9.5	(21)		33.8	(75)	
Age, y					.36			.58
<18	34.2	(125)	8.8	(11)		31.2	(39)	
18–49	48.1	(176)	13.6	(24)		36.9	(65)	
≥50	17.8	(65)	9.2	(6)		33.9	(22)	
Work outside home					.86			.14
Yes	30.5	(111)	10.8	(12)		28.8	(32)	
No	69.5	(253)	11.5	(29)		36.8	(93)	
Time outdoors					.32			.20
Little/never	31.2	(114)	8.8	(10)		29.8	(34)	
Sometimes/all day	68.8	(251)	12.4	(31)		36.6	(92)	
Repellent use, prior 30 d					.65			.87
Yes	60.1	(220)	11.8	(26)		34.1	(75)	
No	39.9	(146)	10.3	(15)		34.9	(51)	
Household attributes								
Size					.81			.05
2–3 persons	32.6	(119)	11.8	(14)		36.1	(43)	
4–5 persons	54.2	(198)	11.1	(22)		29.8	(59)	
≥6 persons	13.2	(48)	8.3	(4)		47.9	(23)	
Household income					.74			.60
$0–$9999	45.4	(147)	10.2	(15)		32.7	(48)	
$10 000–$19 999	34.9	(113)	13.3	(15)		37.2	(42)	

Characteristic	Distribution		ZIKV Test Results					
			PCR Positive			PCR Positive or IgM Positive		
	Column %	(No.)	Row %	(Pos)	Unadjusted *P* Value	Row %	(Pos)	Unadjusted *P* Value
≥$20 000	19.8	(64)	10.9	(7)		39.1	(25)	
Windows and doors					.05			.0004
Never remain open	20.2	(74)	4.1	(3)		16.2	(12)	
Open, all screened	26.0	(95)	15.8	(15)		33.7	(32)	
Open, not all screened	53.8	(197)	11.7	(23)		41.6	(82)	
Use air conditioning					.84			.24
Yes	50.3	(184)	10.9	(20)		31.5	(58)	
No	49.7	(182)	11.5	(21)		37.4	(68)	
Use mosquito coils					.32			.005
Yes	44.0	(161)	13.0	(21)		42.2	(68)	
No	56.0	(205)	9.8	(20)		28.3	(58)	

Abbreviations: IgM, immunoglobulin M; PCR, polymerase chain reaction; Pos, positive; ZIKV, Zika virus.

Table 2.

Prevalence of Zika Virus Infection by Relationship to Index Case Patient and Other Features—Zika Persistence Study, Puerto Rico, 2016–2017

	PCR Positive					PCR Positive or IgM Positive				
	Adult Sex Contact of Index		Not Adult Sex Contact			Adult Sex Contact of Index		Not Adult Sex Contact		
Characteristic	**%**	**(No.)**	**%**	**(No.)**	***P* Value**	**%**	**(No.)**	**%**	**(No.)**	***P* Value**
Overall	15.0	(9/60)	10.5	(32/306)	.31	41.7	(25/60)	33.0	(101/306)	.20
Sex of household contact										
Male	26.1	(6/23)	11.6	(14/121)	.09[a]	52.2	(12/23)	32.2	(39/121)	.07
Female	8.1	(3/37)	9.7	(18/185)	~1.0[a]	35.1	(13/37)	33.5	(62/185)	.85
Age of household contact, y										
<18	…	…	8.5	(11/129)	…	…	…	33.3	(43/129)	…
18–49	14.0	(7/50)	13.7	(18/131)	.96	38.0	(19/50)	38.2	(50/131)	.98
≥50	23.1	(3/13)	7.6	(4/53)	.13[a]	61.5	(8/13)	28.3	(15/53)	.05[a]
Sexual activity (adult contacts and index only)										
Sexual activity, previous 7 d	14.0	(7/50)	7.4	(2/27)	.48	36.0	(18/50)	33.3	(9/27)	.82
No sexual activity, previous 7 d	20.0	(2/10)	9.2	(6/65)	.29[a]	70.0	(7/10)	277	(18/65)	.01[a]

Abbreviations: IgM, immunoglobulin M; PCR, polymerase chain reaction.

[a]Fisher exact test used because of small expected cell counts. Otherwise, *P* values are from the χ^2 test of independence.

Table 3.

Prevalence of Zika Virus Infection Among All Household Dyads by Sexual Relationship—Zika Persistence Study, Puerto Rico, 2016–2017

Characteristic	Both Dyad Members PCR Positive					Both Dyad Members PCR Positive or IgM Positive				
	Sexual Dyad		Not Sexual Dyad		*P* Value	Sexual Dyad		Not Sexual Dyad		*P* Value
Overall, % (No.)	12.1	(11/91)	5.9	(37/633)	.03	33.0	(30/91)	27.7	(175/633)	.29
Unadjusted OR (95% CI)	2.2	(1.1–4.5)	…	…	.03	1.3	(.80–2.1)	…	…	.29
Multivariable GEE model of households, OR (95% CI)	1.9	(1.00–3.7)	…	…	.05	1.2	(.84–1.8)	…	…	.31
Matched analysis of households, OR (95% CI)	2.8	(0.95–8.1)	…	…	.06	1.1	(.45–2.7)	…	…	.84

Abbreviations: CI, confidence interval; GEE, generalized estimating equation; IgM, immunoglobulin M; OR, odds ratio; PCR, polymerase chain reaction.

Table 4.

Incident Zika Virus infections Among Household Contacts at Follow-up Visit—Zika Persistence Study, Puerto Rico, 2015–2017

	Distribution		ZIKV Test Results at Follow-up			
			PCR Positive		PCR Positive or IgM Positive	
Characteristic	**Column %**	**(No.)**	**Row %**	**(No.)**	**Row %**	**(No.)**
Overall	…	(165)	1.2	(2)	6.1	(10)
Era						
October–December 2016	53.3	(88)	1.1	(1)	6.8	(6)
January–June 2017	46.7	(77)	1.3	(1)	5.2	(4)
Sexual history at enrollment visit						
Sexual contact of PCR-positive index participant	13.9	(23)	8.7	(2)	8.7	(2)
Sexual contact of PCR-positive household member	2.4	(4)	0.0	(0)	0.0	(0)
Sexual contact of PCR-negative/IgM-positive household member	0.6	(1)	0.0	(0)	100.0	(1)
None of the above	86.1	(137)	0.0	(0)	5.1	(7)

Abbreviations: IgM, immunoglobulin M; PCR, polymerase chain reaction; ZIKV, Zika virus.