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Network Interconnectivity and Community Detection in HIV/Syphilis Contact Networks among Men who have Sex with Men

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Abstract

Background: Despite persistent HIV and syphilis epidemics among men who have sex with men (MSM), the relationship between HIV and syphilis contact networks has not been well characterized. We aimed to measure interconnectivity between HIV and syphilis contact networks among MSM and identify network communities with heightened interconnectivity of the syphilis network with the HIV network.

Methods: Using contact tracing data, we generated independent and combined HIV and syphilis networks for all MSM diagnosed with HIV or early syphilis, respectively, in North Carolina between 2015 and 2017. We treated the independent networks as layers and identified network communities, or groups of densely connected nodes, in the two-layer network. We assessed interconnectivity by comparing the mean node degree among syphilis network members in the syphilis network alone vs. the combined HIV/syphilis network, both overall and by network community.

Results: The syphilis network was interconnected with the HIV network, especially in network communities with younger median age, higher proportions of persons self-identifying as Black, non-Hispanic, and higher proportions of syphilis cases diagnosed at sexually transmitted disease clinics.

Conclusions: Interconnected contact networks underlie HIV and syphilis epidemics among MSM, particularly among young, Black MSM. Intensified transmission prevention interventions within highly interconnected network communities may be particularly beneficial.

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SUPPLEMENTAL DIGITAL CONTENT
Supplemental materials.docx

Short Summary:

A study of sexual contact tracing networks found that HIV and syphilis networks are interconnected among men who have sex with men (MSM), particularly among young, Black MSM.

Keywords

HIV; syphilis; network communities; network interconnectivity

INTRODUCTION

In the United States (US), HIV and syphilis constitute substantial public health burdens, particularly among men who have sex with men (MSM).^{1,2} In the US in 2017, 25,748 and 17,736 MSM became diagnosed with HIV¹ and syphilis,² respectively. Although estimated HIV incidence has decreased among US MSM overall in recent years, HIV incidence has remained steady among Black MSM and is rising among Hispanic/Latino MSM.¹ Syphilis diagnoses increased steadily from 2013 through 2017 within all populations in the US, with the highest rates also observed among minority MSM.² Black, non-Hispanic MSM and Hispanic MSM are diagnosed with primary/secondary syphilis at 4.5 and 1.8 times the rate observed among white, non-Hispanic MSM, respectively.³ Novel intervention strategies are needed to curtail the ongoing HIV and syphilis epidemics, particularly among MSM of color.

Although numerous studies of HIV and sexually transmitted disease (STD) networks have been undertaken to guide prevention and treatment efforts for a single infection,⁴ few analyses have generated combined networks containing persons diagnosed with HIV or syphilis and their sexual contacts. Each of the existing combined-network analyses^{5–8} primarily evaluated the union of the two networks as a single network, rather than interrogating how the networks interact. New approaches that assess the relationship between HIV and syphilis contact networks could inform the design of interventions deployed through these networks.

We conducted a statewide evaluation of HIV and syphilis contact networks among MSM in North Carolina (NC), a setting where the burden of both infections is high.^{9,10} Using surveillance-based diagnosis and contact tracing data for both infections, we sought to characterize the independent and combined HIV and syphilis networks and identify populations in which these networks are directly connected. We devised a simple measure to quantify the amount and distribution of overlap across two networks; we termed this measure “interconnectivity” and posited that interconnectivity between HIV and syphilis contact-tracing networks could allow infection transmission to cross networks. We then identified distinct network communities, or groups of densely connected nodes,¹¹ in which the syphilis network showed comparatively heightened interconnectivity with the HIV network. Detection of these communities may guide resource allocation to portions of the syphilis network that experience elevated exposure to the HIV network and may thus disproportionately benefit from HIV prevention efforts.

MATERIALS AND METHODS

Study Data

All data were drawn from the NC Electronic Disease Surveillance System (NC EDSS), which is operated by the NC Division of Public Health. NC EDSS captures demographic, medical, and intervention data for all reportable communicable diseases in NC, including HIV and syphilis.¹² Contact tracing data in NC EDSS are collected by Disease Intervention Specialists (DIS) who interview persons newly diagnosed with HIV or early (primary, secondary, or early latent) syphilis in NC to identify recent sexual and injection drug use contacts for tracing and infection screening. Sexual contacts are elicited for the twelve months prior to DIS interview for persons newly diagnosed with HIV and for the twelve, six, and three months prior to symptom onset for persons diagnosed with early latent, secondary, and primary syphilis, respectively (corresponding to mean incubation times for these phases of early syphilis). Contact tracing is not performed for persons diagnosed with late latent syphilis.

Data were extracted from NC EDSS using SAS 9.4 (SAS Institute Inc., Cary, NC), and analyses were conducted in R v. 3.5.0¹³ and MATLAB 9.3 (The MathWorks Inc., Natick, MA). The Non-Biomedical Institutional Review Board at the University of North Carolina at Chapel Hill approved this study.

Independent and Combined Contact Network Generation

We defined a *network event* as either: a) becoming diagnosed with HIV or early syphilis (a *diagnosis event*), or b) being named as a sexual contact by someone becoming diagnosed with HIV or early syphilis (a *contact event*). Each network event was assigned a *network event status*: HIV *diagnosis*, early syphilis *diagnosis*, HIV *contact*, or early syphilis *contact*.

We included all new HIV and early syphilis diagnoses among self-identified cisgender, MSM aged 18 years who were diagnosed in NC between 2015 and 2017 as HIV and syphilis diagnosis events, respectively. Adult, cisgender men named as sexual contacts at these diagnosis events were included as HIV and early syphilis contact events, respectively. Persons diagnosed with both HIV and syphilis had both diagnoses included as separate HIV and syphilis diagnosis events, and thus were included in both networks. Persons diagnosed with HIV or syphilis and named as contacts had each event included as diagnosis and contact events, respectively. We excluded diagnosis events among persons who were not reached by DIS for interview or who refused DIS interview (N = 283), as these persons could not offer any information for network analysis. Events among self-identified transgender persons (N = 199) were not included because gender identity was not collected for persons diagnosed with syphilis during the study time frame, preventing network analyses specific to this vulnerable population.

In social network analysis, persons are represented as *nodes* and relevant connections between persons are included as *edges*.¹⁴ We generated an independent *HIV network* comprising HIV cases and contacts as nodes, with sexual relationships reported between these persons during HIV contact tracing as edges. We generated an analogous independent *syphilis network* comprising syphilis cases and contacts as nodes, linked by edges

representing sexual relationships reported during syphilis contact tracing. Finally, we generated a *combined HIV/syphilis network* comprising all nodes and edges from both independent networks.

Network Description

We calculated descriptive statistics for the combined network population and by network event status, summarizing the number and percentage of network events according to age and self-identified race/ethnicity. We also described the diagnostic site for persons diagnosed with early syphilis, categorizing sites as 1) primary care physician's office or health maintenance organization (HMO) provider; 2) STD clinic; 3) other clinic; 4) emergency department; and 5) other (e.g., inpatient care, correctional facility, blood bank).

We calculated standard network parameters for the independent and combined networks. We identified *isolates*, defined as nodes that are not connected by an edge to any other node, and *components*, defined as groups of two or more nodes in which each node is connected by an edge to at least one other node in the component.¹⁴ We calculated the largest component size and characterized the corresponding component size distribution for each network. We also calculated the mean *node degree*, or the number of nodes to which each node was connected by an edge,¹⁴ in each network population. Finally, we assessed *homophily*, also termed assortative mixing, which measures the tendency for nodes to be connected to other nodes that share a set characteristic.¹⁵ We characterized homophily by age by calculating the median absolute difference in age between nodes in each diagnosis-contact pair. We evaluated homophily by race/ethnicity via homophilic preference, or the proportion of edges within diagnosis-contact pairs with concordant self-identified race/ethnicity classifications¹⁵ (Black, non-Hispanic; white, non-Hispanic; Hispanic; Asian, non-Hispanic; or other/multiracial).

Network Overlap and Interconnectivity

We used the Jaccard node similarity to quantify direct overlap between the independent HIV and syphilis networks, where a value of 1 represents complete overlap and a value of 0 represents no overlap. We calculated the Jaccard node similarity as the number of nodes belonging to both independent networks (intersection) divided by the number in the combined network (union).¹⁶ We calculated the Jaccard edge similarity analogously as the number of edges in the intersection divided by the number in the union.

Jaccard node and edge similarities do not fully describe the potential for HIV to propagate across the syphilis network because opportunities for transmission of HIV through the syphilis network are dependent on both the amount and distribution of overlap [Figure 1]. If the HIV network overlaps with only a distinct segment of the syphilis network, few persons within the syphilis network are directly connected to the HIV network. However, if the HIV and syphilis networks are widely interwoven, a larger proportion of syphilis network members may be directly connected to the HIV network. We devised a simple measure of *interconnectivity* to reflect this phenomenon.

We conceptualized interconnectivity as the relative percentage increase in mean node degree (mean number of nodes to which each node is connected) following combination of an index

network with a partially overlapping network. To estimate interconnectivity of the syphilis network (the index network) with the HIV network (the partially overlapping network), we thus compared the mean node degree among syphilis network members in the independent syphilis vs. combined HIV/syphilis networks. If there were no interconnectivity between the syphilis and HIV networks, we would observe no increase in mean node degree; higher relative increases represent greater interconnectivity. This measure is similar to the approach proposed by Dickison et al.¹⁷ for evaluation of coupled, disjoint network systems, but our simpler measure allows for nodes and edges to be shared between networks. Further, our measure does not require that networks' degree distributions demonstrate an internal scale, a requirement violated by scale-free networks, including many sexual contact networks.

Network Community Detection

Network community detection divides a network into clusters of nodes that are more densely connected to each other than to the remainder of the network.¹⁸ We employed this approach to identify clusters of nodes within the combined HIV/syphilis network in which the syphilis network was highly interconnected with the HIV network, suggesting greater potential for exogenous HIV entry into the syphilis network. We applied a generalized Louvain method for network community detection, including the independent HIV and syphilis networks as two distinct network layers.¹⁸ Although phylogenetic network data could be included as an additional layer, we chose not to do so due to challenges in interpretation. Specifically, while contact tracing edges are restricted to a set time frame, edges representing genetically similar viral sequences may represent direct or indirect connections between PLWH over a variable (and uncertain) time frame.

The generalized Louvain method maximizes a quality function Q , also termed the *modularity* of the network, to identify the set of network community assignments that produces the highest concentration of edges within network communities. Larger values of Q (maximum possible value = 1) indicate that more edges occur within network communities (rather than between communities), while $Q = 0$ indicates that edges are uncorrelated with shared network community membership. The quality function and its application in this study are detailed in the Supplemental Materials. Network community detection analyses were restricted to the largest connected component in the combined network to prevent disconnected components from being grouped into spurious network communities, as can happen with this community detection method when the network includes many small, disconnected components and isolates.¹⁸

Heterogeneity of Syphilis/HIV Network Interconnectivity by Network Community

We repeated our analysis of syphilis network interconnectivity with the HIV network in each network community to assess heterogeneity of interconnectivity across network communities. Using a threshold set *a priori* and based loosely on the Central Limit Theorem,¹⁹ we restricted this analysis to network communities containing ≥ 30 members of the syphilis network to allow for reliable estimates of interconnectivity.

To determine whether highly interconnected communities had any distinguishing features that might guide resource allocation, we used simple linear regression to assess the

unadjusted association between single network community characteristics and community-level interconnectivity. Independent variables included median age of network community members at first network event; proportion of network community members who self-identified as Black, non-Hispanic; and proportion of persons with syphilis diagnoses who received their diagnoses at STD clinics in each network community.

RESULTS

Network Populations

There were 2,090 and 3,419 HIV and early syphilis diagnoses, respectively, that met our inclusion criteria between 2015 and 2017 in NC [Table 1]. These diagnosis events produced 2,439 eligible HIV contact events and 3,545 eligible syphilis contact events, for a total of 11,493 network events among 8,020 unique network members. Most network events were among persons who self-identified as Black, non-Hispanic (60%) or white, non-Hispanic (29%) and the median age at the first eligible network (diagnosis or contact) event was 28.7 (interquartile range [IQR]: 24.2–36.8) years. Age at first network event was lower for HIV vs. syphilis network members (median age 27.7 vs. 29.0 years), and HIV network events were more likely than syphilis network events to occur among persons self-identifying as Black, non-Hispanic (62% vs. 58%). Persons diagnosed with early syphilis were most commonly diagnosed by a primary care physician or HMO provider (37%) or at an STD clinic (36%).

Independent and Combined Network Characteristics

The largest connected component in the syphilis network comprised 13% of all syphilis network members, whereas the largest connected component in the HIV network comprised 9% of all HIV network members [Table 2, Supplemental Figure A]. In the combined network, edges in each of the independent networks bridged disconnected components across the other, creating a largest connected component containing 2,350 persons (29% of all combined network members). Similar proportions of persons were identified as isolates in the HIV, syphilis, and combined networks (19%, 20%, and 20%, respectively).

The overall mean node degree, including isolates, in the combined HIV/syphilis network (1.49; 95% CI: 1.45, 1.53) was greater than that observed in the independent HIV (1.24; 95% CI: 1.19, 1.29) and syphilis (1.34; 95% CI: 1.30, 1.38) networks, while levels of homophily were similar across all three networks. In the combined HIV/syphilis network, the median absolute difference in age between persons diagnosed with HIV and/or syphilis and their named contacts was 5.3 years (younger or older) and 70% of case-contact pairs shared concordant racial and ethnic self-identities. Index cases were typically younger than their named contacts in the HIV, syphilis, and combined networks (median difference: –1.9, –0.5, and –1.2 years, respectively).

We observed minimal direct overlap between the independent networks according to Jaccard measures, with just 15% of nodes and 6% of edges found in both the HIV and syphilis networks, including isolates. Overlapping nodes encompassed all persons who were found in both networks, with any combination of event statuses, during the three-year study time

frame. Only 430 (5.4%) nodes were diagnosed with both HIV and syphilis during the study time frame. Of the 376 edges found in both networks, 185 (49%) represented a link between a person who was simultaneously diagnosed with both HIV and syphilis and a contact named by that person for both HIV and syphilis contact tracing. The remaining 191 (51%) resulted from one person being diagnosed with HIV and syphilis at separate times and naming the same contact at both events, or from one person in the edge being diagnosed with HIV and naming the other person, who was diagnosed with syphilis and named the first person at a separate time.

The mean node degree among members of the syphilis network increased by a relative 26% following combination with the HIV network (1.34 vs. 1.69; interconnectivity = 26%).

Network Communities

We identified twenty-six distinct network communities within the largest connected component of the combined network [Supplemental Figure B]. We observed modularity (Q) = 0.97 out of a maximum value of 1.0, indicating that the vast majority of network edges, and consequently opportunities for transmission, occur within network communities rather than between members of different network communities. Twenty-one network communities comprising 2,268 persons (97% of persons in the largest connected component) contained

30 members of the syphilis network each and were further evaluated for within-community interconnectivity. The mean relative increase in node degree among members of the syphilis network following combination with the HIV network spanned 15% to 72% across network communities. Thus, some portions of the combined network had greater interconnectivity of the syphilis network with the HIV network and greater potential for exogenous entry of HIV into the syphilis network.

Our regression analyses revealed associations between demographic identifiers and interconnectivity that could prove useful in the development and deployment of enhanced HIV prevention efforts for specific sub-populations at heightened risk of HIV exposure. More specifically, a one-year decrease in the median age of network community members, compared to the highest observed value, was associated with an absolute increase of 1.7 (95% CI: -0.4, 3.8) percentage points in interconnectivity. A ten-percentage-point increase in the percentage of persons who self-identified as Black, non-Hispanic, compared to the lowest observed value, was associated with an absolute increase of 3.2 (95% CI: 0.7, 5.7) percentage points in interconnectivity. Median age and race/ethnicity within network communities were also associated with each other [Figure 2].

Regression analyses also indicated that persons diagnosed with syphilis at STD clinics may experience substantial exposure to the HIV network: a ten-percentage-point increase in the percentage of persons diagnosed with syphilis at STD clinics, compared to the lowest observed value, was associated with an absolute increase of 2.5 (95% CI: -1.7, 6.7) percentage points in interconnectivity.

DISCUSSION

Despite persistent, coinciding HIV and syphilis epidemics among MSM, the relationship between HIV and syphilis contact networks has not been well characterized. Improved understanding of interactions between these networks may allow for development of efficient intervention approaches, including HIV prevention strategies prioritizing sub-populations in which the syphilis network is highly interconnected with the HIV network. In this study, we devised and applied a simple measure of network interconnectivity in statewide HIV/syphilis contact networks as an initial step toward such an approach.

Our application of network community detection is a novel strategy for identifying network subsets with potentially increased risk of infection entry. Network community structures have been widely observed across biological, neural, computational, and social networks, including contact networks in human and animal populations.^{20,21} Our network showed extremely high modularity, or concentration of edges within network communities, which is associated with explosive transmission within network communities and rare transmission across network communities.²⁰ High modularity was also observed in an analysis of a sexual contact network of PLWH in Cuba under a different network community detection algorithm.²¹

In the absence of real-time network community detection analysis, it may be useful to guide resource allocation to specific sub-populations that tend to belong to network communities in which the syphilis network is particularly interconnected with the HIV network. If enhanced HIV prevention interventions must be prioritized within the syphilis network due to resource constraints, young, Black MSM appear to be optimal recipients due to their increased membership in network communities with heightened interconnectivity of the syphilis network with the HIV network. Persons diagnosed with syphilis at STD clinics, many of which are housed in city and county health departments, may also experience substantial exposure to the HIV network and may benefit disproportionately from additional support. Supplemental interventions could include pre-exposure prophylaxis (PrEP) care navigation and ongoing support for PrEP maintenance, routine HIV testing reminder notifications, and prioritization of these persons for digital contact tracing services to reach contacts for whom little traditional contact information is available.

Homophily contributes to the formation of network community structure,²² which may drive heightened transmission within vulnerable demographic sub-groups that have historically suffered higher HIV prevalence. Syphilis network members who belong to network communities with high interconnectivity with the HIV network are more likely to be exposed to HIV than those in network communities with low interconnectivity, and the composition of these network communities is tightly associated with demographic characteristics. In the network assessed here, younger median age and greater proportions self-identifying as Black, non-Hispanic among network community members were associated with heightened interconnectivity of the syphilis network with the HIV network. This finding is congruent with prior studies illustrating the role of racial homophily, alongside existing racial and ethnic disparities in HIV prevalence and treatment,²³ in driving HIV incidence among Black MSM.^{24,25}

Beyond the detection of specific network communities with elevated interconnectivity and potentially heightened risk of HIV exposure among syphilis network members, we observed interconnectivity between the HIV and syphilis networks overall. There is a robust history of combined HIV and syphilis control efforts,²⁶ and in the absence of constraints necessitating more focused interventions, HIV and syphilis prevention interventions that attempt to reach the full combined network have the potential to make a strong impact. For example, NC and other jurisdictions have recently expanded HIV prevention services to include referrals for PrEP by DIS during contact tracing for both HIV and syphilis.²⁷ Another recent analysis evaluated venues (physical or digital spaces where persons met sex partners) named by persons diagnosed with HIV or syphilis and identified high levels of venue co-affiliation in the HIV and syphilis networks.²⁸ Venue-based interventions against both HIV and syphilis in the full combined network may also be highly effective.

Our analysis is limited to assessment of network interconnectivity and does not attempt to quantify individual HIV exposure risk among syphilis network members, as our networks aggregated sexual partnerships over several years and did not capture the time-course of individual infection statuses or the spread of infection within or across networks. This approach smooths over the dynamism of true contact networks and is unable to describe the dendritic, forward movement of infection transmission through a network. Rather than examining individual-level exposure risk, we aimed to evaluate the HIV and syphilis epidemics from a network perspective by identifying populations in which the syphilis network is more likely to be interconnected with the HIV network, irrespective of individual syphilis network members' HIV statuses. With this exploratory inquiry, we aim to spark future research on network interconnectivity and network community detection in public health.

We acknowledge that persons diagnosed with HIV and syphilis and their named sexual contacts do not represent the complete HIV and syphilis transmission networks in NC. Network membership was subject to selection bias because members were identified via self-reported sexual orientation and gender identity, and our networks only included persons receiving infection diagnoses who consented to a DIS interview and persons named as sexual contacts.²⁹ Further, contact tracing data can suffer from social desirability bias and recall error.²⁹ Although these factors limit generalizability beyond the reported network population, our findings are highly germane to the development of MSM-focused HIV prevention interventions for deployment within the existing HIV and syphilis contact tracing infrastructure. Future analyses may extend these methods to dynamic networks and to additional populations, transmission modes, and network layers, including phylogenetic and geographic networks. In particular, future analyses could examine the network positioning of and guide resource allocation for transgender individuals within the combined HIV/syphilis network as more data become available on these populations.

Sexual contact networks containing HIV and syphilis are interconnected among MSM in NC, and the sexual network of known HIV and syphilis cases and contacts offers an efficient platform for deployment of intensified HIV prevention interventions. Limited HIV prevention resources may be most efficiently utilized by leveraging existing contact tracing infrastructure to reach populations in which the syphilis network is highly interconnected

with the HIV network. Modernization of surveillance systems to include real-time automated analyses utilizing available network data may allow for targeted delivery of interventions to specific persons, rather than the generalized populations highlighted here. In an era where “Ending the HIV Epidemic” campaigns are being mounted across the US,³⁰ this type of information may be helpful in the design and deployment of interventions against persistent HIV incidence in particularly vulnerable populations.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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Figure 1.

Interconnectivity vs. overlap. The top row provides a high-level visualization and the bottom row illustrates this concept in a mock network. Example networks on the left and right have the same number and proportion of overlapping nodes (3/15), but divergent levels of interconnectivity (12.5% vs. 50%). Members of the HIV network only are shown in blue, members of the syphilis network only are shown in red, and members of both the HIV and syphilis networks are shown in yellow. Nodes within the HIV network that contribute to the observed percentage increase in node degree among syphilis network members upon combination with the HIV network are distinguished with bold borders. The network on the left shows comparatively low interconnectivity of the syphilis network with the HIV network. Members of both networks are clustered together, bridging distinct HIV and syphilis networks, and a large portion of the syphilis network is relatively insulated from the HIV network. The network on the right shows comparatively high interconnectivity of the syphilis network with the HIV network. The HIV network is embedded within the syphilis network, directly connecting much of the syphilis network with the HIV network.

Figure 2. Demographic characteristics of members of the twenty-one network communities containing 30 members of the syphilis network in the largest connected component of the combined HIV/syphilis sexual contact network among men who have sex with men in North Carolina. The relative percentage increase in mean node degree among members of the syphilis network following combination with the HIV network (interconnectivity) in each community is indicated by color and community size is represented by point size. The percentage of community members who self-identify as Black, non-Hispanic on the y-axis is compared to the median age of community members at their first included network event on the x-axis.

Individual characteristics by network event status within the combined HIV/syphilis network among men who have sex with men in North Carolina 2015–2017.

Table 1.

Individual characteristics (N, %)	Combined HIV/syphilis network	Network event status			
		HIV diagnoses	HIV contacts	Early syphilis diagnoses	Early syphilis contacts
Age at network event					
18–24	3342 (29.1)	741 (35.4)	774 (31.7)	872 (25.5)	955 (26.9)
25–34	4643 (40.4)	822 (39.3)	1047 (42.9)	1319 (38.6)	1455 (41.0)
35–44	1871 (16.3)	251 (12.0)	383 (15.7)	612 (17.9)	625 (17.6)
45+	1637 (14.2)	276 (13.2)	235 (9.6)	616 (18.0)	510 (14.4)
Race/ethnicity					
White, non-Hispanic	3339 (29.0)	533 (25.5)	601 (24.6)	1082 (31.6)	1123 (31.7)
Black, non-Hispanic	6865 (59.7)	1266 (60.6)	1581 (64.8)	2011 (58.8)	2007 (56.6)
Hispanic	814 (7.1)	211 (10.1)	126 (5.2)	263 (7.7)	214 (6.0)
Asian, non-Hispanic	76 (0.7)	14 (0.7)	7 (0.3)	32 (0.9)	23 (0.6)
Other	121 (1.0)	19 (0.9)	22 (0.9)	31 (0.9)	49 (1.4)
Missing	278 (2.4)	47 (2.2)	102 (4.2)	0 (0.0)	129 (3.6)
Syphilis diagnostic site					
STD clinic	---	---	---	1090 (36.2)	---
Private physician/HMO	---	---	---	1110 (36.8)	---
Other clinic	---	---	---	405 (13.4)	---
Emergency room	---	---	---	117 (3.9)	---
Other	---	---	---	293 (8.6)	---
Total network events	11493	2090	2439	3419	3545

STD; Sexually transmitted disease. HMO; Health maintenance organization

Network parameters for the combined HIV/syphilis and independent HIV and syphilis sexual contact networks among men who have sex with men in North Carolina 2015–2017.

Table 2.

Network parameter	Combined network	HIV network	Syphilis network
Network size (nodes)	8020	3928	5283
Number of unique edges	5984	2439	3545
Isolates (N, %)	1572 (19.6)	779 (19.8)	1003 (19.0)
Component size (N, %)			
Dyad	883 (63.6)	468 (57.0)	642 (61.4)
Small (3–9)	473 (34.1)	318 (38.7)	365 (34.9)
Medium (10–29)	30 (2.2)	31 (3.8)	30 (2.9)
Large (≥ 30)	2 (0.1)	4 (0.5)	8 (0.8)
Total	2960	1596	2048
Largest connected component (N, %)	2350 (29.3)	334 (8.5)	672 (12.7)
Node degree (mean, 95% CI)	1.49 (1.45, 1.53)	1.24 (1.19, 1.29)	1.34 (1.30, 1.38)
Homophily			
Age in years: age _{case} – age _{contact} (median, IQR)	5.3 (2.2, 7.8)	4.9 (2.1, 7.4)	5.6 (2.4, 8.1)
Race/ethnicity: homophilic preference (mean, 95% CI)	0.7 (0.7, 0.7)	0.7 (0.7, 0.7)	0.7 (0.7, 0.7)
Jaccard node similarity	0.15	---	---
Jaccard edge similarity	0.06	---	---

95% CI; 95% confidence interval. IQR; interquartile range