Preplanned Studies

Partner Tracing Survey and Phylogenetic Analysis Among Newly Diagnosed HIV-Positive MSM — Shenzhen City, Guangdong Province, China, 2019–2022

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Summary

What is already known about this topic?

Partner tracing (PT) represents an established public health strategy for identifying undiagnosed individuals with human immunodeficiency virus (HIV) infection and contributes to controlling sustained HIV transmission.

What is added by this report?

Partner tracing among newly diagnosed HIV-infected men who have sex with men (MSM) demonstrates effectiveness in identifying undiagnosed infected individuals, with regular sexual partners showing higher likelihood of HIV-positive detection. However, phylogenetic analysis revealed that only a small proportion of epidemiologically linked pairs exhibited genetic linkage.

What are the implications for public health practice?

Sustained implementation and broader application of partner tracing may serve a critical role in HIV epidemic control by facilitating early identification of undiagnosed infections and interrupting potential transmission chains. Integrating partner tracing with phylogenetic analysis enhances the capacity to distinguish actual transmission chains from coincidental behavioral associations, thereby improving transmission linkage identification accuracy and informing more targeted intervention strategies.

ABSTRACT

Introduction: In China, the proportion of men who have sex with men (MSM) among newly diagnosed human immunodeficiency virus (HIV) infections is continuously increasing. This study aimed to identify undiagnosed HIV-infected patients in Shenzhen MSM through partner tracing (PT) and to explore potential transmission linkages using phylogenetic analysis.

Methods: From 2019 to 2022, newly diagnosed HIV-positive MSM were recruited as index cases to participate in PT by convenience sampling. Data were collected through offline questionnaires and the National HIV/AIDS Surveillance Database. Phylogenetic analysis using the maximum likelihood method was conducted based on HIV Pol region gene sequences to determine genetic associations.

Results: Of the 486 index cases, a total of 579 sexual partners were traced, of whom 19.9% tested positive for HIV. Among these HIV-positive partners, 83.9% were newly diagnosed infections, and 33.3% were recent infections. Only 8.9% of epidemiologically linked index cases — HIV-positive partner pairs showed genetic associations. Index cases with regular partners were significantly more likely to identify HIV-positive partners [adjusted odds ratio (a*OR*)=1.81; 95% confidence interval (*CI*): 1.02–3.23].

Conclusion: PT is effective in identifying undiagnosed HIV infection and is recommended for further promotion in the MSM population. However, only parts of the epidemiologically linked infected pairs also exhibited genetic association. Therefore, combining PT with phylogenetic analysis can help to more accurately identify the actual transmission network and inform more targeted intervention strategies.

Men who have sex with men (MSM) represent the population at highest risk for human immunodeficiency virus (HIV) infection, with the proportion of newly diagnosed HIV cases attributed to homosexual transmission steadily increasing in China. Surveillance data reveal that homosexual transmission accounts for more than 60% of new HIV cases in Shenzhen. Understanding partnership networks is essential for identifying transmission links among

MSM and disrupting potential transmission chains. Partner tracing (PT) serves as a behavioral surveillance strategy that encourages HIV-infected individuals to refer their sexual partners for HIV testing and treatment (*1*). Research has demonstrated that PT increases HIV testing rates and condom use among key populations (*2*). More importantly, PT can identify undiagnosed infections before further transmission occurs and detect potential clusters of cases before they expand (*3*). To identify additional undiagnosed HIV-positive MSM and explore transmission associations, this study implemented PT combined with phylogenetic analysis among newly diagnosed individuals.

From 2019 to 2022, we recruited newly diagnosed HIV-positive MSM in Shenzhen through convenience sampling to participate in PT. We employed three PT modalities — passive, contractual, or provider notification — to trace sexual partners and provide HIV testing services. After the initial tracing round, HIV-positive sexual partners continued to participate as index cases for a second round of PT. We collected data through offline questionnaires and the China Comprehensive HIV/Acquired Immunodeficiency Syndrome (AIDS) Prevention and Control Data Information System.

We identified recent infections using the HIV-1 limiting-antigen avidity enzyme immunoassay. Sequence acquisition and HIV-1 subtyping methods followed protocols described in previous studies (*4*). We constructed a sexual partner network using Cytoscape (version 3.10.1, Cytoscape Consortium, Santiago, Chile). We built phylogenetic trees using the Maximum Likelihood (ML) method based on the Kimura 2-parameter model in MEGA (version 6.0, Mega Limited, Auckland, New Zealand) software, with 1,000 bootstrap replicates. We considered sequences that clustered with bootstrap values greater than 95% as genetically linked. We performed statistical analysis using the chi-square test and binary logistic regression.

Between 2019 and 2022, a total of 4,880 newly diagnosed HIV-positive MSM were identified in Shenzhen, of whom 486 participated in PT as index cases. The demographic characteristics of the index cases did not differ significantly from those of the overall population (*P*>0.05) (Table 1). Among the 475 index cases who successfully referred sexual partners, 579 partners were identified, with 19.9% (115/579) testing HIV-positive. Subsequently, 9.6% (11/115) of the HIV-positive sexual partners agreed to serve as new index cases for the second round of PT, referring an additional 13 sexual partners, of whom 23.1% (3/13) tested HIV-positive. The complete sexual contact network comprised 614 edges and 1,067 cases, with 593 individuals (475 index cases and 118 sexual partners) confirmed as HIV-infected MSM. Among the 118 HIV-positive sexual partners, 83.9% (99/118) were newly diagnosed cases. Of the 108 HIV-positive sexual partners whose samples were available for recent infection analysis, 33.3% (36/108) were determined to have recent infections. Logistic regression analysis revealed that index cases with regular sexual partners (a*OR*=1.81, 95% *CI*: 1.02, 3.23) were significantly more likely to have HIV-positive sexual partners identified through tracing (Table 2).

Pol gene sequences were successfully obtained from 92.2% (448/486) of index cases. The predominant HIV-1 subtypes were CRF07_BC (48.4%, 217/448), CRF01_AE (28.3%, 127/448), and CRF55_01B (16.3%, 73/448), with other subtypes comprising 6.9% (31/448). The subtype distribution among index cases did not differ significantly from that of the overall HIV-positive MSM population (*P*>0.05). Among the 121 contact pairs traced between 119 index cases and 118 HIV-positive sexual partners, pol sequences were obtained for 83.5% (101/121) of pairs. However, only 8.9% (9/101) of these epidemiologically linked pairs demonstrated genetic linkage in addition to their behavioral associations. The 101 index cases who successfully traced HIV-positive sexual partners showed the following subtype distribution: 51.5% CRF07_BC, 26.7% CRF01_AE, 11.9% CRF55_01B, and 9.9% other subtypes, which did not differ significantly from the overall HIV-positive MSM population (*P*>0.05). Genetic linkage rates varied substantially by HIV-1 subtype: 7.7% (4/52) for CRF07_BC-infected index cases, 3.7% (1/27) for CRF01_AE-infected cases, 25.0% (3/12) for CRF55_01B-infected cases, and 10.0% (1/10) for other subtypes (Figure 1). Fisher's exact test revealed that index cases infected with CRF55_01B demonstrated significantly higher rates of genetic association with their HIV-positive sexual partners compared to those infected with CRF07_BC and CRF01_AE (*P*=0.034).

DISCUSSION

Following extensive behavioral interventions, the MSM population in Shenzhen has demonstrated declining trends in both HIV incidence and clustering rates within molecular transmission networks (*4*). By

TABLE 1. Demographic characteristics of index cases and total newly diagnosed HIV-infected MSM from 2019 to 2022.

Variable	Total newly diagnosed HIV-infected MSM, *n* (%)	Index cases, *n* (%)	*P*
Age (years)			0.155
16–25	1,456 (29.8)	130 (26.7)	
≥26	3,424 (70.2)	356 (73.3)	
Census registration			0.308
Shenzhen City	811 (16.6)	88 (18.1)	
Guangdong Province except Shenzhen City	936 (19.2)	103 (21.2)	
Others*	3,133 (64.2)	295 (60.7)	
Ethnicity			0.525
Han	4,552 (93.3)	457 (94.0)	
Non-Han	328 (6.7)	29 (6.0)	
Education			0.093
Below senior high school	1,228 (25.2)	102 (21.0)	
Senior high school or technical secondary school	1,539 (31.5)	154 (31.7)	
College or university	2,113 (43.3)	230 (47.3)	
Marital status			0.190
Unmarried	3,940 (80.7)	383 (78.8)	
Divorced or widowed	370 (7.6)	33 (6.8)	
Married	570 (11.7)	70 (14.4)	
Recent infection			0.187
Yes	1,612 (35.2)	174 (38.3)	
No	2,965 (64.8)	280 (61.7)	
HIV subtype			0.144
CRF01_AE	987 (26.0)	127 (28.3)	
CRF07_BC	1,881 (49.6)	217 (48.4)	
CRF55_01B	553 (14.6)	73 (16.3)	
Others	375 (9.9)	31 (6.9)	

Abbreviation: HIV=human immunodeficiency virus; MSM=men who have sex with men.

* Provinces and cities other than Guangdong Province.

2022, the HIV-positive rate among MSM in Shenzhen reached 2.78%, substantially lower than the 5.4% rate reported in national MSM sentinel surveillance data. However, the positive rate among sexual partners identified through PT reached 19.9% in this study, significantly exceeding rates from MSM surveillance conducted through respondent-driven sampling (5.2%) or time-location sampling (2.8%) during the same period in Shenzhen ($P<0.001$). These findings demonstrate that PT represents a highly effective method for detecting HIV-positive MSM with superior efficiency compared to conventional surveillance approaches. The substantial proportion of new diagnoses (83.9%) among HIV-positive partners further underscores PT's effectiveness in identifying previously undiagnosed HIV-infected MSM. These results strongly support the broader implementation and expansion of PT across diverse settings, which would significantly contribute to achieving the first 95% target of the UNAIDS strategy.

Consistent with previous research (*5*), we observed a higher proportion of HIV positivity among regular sexual partners of index cases, which likely reflects behavioral and psychological factors. Stronger emotional bonds, greater mutual trust, and reduced perceived infection risk characterize these relationships. In certain contexts, condom use may be perceived as indicating mistrust, thereby increasing the likelihood of unprotected sexual encounters. Additionally, the stability and continuity inherent in regular partnerships may create cumulative risk effects, where frequent and prolonged unprotected sexual activity in the absence of consistent protective measures substantially increases overall infection probability.

TABLE 2. Sociodemographic and behavioral characteristics of index cases successfully traced to HIV-positive sexual partners.

Variable	Successfully traced to sexual partners, *n* (*N*=486)	Index cases successfully traced to HIV-positive sexual partners		*P*	a*OR* (95% *CI*)
		n	**%**		
Age (years)				0.873	
16–25	128	31	24.2		
≥26	353	88	24.9		
Census registration				0.961	
Shenzhen	88	22	25.0		
Guangdong except Shenzhen	102	24	23.5		
Others*	295	73	24.7		
Ethnicity				0.197	
Han	457	109	23.9		
Non-Han	29	10	34.5		
Education				0.734	
Below senior high school	101	22	21.8		
Senior high school or technical secondary school	154	40	26.0		
College or university	227	57	25.1		
Employment status				0.591	
Employed	400	96	24.0		
Unemployed	86	23	26.7		
Annual income (10,000 CNY)				0.374	
<60,000	90	24	26.7		
60,000–120,000	251	56	22.3		
>120,000	111	32	28.8		
Residence time in Shenzhen (years)				0.518	
≤0.5	25	6	24.0		
0.6–1.0	23	5	21.7		
1.1–2.0	66	12	18.2		
>2.0	330	88	26.7		
Marital status				0.441	
Unmarried	379	89	23.5		
Divorced or widowed	33	9	27.3		
Married	69	21	30.4		
Method of finding sexual partners				0.862	
Offline	37	10	27.0		
Online	294	73	24.8		
Both	105	24	22.8		
Drug use				0.448	
Yes	37	11	29.8		
No	431	104	24.1		
Number of sexual partners				0.086	
≤2	142	40	28.2		
3–5	288	65	22.6		

Continued

Variable	Successfully traced to sexual partners, *n* (*N*=486)	Index cases successfully traced to HIV-positive sexual partners		*P*	a*OR* (95% *CI*)
		n	%		
6–9	34	12	35.3		
≥10	22	2	9.1		
With regular sexual partners				0.041	
Yes	222	63	28.4		1.81 (1.02–3.23)
No	106	19	17.9		1
Condomless anal intercourse				0.755	
Yes	209	53	25.4		
No	249	60	24.1		
Recent infection				0.437	
Yes	174	46	26.4		
No	280	65	23.2		

Abbreviation: a*OR*=adjusted odds ratio; *CI*=confidence interval; CNY=Chinese Yuan.

* Provinces and cities other than Guangdong Province.

A striking finding of this study is the remarkably low proportion of genetic linkage between index cases and their HIV-positive sexual partners, which was substantially lower than previously reported in Zhejiang Province (8.9% *vs.* 50.8%) (*6*). Several factors may account for this significant discrepancy. Shenzhen, as China's largest migrant city, had only 16.6% of HIV-positive MSM in this study being local residents. Previous research has demonstrated that HIV epidemics in Shenzhen are predominantly driven by the migrant population (*7*). High population mobility substantially increases individuals' exposure to diverse sexual networks and elevates the likelihood of acquiring HIV from genetically unrelated sources, resulting in fragmented transmission chains and disrupted social networks. Additionally, 67.5% of cases in this study were identified as late diagnoses with CD4 counts below 350 cells/μL, suggesting that many infections occurred more than four years earlier (*8*), likely prior to migration to Shenzhen. In chronic HIV infections, the absence of proofreading mechanisms during prolonged viral replication leads to the accumulation of genetic mutations, which may obscure detectable genetic relatedness even when true transmission has occurred. Furthermore, 70.8% of index cases reported having more than three sexual partners in the past six months, substantially increasing the probability that both the index case and their HIV-positive partners acquired infections independently from different sources. Moreover, the widespread use of online dating platforms — reported by over 90% of index cases — facilitates casual and transient sexual encounters (*9*), potentially leading to partnerships between individuals infected by unrelated sources who are not part of the same transmission chain. The fragile and anonymous nature of these relationships also impedes effective partner tracing and mutual reporting, thereby limiting the identification of transmission links. Nonetheless, when index cases were infected with CRF55_01B, a regional hotspot strain originating from the Shenzhen MSM community (*10*), they demonstrated significantly higher likelihood of genetic linkage with their HIV-positive sexual partners. This finding suggests that PT may be more effective in detecting local transmission networks.

This study presents two primary limitations. First, we employed convenience sampling for participant recruitment. Although comparisons of key demographic characteristics between our study sample and the target population revealed no statistically significant differences, the potential for selection bias cannot be entirely eliminated, which may limit the generalizability of our findings. Second, our analysis utilized Sanger sequencing methodology, which lacks the capability to detect multiple concurrent infections. This technical constraint may compromise the accuracy of genetic linkage assessments and could potentially underestimate the complexity of transmission dynamics within the study population.

In conclusion, partner tracing demonstrates significant effectiveness in identifying undiagnosed HIV infections and remains a cornerstone strategy for HIV prevention and control efforts. To maximize overall efficiency, partner tracing should be integrated with complementary surveillance approaches. Furthermore, partner tracing must be combined with

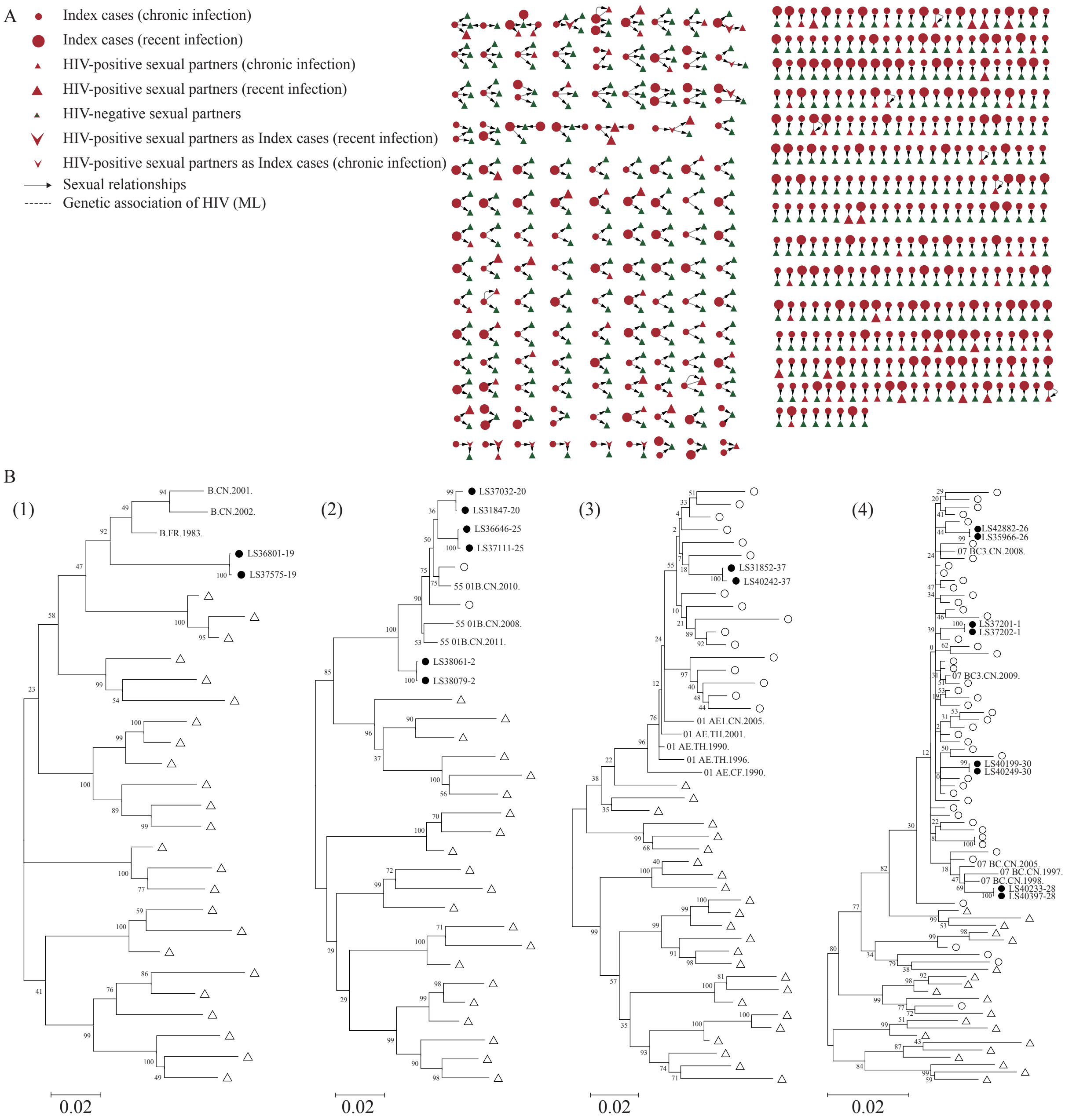

FIGURE 1. Social network of index cases and their partners, with a phylogenetic analysis of HIV-positive partners. (A) Sexual network of Index cases of traced partners and sexual partners; (B) ML tree of subtype B; (C) ML tree of CRF55_01B; (D) ML tree of CRF01_AE; (E) ML tree of CRF07_BC.

Note: For (B)–(E), ML trees were created with the same HIV subtype of index case-HIV-positive partner pairs. ● means with both epidemiologic and genetic association; ○ means with only epidemiologic association, and △ means reference sequences of subtype A, B, C, D, F, and G.

Abbreviation: HIV=human immunodeficiency virus; ML=maximum likelihood.

both epidemiologic and molecular evidence to accurately infer transmission associations and assess local HIV prevalence patterns, ensuring that transmission dynamics are precisely characterized and intervention strategies appropriately targeted.

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REFERENCES

1. World Health Organization. Guidelines on HIV self-testing and partner notification: supplement to consolidated guidelines on HIV testing services. Geneva: World Health Organization; 2016. https://iris.who.int/handle/10665/251655.
2. Dalal S, Johnson C, Fonner V, Kennedy CE, Siegfried N, Figueroa C, et al. Improving HIV test uptake and case finding with assisted partner notification services. AIDS 2017;31(13):1867 – 76. https://doi.org/10.1097/QAD.0000000000001555.
3. Hossain AD, Jarolimova J, Elnaiem A, Huang CX, Richterman A, Ivers LC. Effectiveness of contact tracing in the control of infectious diseases: a systematic review. Lancet Public Health 2022;7(3):e259 – 73. https://doi.org/10.1016/S2468-2667(22)00001-9.
4. Zhang D, Li HP, Zheng CL, Han JW, Li H, Liu YJ, et al. Analysis of HIV-1 molecular transmission network reveals the prevalence characteristics of three main HIV-1 subtypes in Shenzhen, China. J Infect 2022;85(6):e190 – 2. https://doi.org/10.1016/j.jinf.2022.08.024.
5. Kachur RE, Copen CE, Strona FV, Bernstein KT, Furness BW, Hogben M. Factors associated with online sex partners among gay, bisexual and other men who have sex with men: results from a national survey. Sex Transm Dis 2021;48(8):542 – 6. https://doi.org/10.1097/OLQ.0000000000001376.
6. Ding XB, Luo MY, Pan XH, Zhang JF, Fan Q, Jiang J, et al. Analysis on the relationship of molecular transmission between HIV infected men who have sex with men and their sexual partners. Chin J Epidemiol 2021;42(12):2106 – 11. https://doi.org/10.3760/cma.j.cn112338-20210811-00634.
7. An MH, Zheng CL, Li H, Chen L, Yang ZR, Gan YX, et al. Independent epidemic patterns of HIV-1 CRF01_AE lineages driven by mobile population in Shenzhen, an immigrant city of China. Virus Evol 2021;7(2):veab094. https://doi.org/10.1093/ve/veab094.
8. Lodi S, Phillips A, Touloumi G, Geskus R, Meyer L, Thiébaut R, et al. Time from human immunodeficiency virus seroconversion to reaching CD4+ cell count thresholds <200, <350, and <500 Cells/mm^3: assessment of need following changes in treatment guidelines. Clin Infect Dis 2011;53(8):817 – 25. https://doi.org/10.1093/cid/cir494.
9. Wang Z, Wu X, Lau J, Mo P, Mak W, Wang X, et al. Prevalence of and factors associated with unprotected anal intercourse with regular and nonregular male sexual partners among newly diagnosed HIV-positive men who have sex with men in China. HIV Med 2017;18(9):635 – 46. https://doi.org/10.1111/hiv.12500.
10. Wei L, Li H, Lv X, Zheng CL, Li GL, Yang ZR, et al. Impact of HIV-1 CRF55_01B infection on the evolution of CD4 count and plasma HIV RNA load in men who have sex with men prior to antiretroviral therapy. Retrovirology 2021;18(1):22. https://doi.org/10.1186/s12977-021-00567-z.