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Systematic review and meta-analysis of the global prevalence of sexually transmitted infections in people living with HIV and associated risk factors

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Abstract

People living with HIV (PLWH) constitute a vulnerable population for acquiring additional sexually transmitted infections (STIs). This study was conducted to provide a summary of the evidence on the global prevalence of STIs in PLWH with an emphasis on infectious agents, diagnostic methods, and related risk factors. PubMed, Scopus, and Web of Science were systematically searched to include records published from January 01, 1990, to January 31, 2022, and the Google Scholar search engine was used to check the search strategy. In total, 132 eligible studies reporting STIs in PLWH were included, enrolling subjects from 35 countries across five continents. The pooled proportion of STIs was estimated to be 30.23% (95% CI, 26.1-34.45%) in PLWH and 20.01% (95% CI, 17.17-23.01%) in HIV-negative patients. Our meta-analysis indicated that in PLWH, the pooled OR of STIs compared to HIV-negatives was 1.77 (95% CI: 1.58-1.98) (p < 0.0001). The pooled OR of STIs by viral infectious agents was highest in PLWH (52.19% [95% CI: 43.88-60.43]) compared with fungal (22.19% [95% CI: 15.64-29.53]), bacterial (19.07% [95% CI: 13.59-26.63]), and parasitic (14.05% [95% CI: 11.88-16.38]) infections. Our findings show that there is a rather significant frequency of STIs among PLWH. This study highlights the need for new programs for the detection, treatment, and prevention of STIs in this at-risk population.

Keywords

Sexually transmitted disease. Co-infection. Systematic review. Meta-analysis.

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Introduction

Sexually transmitted infections (STIs) are among the most prevalent worldwide health problems and are on the rise in certain populations. The most common factors affecting the presentation of STIs are microbial etiology, geography, the route of infection, and clinical manifestations. The risk of STIs transmission can be increased in the presence of a history of unprotected sexual contact, multiple partners, rape, prior history of STIs, alcoholism, recreational drugs, and intravenous drug use[1,2].

Although adolescents (between 15 and 25 years) make up only 25% of people with sexual experience, they account for 50% of all new STIs[3]. STIs may cause a number of destructive, often irreversible, and costly clinical problems such as pelvic inflammatory disease, fetal and pregnancy health complications, reproductive health problems, ectopic pregnancy, infertility, and cancers, and facilitate sexual HIV transmission[3,4].

HIV and AIDS remain one of the world's most important health challenges and a leading cause of premature death worldwide[5-7]. To date, approximately 76 million individuals in the world have been infected with HIV[8], of whom 38 million are living with HIV nowadays[9]. Remarkably, STIs facilitate the risk of acquiring HIV due to sharing the same routes of transmission[10]. Coinfection with STIs is the leading cause of reduced disability-adjusted life years among women of reproductive age[11]. Indeed, there is a bidirectional relationship between viral STIs and HIV; HIV can increase the risk of STIs, and STIs can pave the way for HIV disease progression[12].

In the present systematic review and meta-analysis, we aim to investigate the prevalence of STIs in HIV-positive individuals and to assess risk factors in this population.

Methods

Search strategy

This systematic review was conducted according to the principles outlined in the statement preferred reporting items for systematic and meta-analysis[13] (Supplemental Table S1). Search methods attempted to identify all relevant studies regardless of language, date of publication, or publication status. Two independent investigators (ME and HS) systematically searched electronic databases, including Medline (through PubMed) (https://www.ncbi.nlm.nih.gov/pubmed/), Scopus (https://www.scopus.com/), and Web of Science (https://www.webofnowledge.com/) with no restriction on language from January 01, 1990, to January 31, 2022. Search terms included a combination of medical subject heading terms and free-text words in titles, abstracts, and full texts.

The systematic search for PubMed was performed using the following search syntax: HIV OR "human immunodeficiency virus" OR ("immunodeficiency virus" AND human) OR "human T-cell lymphotropic virus type III" OR "human T-cell lymphotropic virus type III" OR "human T-cell leukemia virus type III" OR "human T-cell leukemia virus type III" OR LAV-HTLV-III OR "human T-cell leukemia virus type III" OR "lymphadenopathy-associated virus" OR (virus AND lymphadenopathy-associated) OR "human T lymphotropic virus type III" OR "human T-lymphotropic virus type III" OR "acquired immune deficiency syndrome virus" OR "acquired immunodeficiency syndrome virus" OR "AIDS virus" OR (virus AND AIDS) AND ("hepatitis A virus" OR ("B virus" AND hepatitis) OR "hepatitis B viruses" OR ("hepatitis B" AND viruses) OR ("hepatitis virus" AND "homologous serum") OR "Dane particle" OR (particle AND Dane) OR hepaciviruses OR "hepatitis C virus" OR "hepatitis C-like virus" OR cytomegaloviruses OR ("herpesvirus 5" AND human) OR "human herpesvirus 5" OR "HHV 5" OR ("herpesvirus 5 beta" AND human) OR simplexviruses OR "herpes virus hominis" OR (hominis AND herpes virus) OR "herpes virus homini" OR (homini AND herpesvirus) OR "herpes simplex virus" OR "herpes labialis virus" OR ("labialis virus" AND herpes) OR alpha papilloma viruses OR "human papillomavirus" OR (papillomavirus AND human) OR "HPV human papillomavirus" OR ("human papillomavirus" AND HPV) OR ("cervical neoplasm" AND uterine) OR (neoplasm AND "uterine cervical") OR "uterine cervical neoplasm" OR (neoplasm AND cervical) OR (cervical neoplasm) OR (neoplasm AND cervix) OR "cancer of the uterine cervix" OR "cancer of the cervix" OR "cervical cancer" OR "uterine cervical cancer" OR (cancer AND "uterine cervical") OR ("cervical cancer" AND uterine) OR "cancer of cervix" OR "cervix cancer" OR (cancer AND cervix) OR "*Chlamydia trachomatis*" OR "lymphogranuloma venereum" OR "lymphogranuloma inguinale" OR urethritides OR urethritis OR cervicitis OR (cervicitis AND uterine) OR "uterine cervicitides" OR cervicitides OR "pelvic inflammatory disease" OR (disease AND "pelvic inflammatory") OR ("inflammatory diseases" AND pelvic) OR "pelvic inflammatory diseases" OR "inflammatory pelvic disease" OR (disease AND "inflammatory pelvic")

OR "inflammatory pelvic diseases" OR ("pelvic disease" AND inflammatory) OR ("inflammatory disease" AND pelvic) OR adnexitis OR "*Bacillus ulcers cancerous* " OR "*Coccobacillus ducreyi*" OR "*Haemophilus ducreyi*" OR "*H. ducreyi*" OR "*H. ducreyi*" OR Chancroid OR "*Mycoplasma genitalium*" OR "*Neisseria gonorrhoeae*" OR "*Gonococcus neisseria*" OR "*Micrococcus gonorrhoeae*" OR "*Merismopedia gonorrhoeae*" OR "*Micrococcus der gonorrhoe*" OR "*M. gonococcus*" OR "*Diplococcus gonorrhoeae*" OR *Gonococcus* OR Gonorrhea OR "*N. gonorrhoeae* infection" OR proctitis OR proctitides OR "*Treponema pallidum*" OR syphilis OR "great pox" OR "*Ureaplasma urealyticum*" OR "*U. urealyticum* biovar 2" OR "*Trichomonas vaginalis*" OR (*vaginali* AND *Trichomonas*) OR "*T. vaginali*" OR trichomoniasis OR "*Trichomonas* infection" OR (infection AND *Trichomonas*) OR "*Candida albicans*" OR "*Dematium albicans*" OR "*Monilia albicans*" OR "*Para saccharomyces albicans*" OR "*Myceloblastanon albicans*" OR "*Syringospora albicans*" OR "*Pro candida albicans*" OR "*C. albicans var. stellatoidea*" OR "*P. candida stellatoidea*" OR "*Candida stellatoidea*" OR "*Saccharomyces albicans*" OR "*Mycotorula albicans*" OR "vaginal candidiasis" OR "vulvovaginal candidiasis" OR "vulvovaginal moniliasis" OR (moniliasis AND vulvovaginal) OR "genital vulvovaginal candidiasis" OR "monilial vaginitis" OR (vaginitis AND monilial)) AND 1990/01/01:2022/01/31[dp]. In addition, Scopus and Web of Science were searched using the same strategy. The Google Scholar search engine was used for checking the search strategy. The reference lists of all included articles and relevant reviews were hand searched for potentially eligible literature. In addition, authors and experts in the field were consulted to aid in the identification of relevant conference abstracts related to STIs in HIV.

Study selection

Initial screening by manuscript titles and abstracts was performed independently by two researchers (ME and HS) that also assessed the full texts of all potentially relevant articles. Discrepancies were resolved by consensus. From the retrieved articles, duplicates were removed. For a manuscript to be eligible for our study, it had to satisfy the following eligibility criteria: (i) studies had to provide data on the prevalence of STIs in HIV-positive people; (ii) studies could not duplicate data already published; and (iii) studies needed to be published as full manuscripts. Studies meeting the prevalence of STIs in people living with HIV (PLWH) with a total sample size smaller than 20, experimental studies, articles that only presented the final result and did not provide the raw data, or those without definite sample size, abstracts presented in congresses without full text, and case–control studies and clinical trials that could not report a correct estimate of prevalence were excluded from the study.

Data extraction and quality assessment

A standardized data collection form was used to extract the following data from each study: first author, publication year, country, number of patients with HIV and STI, education status, marital status, the count of $CD4^+$ T-cells in HIV-positive patients, antiretroviral therapy (ART) status, and detection methods for STIs. If one study reported data on infection with multiple pathogenic microorganisms, data for each microorganism were entered as an independent study.

Two authors independently assessed the quality of the studies using the Joanna Briggs Institute checklist[14]. These tools rate the quality of selection, measurement, and comparability and give a score to the studies. This tool comprised nine items with four options: "yes," "no," "unclear," and "not applicable." "Yes," answers were used to calculate the final score for each article.

Statistical analysis

Statistical analyses were achieved using Stats Direct (version 2.7.2). $p < 0.05$ was defined as statistically significant. Pooled OR with 95% CI was calculated using a random/fixed effect model to assess the association of bacterial, viral, parasitic, and fungal infections with the risks of STIs in PLWH. Since $I^2 > 50\%$, the random effects model was selected.

Forest plots were provided to demonstrate the detailed representation of the included studies based on effect size and CI. Incoherence and heterogeneity among studies were assessed using the I^2 index and Cochran's Q test, respectively. In addition, a funnel plot with Egger's regression asymmetry test to assess the study's small effects and the population bias were provided.

Results

Study characteristics

A total of 186,076 studies were identified by exploration of three selected databases, and finally, 132 records were found to be eligible for the current systematic review and meta-analysis (Fig. 1).

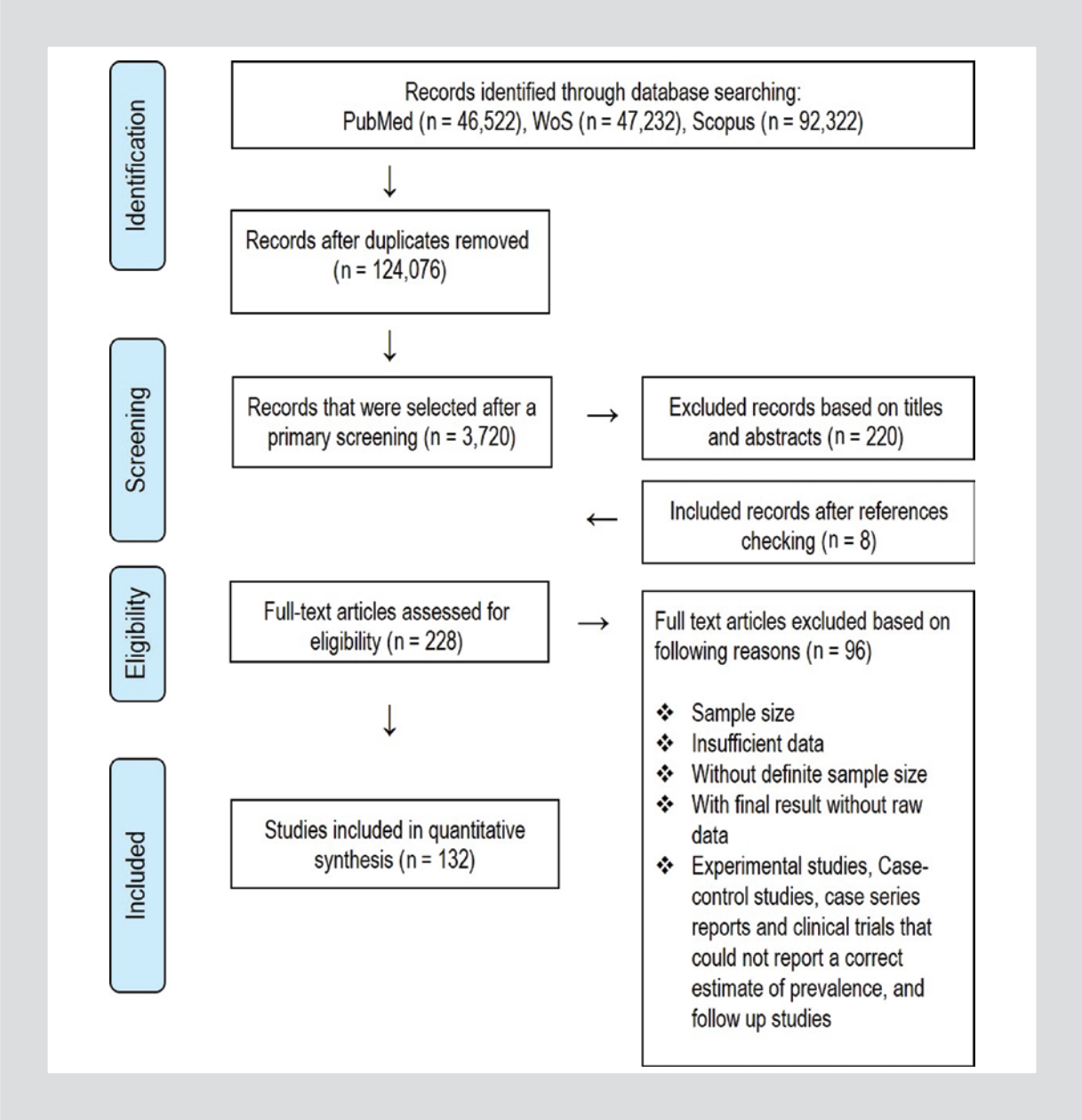

Figure 1. *Flow chart for literature selection.*

Chosen studies had been conducted in 35 countries across all five continents. Many studies were conducted on viruses (n = 81), followed by bacteria (n = 58), parasites (n = 51), and fungi (n = 23).

At least, four different diagnostic tools were used, including culture, molecular, serological, and microscopy. The most widely used diagnostic test to screen bacterial and viral infections in PLWH patients was molecular detection. Microscopic and culture methods were the most widely used diagnostic tests for parasitic and fungal infections, respectively. The main baseline characteristics of publications are recorded in Table 1[15-146].

Meta-analysis results

The estimated pooled global prevalence of STIs in PLWH and HIV-negative subjects using the random effects model for meta-analysis were 30.23% (95% CI, 26.18-34.45%) and 20.01% (95% CI, 17.17-23.01%), respectively (Table 2). The pooled OR of STI for viral

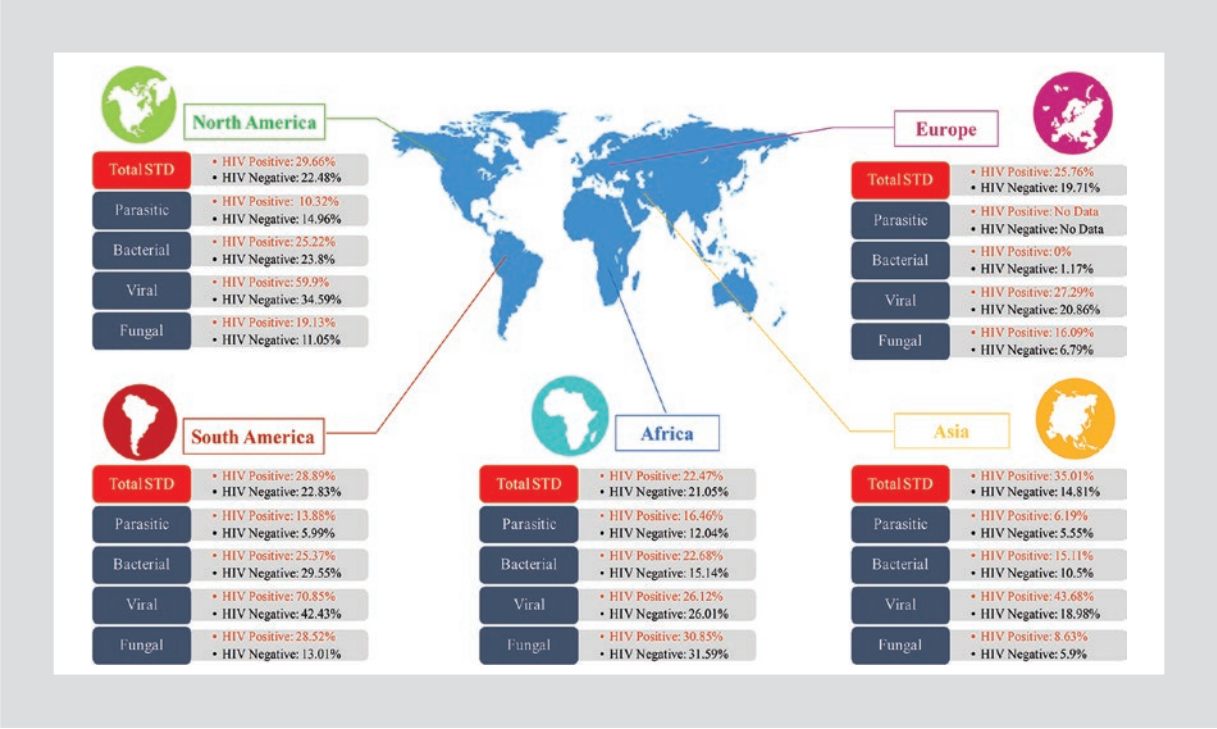

Figure 2. *Worldwide prevalence of sexually transmitted infections in people living with HIV. Data are reported as mean (range).*

agents was highest in PLWH (52.19% [95% CI: 43.88-60.43]) compared to fungal (22.19% [95% CI: 15.64-29.53]), bacterial (19.07% [13.59-26.63]), and parasitic (14.05% [11.88-16.38]) infections.

Figure 2 shows the prevalence of STIs caused by viral, parasitic, bacterial, and fungal infections in PLWH and HIV-negative individuals across continents. The total STI prevalence was higher in Asia (35.01%). The lowest coinfection rate was seen in Africa (22.47%). As shown in table 2, the pooled OR of STI due to infectious agents in HIV-positive patients was 1.77 (95% CI: 1.58-1.98) ($p < 0.0001$). The forest plot for the pooled odds ratios (ORs) of STIs caused by viral, fungal, bacterial, and parasitic agents in HIV-positive patients with random-effects analysis is shown in figures 3-6.

Furthermore, there was significant heterogeneity among studies with I^2 values of > 50% ($p < 0.05$) (Table 2). Publication bias was assessed by Egger's test and the results showed no publication bias ($p > 0.05$). Furthermore, funnel plots to assess publication bias in the meta-analysis are shown in figures 3-6.

Sub-group analysis

As reported in table 3, the most pooled prevalence of STIs in HIV-positive patients due to parasitic agents was estimated by serology methods (37.59% [95% CI: 7.78-74.14]), as well as bacterial agents by microscopy methods (27.28% [95% CI: 14.67-42.1]), viral infections using molecular test (60.52% [95% CI: 54.54-66.35]), and fungal agents by culture methods (26.9% [95% CI: 15.56-40.05]). There was a significant difference between sub-groups based on diagnostic methods and type of infection ($p < 0.05$), except in microscopy and culture methods were caused by bacterial infection (Table 3).

Risk factors reviewed in this research were $CD4^+$ T-cell counts, ART, marital status, education level, and developing or developed countries. Results of the meta-analysis showed a significant difference between a higher infection rate of STIs in HIV patients and $CD4^+$ cell count, ART, and countries ($p < 0.05$) (Table 4). One important point of this study is the prevalence of STI among PLWH in developing and developed countries' populations which was significantly different from HIV-negative individuals. Results of heterogeneity of meta-analysis for two risk factors including marital status and education showed that there were not homogeneous ($p > 0.05$). However, significant heterogeneity was seen in $CD4^+$ cell count, ART, and developing or developed countries ($p < 0.0001$) (Table 4).

Table 1. Baseline characteristics of the included studies

First author	Year of publication	Country	Infectious agent	Number of participants (HIV+)	Number of positives	Number of participants (HIV-)	Number of positives	Quality assessment	Ref.
Parasitic infection									
Microscopic method									
Cu-Uvin S	1999	U.S	T.v	824	100	430	43	7	Cu-Uvin et al., 1999
Warren D	2001	U.S	T.v	402	78	190	32	6	Warren et al., 2001
Cu-Uvin S	2002	U.S	T.v	864	100	435	43	8	Cu-Uvin et al., 2002
Watts DH	2005	U.S	T.v	1617	97	475	38	9	Watts et al., 2005
Watts DH	2006	U.S	T.v	2056	116	554	41	9	Watts et al., 2006
Tohill BC	2007	U.S	T.v	369	66	184	27	7	Tohill et al., 2007*
Micheletti AMR	2009	Brazil	T.v	153	11	169	8	6	Micheletti et al., 2009
deLemos P	2009	Brazil	T.v	125	22	112	10	5	de Lemos et al., 2009
deLemos P	2009	Brazil	T.v	125	19	112	8	5	de Lemos et al., 2009
Menéndez C	2010	Mozambique	T.v	30	9	226	67	7	Menéndez et al., 2010
Oyewole IO	2010	Nigeria	T.v	34	4	66	1	5	Oyewole et al., 2010
King CC	2011	U.S	T.v	756	96	380	40	7	King et al., 2011
Chiduo M	2012	Tanzania	T.v	105	16	100	5	7	Chiduo et al., 2012
Balkus JE	2013	Kenya	T.v	282	42	288	35	6	Balkus et al., 2013
Mullins TLK	2013	U.S	T.v	257	5	142	4	7	Mullins et al., 2013
Chopra D	2015	India	T.v	50	6	50	9	8	Chopra et al., 2015
Mukanyangezi MF	2017	Rwanda	T.v	205	13	156	9	7	Mukanyangezi et al., 2018
Haley DF	2017	U.S	T.v	530	34	207	12	7	Haley et al., 2017
Ijasan O	2018	Nigeria	T.v	160	16	160	13	7	IJASAN et al., 2018
Haley DF	2018	U.S	T.v	471	32	195	12	7	Haley et al., 2018
Ingabir R	2019	Rwanda	T.v	587	121	581	72	7	Ingabire et al., 2019
Mukanyangezi MF	2019	Rwandan	T.v	137	4	100	5	9	Mukanyangezi et al., 2019
Dionne-Odom J	2019	U.S	T.v	171	29	149	19	8	Dionne-Odom et al., 2019
Kristin M. Wall	2021	Rwanda	T.v	75	15	504	57	9	Wall et al., 2021
Nava-Memije K	2021	Mexico	T.v	267	22	82	1	8	Nava-Memije et al., 2021
Culture method									
Leroy V	1995	Rwanda	T.v	384	77	381	41	7	Leroy et al., 1995
Wilson T	1997	U.S	T.v	232	49	445	102	6	Wilson et al., 1998
Rugpao S	1998	Thailand	T.v	192	9	220	6	8	Rugpao et al., 1998
Madeline Y	1999	Congo	T.v	215	40	206	21	7	Sutton et al., 1999

(Continues)

Table 1. Baseline characteristics of the included studies *(continued)*

First author	Year of publication	Country	Infectious agent	Number of participants (HIV+)	Number of positives	Number of participants (HIV-)	Number of positives	Quality assessment	Ref.
				Parasitic infection					
Minkoff HL	1999	U.S	T.v	292	58	681	163	8	Minkoff et al., 1999
Vermund SH	2001	U.S	T.v	217	31	125	4	8	Vermund et al., 2001a
Vermund SH	2001	U.S	T.v	271	33	164	5	7	Vermund et al., 2001b
Rodríguez ME	2005	Cuba	T.v	60	6	60	1	5	Rodríguez et al., 2005
deLemos P	2009	Brazil	T.v	125	23	112	10	5	de Lemos et al., 2009
Sebitloane HM	2011	South Africa	T.v	418	56	383	30	5	Sebitloane et al., 2011
Nwadioha SI	2012	Nigeria	T.v	350	84	350	36	7	Nwadioha et al., 2012
Molecular Method									
Miller MJ	2008	U.S	T.v	38	20	190	64	7	Miller et al., 2008
Remis RS	2013	Canada	T.v	124	9	286	13	8	Remis et al., 2013
Masson L	2015	South Africa	T.v	37	4	227	47	6	Masson et al., 2015
Kinuthia J	2015	Kenya	T.v	25	2	1279	81	9	Kinuthia et al., 2015
Kriek JM	2016	South Africa	T.v	93	22	72	10	8	Kriek et al., 2016
Davis A	2017	U.S	T.v	44	16	287	61	7	Davis et al., 2016
Wynn A	2017	Botswana	T.v	90	9	305	12	7	Wynn et al., 2018
Ferré VM	2019	Togo	T.v	33	1	277	19	7	Ferré et al., 2019
Rodrigues LLS	2019	Brazil	T.v	41	4	112	1	7	Rodrigues et al., 2019
Tchankoni MK	2021	Togo	T.v	33	0	227	20	6	Tchankoni et al., 2021
Aude Jary	2021	Mali	T.v	44	4	96	6	8	Jary et al., 2021
Serological method									
Strathdee SA	2011	Mexico	T.v	33	19	587	199	7	Strathdee et al., 2011
Joseph Davey DL	2019	South Africa	T.v	107	22	135	13	7	Joseph Davey et al., 2019
Gorgens M	2020	Eswatini	T.v	397	50	4443	150	8	Gorgens et al., 2020
Nyemba DC	2020	South Africa	T.v	534	109	135	14	9	Nyemba et al., 2021
				Bacterial infection					
Microscopic method									
Cu-Uvin S	1999	U.S	C.t	651	27	365	17	7	Cu-Uvin et al., 1999
Helfgott A	2000	U.S	T.p - N.g - C.t	159	28	144	38	5	Helfgott et al., 2000
Warren D	2001	U.S	BV	854	402	434	190	7	Warren et al., 2001

(Continues)

Table 1. Baseline characteristics of the included studies *(continued)*

First author	Year of publication	Country	Infectious agent	Number of participants (HIV+)	Number of positives	Number of participants (HIV-)	Number of positives	Quality assessment	Ref.
				Bacterial infection					
Cu-Uvin S	2002	U.S	BV	852	402	190	429	8	Cu-Uvin et al., 2002
Watts DH	2005	U.S	BV	1736	743	493	232	9	Watts et al., 2005
Watts DH	2005	U.S	C.t	1725	10	491	8	9	Watts et al., 2005
Watts DH	2006	California	BV	2056	849	554	253	9	Watts et al., 2006
Mayaud P	2008	Burkina Faso	BV	98	35	22	3	8	Mayaud et al., 2008
Djigma F	2010	Burkina Faso	M.h - U.u	251	83	200	11	7	Djigma et al., 2011
C King C	2011	U.S	BV	756	361	380	164	7	King et al., 2011
Nwadioha S	2011	Nigeria	BV	350	126	350	70	8	Nwadioha et al., 2011*
Mavedzenge SN	2012	Uganda	BV	181	70	302	111	8	Mavedzenge et al., 2012
Remis RS	2013	Canada	BV	123	19	283	49	8	Remis et al., 2013
Chopra D	2015	India	BV - N.g	50	7	50	15	8	Chopra et al., 2015
Mukanyangezi MF	2017	Rwanda	BV	203	1	155	9	7	Mukanyangezi et al., 2018*
Nava-Memije K	2021	Mexico	BV	186	61	82	9	8	Nava-Memije et al., 2021
Apalata T	2021	South Africa	BV	61	49	39	21	8	Apalata et al., 2021
Culture method									
Rugpao S	1998	Thailand	BV - C.t - N.g	224	58	257	56	8	Rugpao et al., 1998
Cu-Uvin S	1999	U.S	N.g	777	6	397	1	7	Cu-Uvin et al., 1999
Minkoff HL	1999	U.S	C.t - N.g	292	15	681	105	8	Minkoff et al., 1999
Mbu	2008	Cameroon	C.t - N.g - T.p	198	76	1810	274	5	Mbu et al., 2008
Sebitloane HM	2011	South Africa	T.p	418	26	383	14	8	Sebitloane et al., 2011
Molecular method									
Wattana PC	1997	Thailand	C.t - N.g	222	42	219	23	7	Chaisilwattana et al., 1997
Peralta L	2001	San Francisco	C.t - N.g	187	49	82	12	8	Peralta et al., 2001
Vermund SH	2001	U.S	N.g - T.p - C.t	217	53	125	26	8	Vermund et al., 2001a
Vermund SH	2001	U.S	C.t - N.g - T.p	271	90	164	39	7	Vermund et al., 2001b
Watts DH	2006	U.S	C.t	2056	12	554	8	9	Watts et al., 2006
Suntoke TR	2008	Uganda	T.p - H.d	43	1	57	5	8	Suntoke et al., 2009
Vandepitte J	2011	Uganda	M.g	382	68	643	80	7	Vandepitte et al., 2012
King CC	2011	U.S	C.t - N.g	756	14	380	6	8	King et al., 2011
Mavedzenge SN	2012	Uganda	C.t - N.g	181	37	302	17	8	Mavedzenge et al., 2012
Bhattar S	2013	India	C.T	60	4	60	1	7	Bhattar et al., 2013
Souza RP	2013	Brazil	C.t - N.g - T.p - M.g	178	40	378	88	6	Souza et al., 2013
Vandepitte J	2013	Uganda	M.g	53	46	66	65	5	Vandepitte et al., 2013

(Continues)

Table 1. Baseline characteristics of the included studies *(continued)*

First author	Year of publication	Country	Infectious agent	Number of participants (HIV+)	Number of positives	Number of participants (HIV-)	Number of positives	Quality assessment	Ref.
Viral infection									
Remis RS	2013	Canada	C.t	124	0	286	11	8	Remis et al., 2013
Remis RS	2013	Canada	N.g	124	0	285	0	8	Remis et al., 2013
Vandepitte J	2014	Uganda	C.t - N.g - M.g	42	21	126	27	7	Vandepitte et al., 2014
Mafokwane TM	2016	South Africa	C.t	235	75	8	3	7	Mafokwane and Samie, 2016
Kriek JM	2016	South Africa	C.t - N.g - M.g	93	11	72	5	8	Kriek et al., 2016
Ferré VM	2019	Togo	C.t - N.g - M.g	54	33	153	42	7	Ferré et al., 2019
Rodrigues LLS	2019	Brazil	C.t	8	8	112	41	8	Rodrigues et al., 2019
Rodrigues LLS	2019	Brazil	N.g	3	2	112	41	8	Rodrigues et al., 2019
Rodrigues LLS	2019	Brazil	M.g	12	1	112	41	8	Rodrigues et al., 2019
Joseph Davey DL	2019	South Africa	C.t - N.g	107	32	135	31	8	Joseph Davey et al., 2019
Nouchi A	2019	France	C.t - N.g – T.p	56	43	84	30	8	Nouchi et al., 2019
Nava-Memije K	2021	Mexico	C.t	186	5	82	5	8	Nava-Memije et al., 2021
Serological method									
Cu-Uvin S	1999	U.S	BV	817	285	412	136	7	Cu-Uvin et al., 1999
Cu-Uvin S	1999	U.S	T.p	841	71	431	24	7	Cu-Uvin et al., 1999
Minkoff HL	1999	U.S	T.p	292	40	681	56	8	Minkoff et al., 1999
Stanekova D	2006	Slowakia	T.p	7	0	85	1	8	Staneková et al., 2006
Nag VL	2009	India	T.p	49	3	171	4	8	Nag et al., 2009
Remis RS	2013	Canada	T.p	126	1	291	1	8	Remis et al., 2013
Vandepitte J	2014	Uganda	T.p	42	9	126	13	8	Vandepitte et al., 2014
Chopra D	2015	India	T.p	50	3	50	1	8	Chopra et al., 2015
Mukanyangezi MF	2017	Rwanda	T.p	197	4	100	6	7	Mukanyangezi et al., 2018
Ferré VM	2019	Togo	T.p	54	0	153	0	7	Ferré et al., 2019
Joseph Davey DL	2019	South Africa	T.p	107	1	135	1	8	Joseph Davey et al., 2019
Nava-Memije K	2021	Mexico	U.u	186	87	82	27	8	Nava-Memije et al., 2021
Microscopic method									
Rugpao S	1998	Thailand	HPV	224	103	257	127	8	Rugpao et al., 1998
Ferré VM	2019	Togo	HPV	54	48	153	49	7	Ferré et al., 2019
Culture method									
Minkoff HL	1999	U.S	CMV-HSV	292	44	163	11	8	Minkoff et al., 1999
King CC	2011	U.S	HSV-2	756	491	380	207	7	King et al., 2011
Molecular method									
Minkoff HL	1999	U.S	HPV	292	82	681	37	8	Minkoff et al., 1999
Cu-Uvin S	1999	U.S	HPV	840	540	431	119	7	Cu-Uvin et al., 1999
Ahdieh L	2001	U.S	HPV	871	639	439	237	5	Ahdieh et al., 2001
Branca M	2003	Italy	HPV	89	34	48	13	7	Branca et al., 2003*

(Continues)

Table 1. Baseline characteristics of the included studies *(continued)*

First author	Year of publication	Country	Infectious agent	Number of participants (HIV+)	Number of positives	Number of participants (HIV-)	Number of positives	Quality assessment	Ref.
Viral infection									
Zehender G	2004	Italy	HTLV	167	8	226	2	7	Zehender et al., 2004*
Watts DH	2005	U.S	HPV	1606	1023	462	138	9	Watts et al., 2005
Watts DH	2006	U.S	HPV	2056	1237	554	154	9	Watts et al., 2006
Ng'andwe C	2007	Zambia	HPV	30	24	40	22	7	Ng'andwe et al., 2007
Mayaud P	2008	Burkina Faso	HSV	98	65	22	10	8	Mayaud et al., 2008
Jamieson DJ	2008	Thailand	HCV	1429	54	342	1	9	Jamieson et al., 2008*
Hessol NA	2009	U.S	HPV	470	163	185	12	9	Hessol et al., 2009
Singh DK	2009	Rwandan	HPV	710	445	226	188	7	Singh et al., 2009
Desruisseau AJ	2009	Cameroon	HPV	32	26	29	15	7	Desruisseau et al., 2009
Sarkar K	2011	India	HPV	93	30	1106	101	5	Sarkar et al., 2011
Nowak RG	2011	Zimbabwe	HPV	154	99	478	227	8	Nowak et al., 2011
King CC	2011	U.S	HPV	756	482	380	109	7	King et al., 2011
Veldhuijzen NJ	2011	Rwanda	HPV	126	91	349	164	8	Veldhuijzen et al., 2011
Aggarwal R	2012	India	HPV	130	26	64	12	6	Aggarwal et al., 2012*
Blitz S	2013	Canada	HPV	750	338	323	211	5	Blitz et al., 2013
Remis RS	2013	Canada	HPV	124	60	283	49	8	Remis et al., 2013
Adler DH	2014	South Africa	HPV	35	31	50	24	7	Adler et al., 2014
Pundhir P	2014	India	HPV	100	24	100	4	5	Pundhir et al., 2014
Dartell MA	2014	Tanzania	HPV	334	156	3005	517	8	Dartell et al., 2014*
Massad LS	2014	U.S	HPV	294	147	144	27	8	Massad et al., 2014*
Lima MD	2014	Brazil	HPV	100	47	100	46	8	Lima et al., 2014*
Chisanga C	2015	Zambia	HPV	103	83	93	83	8	Chisanga et al., 2015*
Ursu RG	2015	Romania	HPV	40	18	992	350	6	Ursu et al., 2015
Yar DD	2015	Ghana	HPV	107	93	100	56	6	Yar et al., 2016
Gallagher KE	2016	Tanzania	HPV	161	83	464	225	7	Gallagher et al., 2016
Kriek JM	2016	South Africa	HPV	93	63	72	20	8	Kriek et al., 2016
He X	2016	Kenya	HTLV	113	22	111	4	8	He et al., 2016
Obiri-Yeboah D	2017	Ghana	HPV	163	120	170	72	7	Obiri-Yeboah et al., 2017
Mbatha JN	2017	South Africa	HPV	267	86	956	215	6	Mbatha et al., 2017
Orlando G	2017	Italy	HPV	805	229	1402	166	6	Orlando et al., 2017
Tartaglia E	2017	Italy	HPV	50	24	150	42	7	Tartaglia et al., 2017
Whitham HK	2017	Senegal	HPV	618	365	702	479	5	Whitham et al., 2017*
Carriero C	2018	Italy	HPV	48	11	99	15	5	Carriero et al., 2018*
Cholli P	2018	Cameroon	HPV	384	157	529	463	6	Cholli et al., 2018
Rodrigues LLS	2018	Brazil	HPV	41	40	112	48	8	Rodrigues et al., 2018
Rodrigues LLS	2018	Brazil	Hr-HPV	41	33	112	66	8	Rodrigues et al., 2018
Mudini W	2018	Zimbabwe	HPV	53	51	54	50	7	Mudini et al., 2018

(Continues)

Table 1. Baseline characteristics of the included studies *(continued)*

First author	Year of publication	Country	Infectious agent	Number of participants (HIV+)	Number of positives	Number of participants (HIV-)	Number of positives	Quality assessment	Ref.
Viral infection									
Lin CC	2018	Taiwan	HPV	113	80	166	35	7	Lin et al., 2018
Liu X	2018	China	HPV	160	82	113	24	8	Liu et al., 2019
Rodrigues LL	2019	Brazil	HPV	41	39	112	37	6	Rodrigues et al., 2019
Thay S	2019	cambodia	HPV	129	37	121	19	6	Thay et al., 2019
Ndizeye Z	2019	Burundi	HPV	300	114	300	67	7	Ndizeye et al., 2019*
Tawe L	2019	Botswana	hrHPV	88	88	38	38	8	Tawe et al., 2020*
Visalli G	2021	Italy	HPV	40	13	62	23	8	Visalli et al., 2021
Beliakov I	2021	Russia	HPV	60	40	60	40	7	Beliakov et al., 2021
Beliakov I	2021	Russia	HSV1	60	1	60	3	7	Beliakov et al., 2021
Beliakov I	2021	Russia	HSV2	60	6	60	4	7	Beliakov et al., 2021
Beliakov I	2021	Russia	CMV	60	2	60	0	7	Beliakov et al., 2021
Serological method									
Hershow RC.	1998	U.S	HCV	243	107	53	16	7	HERSHOW et al., 1998
Ayele W	2002	Ethiopia	HCV	2663	29	165	8	6	Ayele et al., 2002
Schuman P	2003	U.S	HPV	774	482	391	110	8	Schuman et al., 2003
Staneková D	2006	Slovakia	CMV	7	6	90	72	7	Staneková et al., 2006
Staneková D	2006	Slovakia	HBV	7	1	90	4	7	Staneková et al., 2006
Staneková D	2006	Slovakia	HCV	7	2	85	0	7	Staneková et al., 2006
Simpore J	2006	Burkina Faso	HBV-HCV	207	34	129	17	7	Simpore et al., 2006
Burnett RJ	2007	South Africa	HBV	710	278	710	214	7	Burnett et al., 2007
Operskalski EA	2008	Thailand	HBV	735	637	134	97	7	Operskalski et al., 2008
Operskalski EA	2008	Thailand	HCV	882	723	167	129	7	Operskalski et al., 2008
Kfutwah AK	2012	Cameroon	HBV	301	28	349	23	6	Kfutwah et al., 2012
Remis RS	2013	Canada	HSV-1	123	111	290	254	8	Remis et al., 2013
Remis RS	2013	Canada	HSV-2	124	107	290	135	8	Remis et al., 2013
Remis RS	2013	Canada	HCV	126	5	290	4	8	Remis et al., 2013
Remis RS	2013	Canada	HBV	126	60	283	60	8	Remis et al., 2013
Remis RS	2013	Canada	CMV	126	125	291	274	8	Remis et al., 2013
Anderson MI	2013	South Africa	HBV	1543	53	1546	44	7	Andersson et al., 2013
Matthews PC	2015	South Africa	HBV	950	66	72	6	5	Matthews et al., 2015
Gallagher KE	2016	Tanzania	HSV-2	161	146	464	394	7	Gallagher et al., 2016
Diale Q	2016	South Africa	HBV	486	10	1882	8	5	Diale et al., 2016
Mukanyangezi MF	2017	Rawanda	HBV-HCV	197	6	151	6	7	Mukanyangezi et al., 2018
Mukanyangezi MF	2017	Rawanda	HPV	205	57	172	20	7	Mukanyangezi et al., 2018
Page K	2017	U.S	HCV	127	69	119	44	6	Page et al., 2017

(Continues)

Table 1. Baseline characteristics of the included studies *(continued)*

First author	Year of publication	Country	Infectious agent	Number of participants (HIV+)	Number of positives	Number of participants (HIV-)	Number of positives	Quality assessment	Ref.
				Viral infection					
Frempong MT	2019	Ghana	HBV-HCV	148	28	100	22	7	Frempong et al., 2019
Lawal MA	2020	Nigeria	HBV	187	9	187	9	7	Lawal et al., 2020
Lawal MA	2020	Nigeria	HCV	187	13	187	14	7	Lawal et al., 2020
Microscopic method									
Duerr A	1997	U.S	C.a	223	60	289	53	7	Duerr et al., 1997
Mostad SB	1997	Kenya	C.a	44	15	274	46	5	Mostad et al., 1997
Greenblatt RM	1998	U.S	C.a	2058	265	567	48	4	Greenblatt et al., 1999
Helfgott A	2000	U.S	C.a	159	25	144	8	5	Helfgott et al., 2000
Hasselrot K	2011	Kenya	C.a	20	1	39	4	7	Hasselrot et al., 2012
Gupta K	2019	India	C.a	26	3	31	3	7	Gupta et al., 2019
Chaubey S	2021	India	C.a	23	2	977	93	6	Chaubey et al., 2021
Culture method									
Rugpao S	1998	Thailand	C.a	220	19	254	15	8	Rugpao et al., 1998*
Minkoff HL	1999	U.S	C.a	292	32	681	19	8	Minkoff et al., 1999
Cu-Uvin S	1999	U.S	C.a	851	26	432	8	7	Cu-Uvin et al., 1999
Sobel JD	2001	U.S	C.a	871	382	439	117	8	Sobel et al., 2001
Ohmit SE	2003	U.S	C.a	868	318	437	91	7	Ohmit et al., 2003
Watts DH	2006	U.S	C.a	2056	190	554	20	9	Watts et al., 2006*
Mbu ER	2008	Cameroon	C.a	198	73	1810	640	5	Mbu et al., 2008
King CC	2011	U.S	C.a	756	273	380	82	7	King et al., 2011
Oliveira PM	2011	Brazil	C.a	64	19	76	11	6	Oliveira et al., 2011
Merenstein D	2012	Colombia	C.a	56	30	24	10	7	Merenstein et al., 2013
Apalata T	2014	South Africa	C.a	97	52	101	38	7	Apalata et al., 2014*
Alczuk SSD	2015	Brazil	C.a	178	36	200	18	6	Alczuk et al., 2015
Mukanyangezi MF	2017	Rwanda	C.a	205	33	156	24	7	Mukanyangezi et al., 2018
Dionne-Odom J	2019	England	C.a	174	28	162	11	8	Dionne-Odom et al., 2019*
Mukanyangez MF	2019	Rwanda	C.a	124	19	88	18	7	Mukanyangezi et al., 2019
Nava-Memije K	2021	Mexico	C.a	267	31	82	9	7	Nava-Memije et al., 2021

T.v: *Trichomonas vaginalis;* C.t: *Chlamydia trachomatis;* T.p: *Treponema pallidum;* N.g: *Neisseria gonorrhoeae;* BV: Bacterial Vaginosis; M.g: *Mycoplasma genitalium;* M.h: *Mycoplasma hominis;* U.u: *Ureaplasma urealyticum;* H.d: *Haemophilus ducreyi;* HPV: Human papillomavirus; HCV: Hepatitis C virus; CMV: Cytomegalovirus; HBV: Hepatitis B virus; HSV: Herpes simplex viruses; HTLV: Human T-lymphotropic virus; C.a: Candida albicans. *Unclear method.

Table 2. Pooled prevalence of STIs in HIV-positive and HIV-negative individuals according to microorganism

Type of infection	Pooled proportion (95% CI)	Pooled odds ratio (95% CI) *p* value	Heterogeneity			Egger's test	
			I_2 (%)	Cochran Q	p-value	T	p-value
Total STD							
HIV+	30.23 (26.18-34.45)		99.3	27758.26	p < 0.0001	11.73	p < 0.0001
HIV–	20.01 (17.17-23.01)		98.8	16438.84	p < 0.0001	9.77	p < 0.0001
		1.77 (1.58-1.98) $p < 0.0001$*	88.5	1820.4	p < 0.0001	0.19	p = 0.6005
Parasitic							
HIV+	14.05 (11.88-16.38)		92.3	571.99	p < 0.0001	3.59	p < 0.0001
HIV–	10 (7.91-12.3)		93.9	726.44	p < 0.0001	4.32	p = 0.004
		1.57 (1.33-1.85) $p < 0.0001$*	67.4	153.5	p < 0.0001	0.607	p = 0.266
Bacterial							
HIV+	19.07 (13.59-26.63)		99.1	6385.04	p < 0.0001	8.83	p < 0.0001
HIV–	15.03 (11.05-19.5)		98.1	2961.29	p < 0.0001	8.78	p < 0.0001
		1.39 (1.16-1.66) $p = 0.0003$*	80.7	284.3	p < 0.0001	0.346	p = 0.4958
Viral							
HIV+	52.19 (43.88-60.43)		99.5	14775.26	p < 0.0001	18.3	p < 0.0001
HIV–	33.73 (27.1-40.7)		99.3	10470.3	p < 0.0001	13.54	p < 0.0001
		2.24 (1.81-2.78) $p < 0.0001$*	93.3	1187.48	p < 0.0001	0.27	p = 0.7382
Fungal							
HIV+	22.19 (15.64-29.53)		98.4	1175	p < 0.0001	6.74	p = 0.0098
HIV–	13.71 (8.42-20.03)		98	959.44	p < 0.0001	6	p = 0.0399
		1.82 (1.54-2.16) $p < 0.0001$*	54.5	48.3	p = 0.001	0.37	p = 0.5801

STIs: sexually transmitted infections.

Table 3. Pooled prevalence of STIs in HIV-positive and HIV-negative individuals with different diagnostic methods

Type of infection	Method	Number of studies	Prevalence (95% CI) HIV+	Prevalence (95% CI) HIV-	Pooled odds ratio (95% CI)	p-value
Parasitic	Culture	12	16.02 (12.71-19.64)	8.97 (5.03-13.91)	1.94 (1.33-2.84)	p = 0.0005
	Molecular	11	16.67 (8.86-26.34)	10.84 (5.72-17.33)	1.72 (1.13-2.62)	p = 0.0102
	Serology	4	37.59 (7.78-74.14)	20.79 (3.14-48.3)	2.53 (1.52-4.23)	p = 0.0004
	Microscopy	24	10.97 (8.67-13.51)	9.19 (7.29-11.29)	1.21 (1.02-1.43)	p = 0.0222
Bacterial	Culture	5	12.08 (2.41-27.66)	9.28 (3.1-18.3)	1.37 (0.51-3.64)	p = 0.5234
	Molecular	24	24.26 (15.16-34.14)	18.77 (11.59-27.22)	1.63 (1.19-2.23)	p = 0.0023
	Serology	12	7.24 (1.97-15.45)	4.79 (1.21-10.56)	1.42 (1.05-1.91)	p = 0.022
	Microscopy	17	27.28 (14.67-42.1)	26.21 (15.5-38.59)	1.02 (0.82-1.26)	p = 0.8544
Viral	Culture	2	38.47 (2.03-86.53)	31.99 (2.25-75.38)	1.48 (1.17-1.86)	p = 0.0007
	Molecular	52	60.52 (54.54-66.35)	37.1 (28.71-45.9)	2.96 (2.04-4.31)	p < 0.0001
	Serology	27	39.7 (23.05-57.67)	27.95 (14.38-43.98)	1.86 (1.38-2.49)	p < 0.0001
Fungal	Culture	16	26.9 (15.56-40.05)	16.78 (8.04-27.9)	1.93 (1.5-2.48)	p < 0.0001
	Microscopy	7	18.94 (11.59-27.6)	11.91 (7.22-17.57)	1.8 (1.37-2.38)	p < 0.0001

STIs: sexually transmitted infections.

Table 4. Risk factors associated with STIs in PLWH

Risk factors	No. of studies	Categories	OR (95% CI)	p-value	I^2 (inconsistency)%	Cochran Q	p-value
$CD4^+$	22	< 200 cells/mL^3 > 200 cells/mL^3	1.86 (1.24-2.79)	p = 0.0026*	74.3	81.84	p < 0.0001
Antiretroviral therapy (ART)	19	Yes No	1.09 (0.43-2.75)	p = 0.8502	92	113.02	p < 0.0001
Marital status	6	Unmarried Married	1.57 (0.81-3.02)	p = 0.1728	48.9	9.78	p = 0.0817
Education	5	Non-academic Academic	1.27 (0.64-2.5)	p = 0.4806	0	3.71	p = 0.4454
Developing countries	116	HIV+ HIV-	1.85 (1.65-2.18)	p < 0.0001	87.4	894.78	p < 0.0001
Developed countries	83	HIV+ HIV-	1.84 (1.56-2.17)	p < 0.0001	91.4	932.39	p < 0.0001

STIs: sexually transmitted infections; PLWH: people living with HIV.

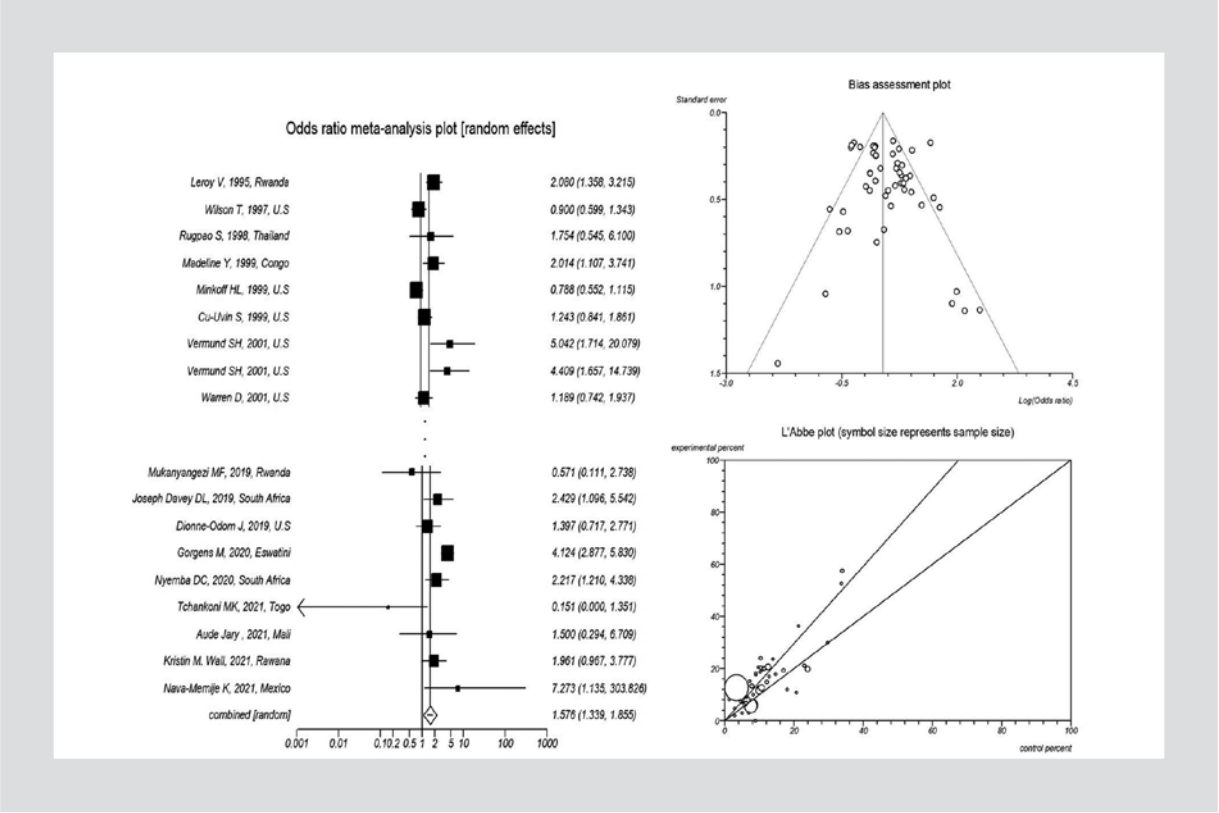

Figure 3. *Forest plot for the pooled odds ratios (ORs) and funnel plots to assess publication bias of STD caused by parasitic agent in PLWH with random-effects analysis.*

Discussion

STIs are a well-known risk factor for acquiring and spreading HIV. Through mucosal injury, inflammation, and enhancement of HIV in genital tract discharge, STIs open a channel for HIV entrance147. This systematic review and meta-analysis, which compiles data published over the past three decades, provides extensive information on the global burden of STIs in PLWH. Based on infectious agents, continents, diagnostic methods, and risk factors, the collected data were grouped.

According to the findings of the present study, the pooled ORs of STIs in persons living with HIV were 1.77 (95% CI: 1.58-1.98). In addition, individuals with HIV were more likely to have STIs overall (30.23 [95% CI: 26.18-34.45]) than those without HIV (20.01 [95% CI: 17.17-23.01]). According to the findings of our meta-analysis, HIV-positive patients had a greater prevalence of STIs brought on by infectious diseases than HIV-negative individuals.

The data information provided demonstrates that there were regional variations in the prevalence of STIs. Accordingly, most STI cases in HIV-positive patients were in the following order: Asia > North America > South America > Europe > Africa. In addition, it was shown that the prevalence of STI among the PLWH populations of developing and developed countries was significantly different from HIV-negative individuals.

The prevalence of STIs caused by different infectious agents in these patients was obtained in the following order: viral > fungal > bacterial > parasitic agents. STIs cause abnormal vaginal or urethral discharges and ulcerative or non-ulcerative genital lesions[148,147]. The prevalence of viral agents was higher in all continents except in Africa. The common viral agents reported in included studies were HPV, HCV, CMV, HBV, HSV, and HTLV which play an important role in the spread of STIs in PLWH. The prevalence of fungal infection was higher in PLWH of Africa. However, according to the previous report in 2006, HSV-2 was the leading cause of genital ulceration in HIV patients, globally and in sub-Saharan Africa[149]. HPV infection is the most frequent viral STI in the world and high-risk oncogenic (HR)-HPV genotypes are responsible for 7.7% of all cancers in developing

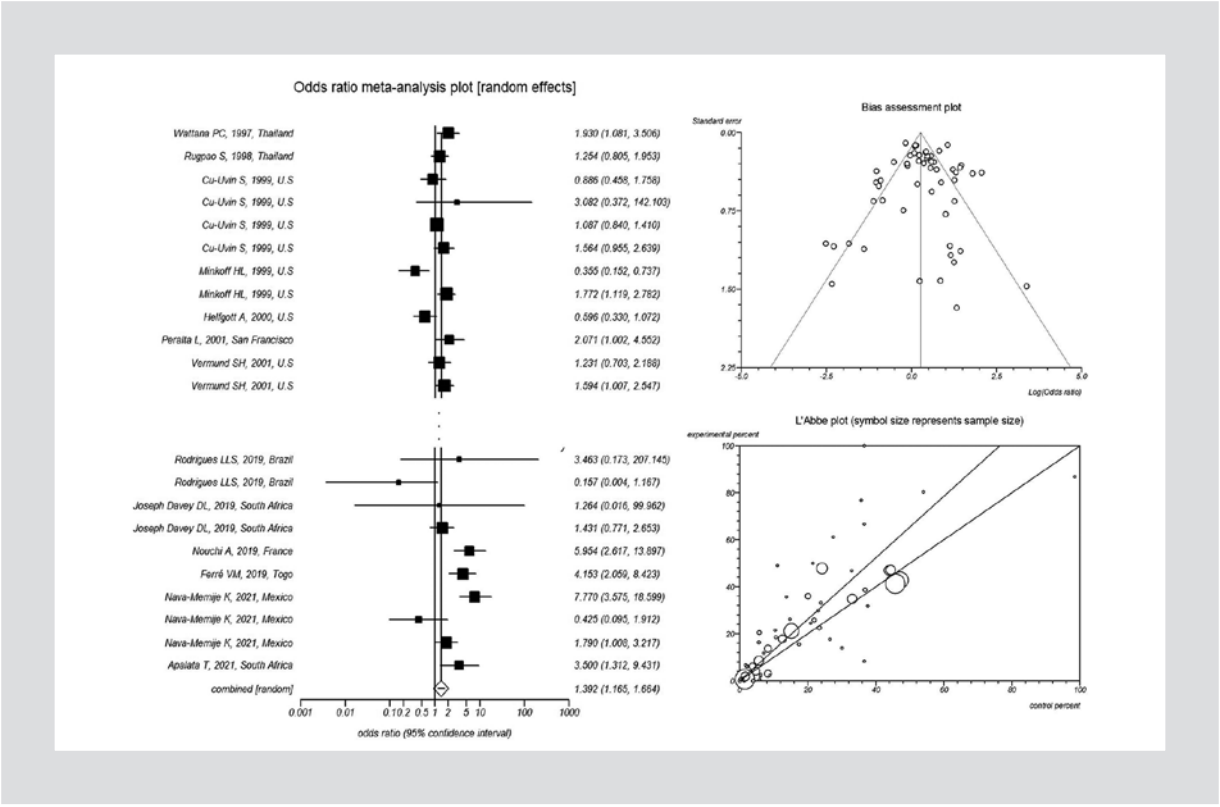

Figure 4. *Forest plot for the pooled odds ratios (ORs) and funnel plots to assess publication bias of STD caused by bacterial agent in PLWH with random-effects analysis.*

countries[150,151]. The significant association between certain HPV types and their clinical characteristics is well-described[152]. The frequency of genital HPV infections is higher in HIV-infected men and women than the healthy control group. The lesions in HIV patients are more commonly diffuse, dysplastic, and subclinical compared to the control group that more frequently indicate condylomatous lesions and rarely subclinical and dysplastic lesions. It has also shown that more types of HPV can infect HIV patients than the control group. HIV infections can potentiate HPV replication and increase the disease progression which may be due to the effect of HIV on the HPV gene transcription. Regardless of the accurate pathway, it is described that HIV-infected individuals show a more frequency of cervical, anal, and other genital malignancy that by be induced by viral infections[152]. This indicates the importance of full genital examinations in HIV-positive patients.

According to a systematic review and meta-analysis study by Arora et al., the viral and bacterial STIs had a similar association with the overall prevalence of HIV in sexually active Ugandan female youths[153]. According to our results, among the protozoan parasites, *T. vaginalis* is a highly prevalent STI in HIV patients similar to previous reports[154,155]. It has been reported that *T. vaginalis* infection is a considerable risk factor for HIV acquisition by several mechanisms[156]. It may injure the epithelial layers, which play an important role as a barrier to infections. *T. vaginalis* has also been reported to induce an inflammatory reaction in the host that may lead to promotion in the population of HIV target cells. *T. vaginalis* infection might increase the likelihood of bacterial vaginosis, which, subsequently, can elevate the risk of HIV infection[157].

Our pooled estimates showed significant variability, which might be the result of several other factors, such as research designs, sample sizes, regional disparities, and changes in the sensitivity and specificity of detection techniques. However, the continuously high STI prevalence and incidence documented in HIV-positive individuals cannot be disregarded, despite the considerable amount of variability between the studies. Moreover, diagnosis and confirmation of STIs using laboratory diagnostic tools is essential to select the most appropriate course of treatment. A significant difference was

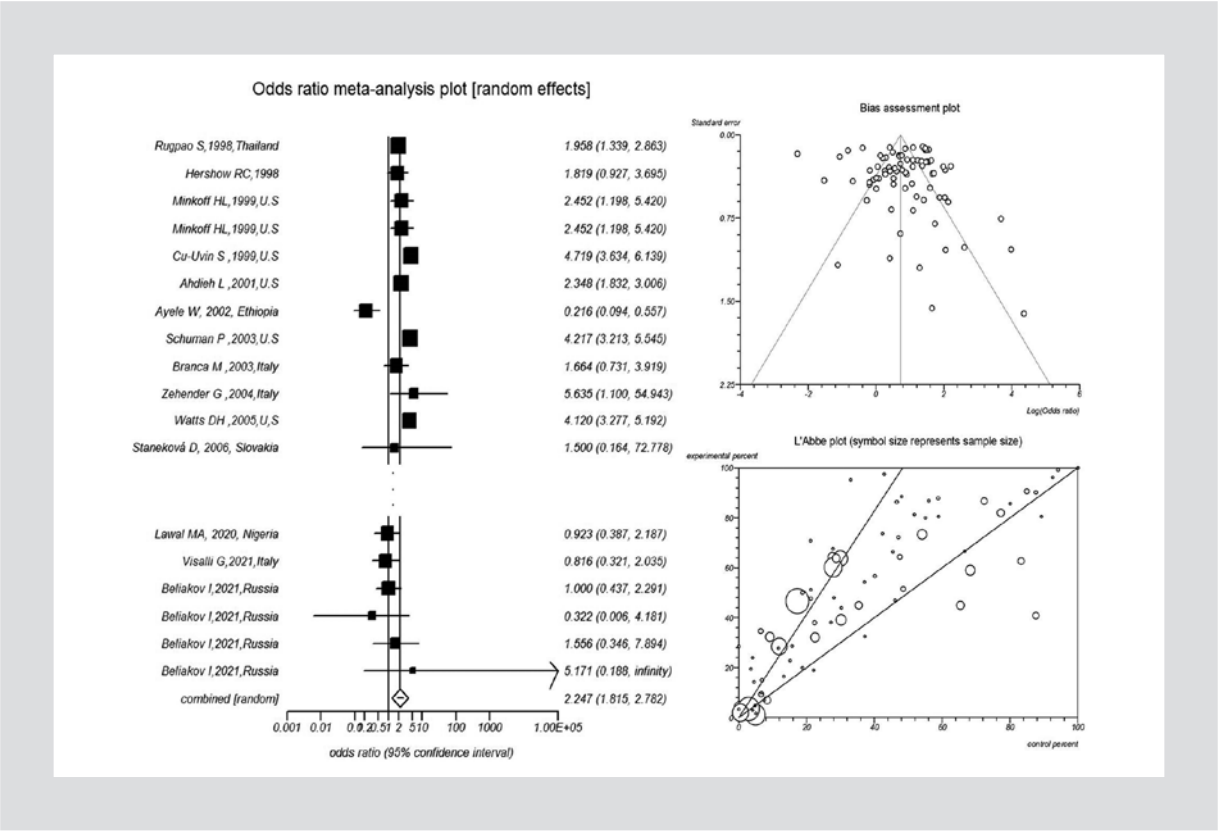

Figure 5. *Forest plot for the pooled odds ratios (ORs) and funnel plots to assess publication bias of STD caused by viral agent in PLWH with random-effects analysis.*

identified between sub-groups based on diagnostic methods with regard to the type of coinfection, that is, parasitic, bacterial, viral, and fungal infection ($p < 0.05$), except in microscopy, and culture methods caused by bacterial infection. The discrepancy in the frequency of STIs in studies reported from different areas may be due to differences in the sensitivity and specificity of the diagnosis methods. The use of molecular approaches provides higher sensitivity than traditional methods such as culture and microscopy at identifying a pathogen. Molecular methods have commonly been used for the detection of viral infections, while fungal infections have been detected by microscopic and culture-based methods. Given the spread of parasitic, bacterial, viral, and fungal infections may be quantified by the asymptomatic carriers, improved surveillance through the development of more rapid and sensitive diagnosis tools based on antigen and DNA/RNA detection is a highly valuable goal for highlighting the possibility of STIs screening in HIV-positive patients[158].

Multivariate analysis showed that there is a statistically significant correlation between the prevalence of STIs in HIV patients and two risk factors including $CD4^+$ cell count and countries. However, risk factors such as ART, marital status, and education were not statistically significant in the results of our study. $CD4^+$ cell counts provide an indicator to detect the immune state of an individual, particularly in HIV-positive patients[159]. Its level is still being applied in some low and medium-income areas where viral load is not commonly accessible as the basis to determine if the serologically positive patient is to start anti-retroviral agent treatment[160]. Lower counts of CD4+ cells with ART-naive may aggravate the risk of secondary infections in patients living with HIV. Therefore, CD4+ cell count monitoring can help guide the appropriate administration of prophylactic interventions against STIs in HIV-positive patients.

Conclusion

To the best of our knowledge, this is the first complete overview of the global burden of STIs in PLWH provided by a systematic review and meta-analysis. Overall, STI rates in HIV-positive individuals are higher than in the general population. Thus, efforts for STI screening and prophylaxis are warranted in this pop-

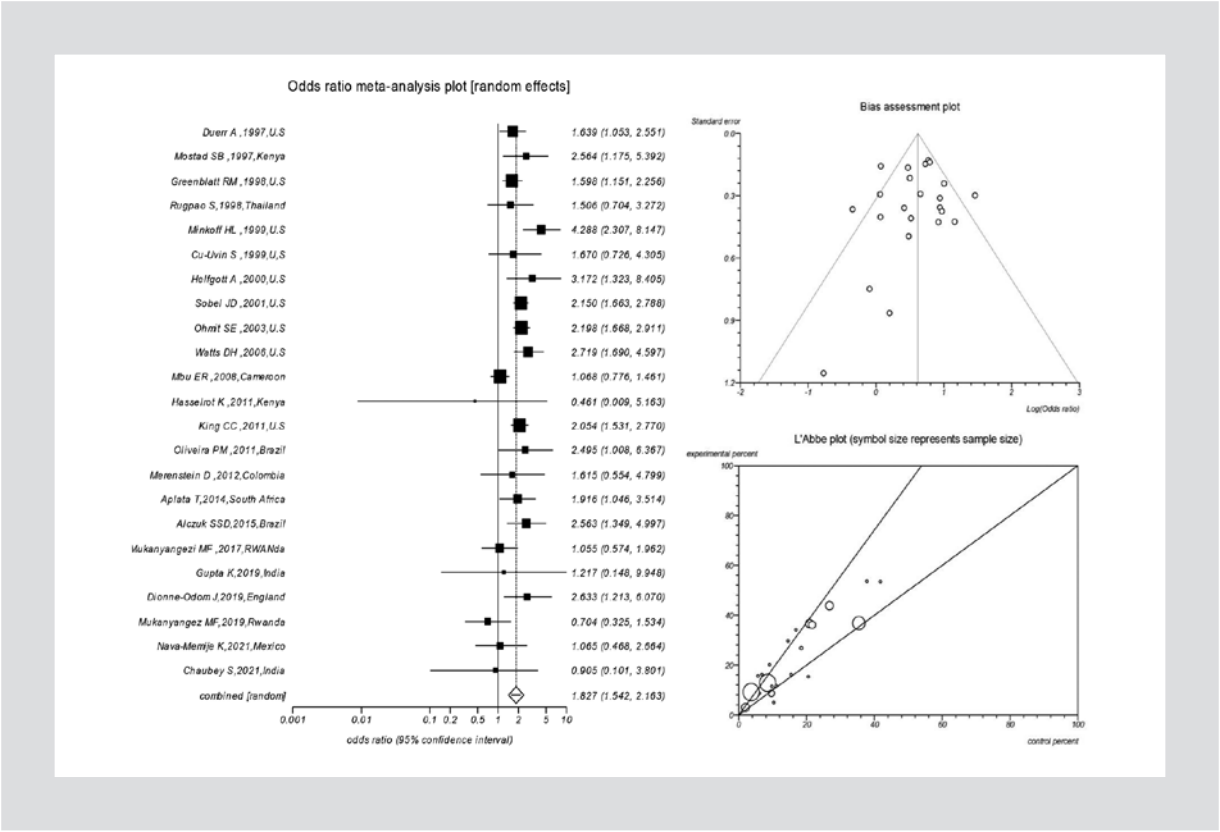

Figure 6. *Forest plot for the pooled odds ratios (ORs) and funnel plots to assess publication bias of STD caused by fungal agent in PLWH with random-effects analysis.*

ulation. New programs and public health initiatives for the identification, management, and prevention of STIs should be prioritized in HIV-positive people.

Supplementary data

Supplementary data are available at DOI: 10.24875/AIDSRev.23000008. These data are provided by the corresponding author and published online for the benefit of the reader. The contents of supplementary data are the sole responsibility of the authors.

Authors' contributions

All authors provided critical feedback and helped shape the research, analysis, and manuscript. All authors read and approved the final manuscript.

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Conflicts of interest

None.

Ethical disclosures

Protection of human and animal subjects. The authors declare that no experiments were performed on humans or animals for this study.

Confidentiality of data. The authors declare that no patient data appear in this article.

Right to privacy and informed consent. The authors declare that no patient data appear in this article.

Use of artificial intelligence for generating text. The authors declare that they have not used any type of generative artificial intelligence for the writing of this manuscript nor for the creation of images, graphics, tables, or their corresponding captions.

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