

Global and regional estimates of genital human papillomavirus prevalence among men: a systematic review and meta-analysis

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Summary

Background The epidemiology of human papillomavirus (HPV) in women has been well documented. Less is known about the epidemiology of HPV in men. We aim to provide updated global and regional pooled overall, type-specific, and age-specific prevalence estimates of genital HPV infection in men.

Methods We conducted a systematic review and meta-analysis to assess the prevalence of genital HPV infection in the general male population. We searched Embase, Ovid MEDLINE, and the Global Index Medicus for studies published between Jan 1, 1995, and June 1, 2022. Inclusion criteria were population-based surveys in men aged 15 years or older or HPV prevalence studies with a sample size of at least 50 men with no HPV-related pathology or known risk factors for HPV infection that collected samples from anogenital sites and used PCR or hybrid capture 2 techniques for HPV DNA detection. Exclusion criteria were studies conducted among populations at increased risk of HPV infection, exclusively conducted among circumcised men, and based on urine or semen samples. We screened identified reports and extracted summary-level data from those that were eligible. Data were extracted by two researchers independently and reviewed by a third, and discrepancies were resolved by consensus. We extracted only data on mucosal α -genus HPVs. Global and regional age-specific prevalences for any HPV, high-risk (HR)-HPV, and individual HPV types were estimated using random-effects models for meta-analysis and grouped by UN Sustainable Development Goals geographical classification.

Findings We identified 5685 publications from database searches, of which 65 studies (comprising 44 769 men) were included from 35 countries. The global pooled prevalence was 31% (95% CI 27–35) for any HPV and 21% (18–24) for HR-HPV. HPV-16 was the most prevalent HPV genotype (5%, 95% CI 4–7) followed by HPV-6 (4%, 3–5). HPV prevalence was high in young adults, reaching a maximum between the ages of 25 years and 29 years, and stabilised or slightly decreased thereafter. Pooled prevalence estimates were similar for the UN Sustainable Development Goal geographical regions of Europe and Northern America, Sub-Saharan Africa, Latin America and the Caribbean, and Australia and New Zealand (Oceania). The estimates for Eastern and South-Eastern Asia were half that of the other regions.

Interpretation Almost one in three men worldwide are infected with at least one genital HPV type and around one in five men are infected with one or more HR-HPV types. Our findings show that HPV prevalence is high in men over the age of 15 years and support that sexually active men, regardless of age, are an important reservoir of HPV genital infection. These estimates emphasise the importance of incorporating men in comprehensive HPV prevention strategies to reduce HPV-related morbidity and mortality in men and ultimately achieve elimination of cervical cancer and other HPV-related diseases.

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Introduction

Human papillomavirus (HPV) is the most common sexually transmitted viral infection worldwide, and previous research has shown that most sexually active

men and women will acquire at least one genital HPV infection during their lives.¹ There are more than 200 HPV types that can be transmitted sexually, and at least 12 types are oncogenic.² The majority of HPV

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For the Spanish translation of the abstract see [Online for appendix 1](#)

For the French translation of the abstract see [Online for appendix 2](#)

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Research in context

Evidence before this study

The epidemiology of human papillomavirus (HPV) in women is well documented. Prevalence data from the general male population, however, are scarce. We searched Embase, Ovid MEDLINE, and the Global Index Medicus without language restrictions for studies published between Jan 1, 1995, and June 1, 2022. Search terms included “((HPV OR papilloma*) AND (male* OR men OR man) AND (prevalence))”. Most studies in men have been conducted in high-income countries and have focused on subpopulations at increased risk of HPV infection, such as men who have sex with men, men living with HIV, symptomatic men attending sexually transmitted infection clinics, and male partners of women with HPV infection or abnormal cervical cytology. The last comprehensive global review of the prevalence of genital HPV in men was published in 2011 and included studies on men at increased risk of HPV infection. The study reported that HPV prevalence was high among sexually active men in all regions but with considerable variation, from 1% to 84% among men at low risk of HPV infection and from 2% to 93% among men at increased risk of HPV infection. Peak HPV prevalence spanned a wide range of ages, and age-specific prevalence curves were relatively flat or declined only slightly following peak prevalence.

Added value of this study

This study provides global and regional mean benchmark values of genital HPV prevalence in men to inform prevention strategies, on the basis of a systematic review and meta-analysis of studies on HPV infection in general populations of sexually active men who are not reported as being in high-risk subgroups for HPV infection. We were able to generate global and regional prevalence estimates for any HPV, high-risk (HR)-HPV, and specific genotypes and assess age patterns

of infection and sources of interstudy heterogeneity. We made a major effort to select only studies that could be considered as representative of the general male population of a country and could be combined by means of meta-analysis with strict selection criteria. We provide support for evidence that the mean global and regional prevalence of high-risk genital HPV in men is very high (globally 21%, 95% CI 18–24) and sustained across the adult lifespan. HR-HPV prevalence estimates were similar across all regions studied except for Eastern and South-Eastern Asia (pooled estimate of 23%, excluding Eastern and South-Eastern Asia), for which estimates were half that of the other regions (10%). We also show that one key factor of interstudy heterogeneity is the anatomical site sampled. HR-HPV prevalence was higher in studies that sampled at least the penile shaft and the glans penis or coronal sulcus (23%) when compared with studies that did not (17%).

Implications of all the available evidence

The results suggest that genital HPV prevalence is high in men and that prevalence remains high throughout heterosexual men's sexual lives. These results are consistent with men being a reservoir of HPV infection and emphasise the importance of incorporating men in efforts to control HPV infection and to reduce the incidence of HPV-related disease. Prevalence data are primarily from high-income countries. Additional epidemiological studies assessing the age-specific prevalence of HPV types in men from additional countries could contribute to impact monitoring efforts both for countries that have HPV vaccination programmes for girls and young women and for the increasing number of countries that are including boys in their vaccination programme.

infections in men and women are asymptomatic, but they can lead to long-term sequelae and mortality. Each year, more than 340 000 women die of cervical cancer.³ In men, HPV infection tends to manifest clinically as anogenital warts, which cause significant morbidity and increase HPV transmission rates.^{4,5} HPV infections are also associated with penile, anal, and oropharyngeal cancers, which are commonly linked to HPV type 16.^{6,7} The International Agency for Research on Cancer estimated that there were about 69 400 cases of cancer in men caused by HPV in 2018.⁴

There are far fewer published reports on the epidemiology of HPV among general populations of men than those among women. Epidemiological studies have primarily focused on women, and data for the prevalence of HPV in men are scarce and predominantly from populations identified as being at increased risk of infection, such as men who have sex with men, men living with HIV, men with symptoms of sexually transmitted infections (STIs) attending STI clinics, and

male partners of women with HPV infection or abnormal cervical cytology. The first global review of genital HPV prevalence in men was published in 2006 and identified 40 publications on men at any risk of infection (appendix 3 p 2).⁸ HPV prevalence in men was 1.3–72.9% in the studies in which more than one anatomical site or specimen were evaluated. HPV prevalence varied on the basis of sampling, testing methods, and the anatomical site or specimen sampled.

A second review in 2011 focused on age-specific prevalence of HPV in men and identified 64 studies, 38 of which included populations at increased risk of HPV infection (appendix 3 p 2).⁹ HPV prevalence was high among these sexually active men in all regions but varied from 1% to 84% among men with low risk of HPV and from 2% to 93% among men with increased risk of HPV. Peak HPV prevalence spanned a wide range of ages, and age-specific prevalence curves were quite flat or declined only slightly following peak prevalence. A study published in 2018 examined risk factors for HPV in men,

See Online for appendix 3

including having sex with men, and estimated a global pooled prevalence of any type of genital HPV in men of 49% (95% CI 35–64) and a prevalence of high-risk (HR)-HPV of 35% (26–45) on the basis of data from 16 studies.¹⁰ Regional-level reviews from sub-Saharan Africa and Europe have consistently documented a prevalence of any HPV in men exceeding 25%.^{11,12}

We aimed to update the global and regional estimates of the overall, type-specific, and age-specific prevalence of genital HPV DNA in general populations of men before the onset of widespread HPV gender-neutral vaccination. HPV prevalence data among men are essential to understand disease burden and transmission risk in both men and women and to support the implementation and evaluation of cervical cancer prevention and elimination programmes.

Methods

Search strategy and selection criteria

This systematic review and meta-analysis is reported according to PRISMA¹³ and GATHER¹⁴ guidelines. We searched Embase, Ovid MEDLINE, and the Global Index Medicus using search strategies with exploded MeSH and Emtree terms and broad search criteria and without language restrictions for studies published between Jan 1, 1995, and June 1, 2022. For Embase Classic, Embase, and Ovid MEDLINE, search terms were “((HPV OR papilloma*) AND (male* OR men OR man) AND (prevalence)).mp.”. The search window went back to 1995 to mirror the data included in a meta-analysis of HPV in women.¹⁵ The search was supplemented by a bibliographic screening of review papers and papers that met the study entry criteria. The search strategies and full search terms are available in appendix 3 (p 2).

The study eligibility criteria for the systematic review and meta-analysis are summarised in appendix 3 (p 3). Briefly, we included articles that reported HPV prevalence among at least 50 men aged 15 years or older with no HPV-related pathology, used PCR or hybrid capture 2 techniques for HPV DNA detection, and collected samples from penile or anal sites (eg, glans, shaft, scrotum, urethra, anus, or foreskin) mostly after 1995. Studies conducted exclusively in populations that were considered at increased risk for HPV infection were excluded, as were studies conducted exclusively among circumcised men because circumcision is considered a protective factor.^{16–18} Studies conducted exclusively among men vaccinated against HPV, and studies based on urine or semen samples because the sensitivity of these samples for HPV detection is low.¹¹ We included baseline HPV prevalence data from cohort studies and from the control groups of case-control studies if men were asymptomatic. Titles and abstracts were screened for relevant publications separately by two authors (MT and LB for Embase and Ovid MEDLINE and MT and JR for the Global Index Medicus). Any differences were discussed by the two screeners and, where there was any

uncertainty over publication titles and abstracts, the publications were included in the list for full-text screening. Full texts were screened for relevance by GA and LB, and discrepancies were discussed by GA, LB, JR, and MT. In the case of studies where we were uncertain about eligibility, we reached out to the corresponding author (with a minimum of three contact attempts made). We also contacted corresponding authors to access detailed information on HPV prevalence by genotype and age where these data were not reported.

Data analysis

Data were extracted by GA and JR and reviewed by LB. Data were extracted using a standardised form. Discrepancies were resolved by consensus. Where the same study population was described in more than one publication, the publication with the highest sample size and most detailed information was used, supplemented by the other publications. Data from multicountry studies were presented by country where possible, and if a study provided data for 2 years or more, we used the starting year or year with the most detailed information (appendix 3 p 4). For studies that reported HPV prevalence data from more than one anatomical site, we prioritised data that included penile shaft, glans, or corona over other sites.¹⁹ We also prioritised data from PCR assays over hybrid capture 2 (Qiagen, Gaithersburg, MD, USA) if a study provided data for both. We extracted data only for mucosal α genus HPVs, because the main oncogenic HPV types and types that cause anogenital warts belong to this genus.²⁶ The full list of variables for which data were extracted is shown in appendix 3 (p 4).

The prevalence of high-risk genotypes was based on the high-risk definition used in each publication. If a publication did not provide an HR-HPV estimate, we estimated it as the sum of the prevalence of the 12 HR-HPV genotypes (types 16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, and 59) and adjusted for multiple infections using the ratio of the total number of HPV infections to number of individuals who were positive for HPV. Analyses of type-specific HPV prevalence were based on the studies reporting information for that HPV type. Each type (as single or multiple infection) was evaluated independently. Prevalence of HPV types that are included in the two-valent (types 16 and 18), four-valent (types 6, 11, 16, and 18), and nine-valent (types 6, 11, 16, 18, 31, 33, 45, 52, and 58) HPV vaccines were estimated at the global level after adjusting for multiple infections.

To be eligible for inclusion in the age-specific analyses, the range of a reported age category had to be 11 years or less. Age-specific prevalence data from each eligible study were transformed into estimates by 1-year age groups, assuming the number of men and prevalence were equally distributed, and then aggregated into 5-year and 10-year age groups.

The quality of studies was appraised by a risk of bias score (ie, low or high) on the basis of how closely the

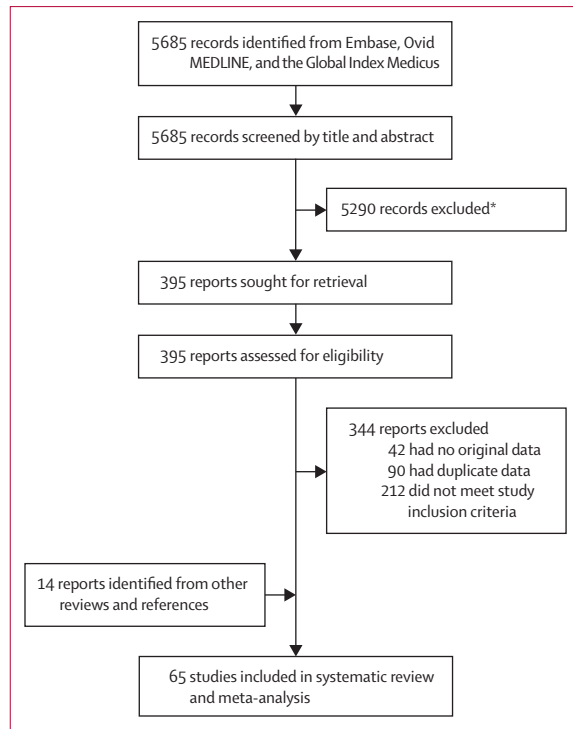


Figure 1: PRISMA flow diagram

*4938 records were excluded during the screening of publication titles and 352 records were excluded during the screening of abstracts.

study population represented the general population of sexually active men, the sampling frame, sample selection, and response rate. The checklist was adapted from publications by Hoy and colleagues²⁰ and Agbor and colleagues²¹ and is summarised in appendix 3 (p 5).

Regional pooled mean estimates for any HPV, HR-HPV, and HPV type were calculated using the geographical classification of the UN Sustainable Development Goals (SDGs)²² and the World Bank classification of income level.²³ Regional estimates were generated only for those regions where the total number of tested men was at least 500.

HPV prevalence estimates were pooled using random-effects models for meta-analyses of binomial data. Meta-analyses were conducted with Stata procedures `metaprop`, `metapreg`, and `metan`.^{24,25} Freeman-Tukey arcsine transformation of the prevalence was used to normalise variance; 95% CIs around the study-specific and pooled prevalences were computed on the basis of the score-test statistic. The percentage of total variation due to interstudy heterogeneity was evaluated using the I^2 measure. Publication bias was evaluated by visual inspection of funnel plots, the Egger test, and the trim-and-fill method.

Sensitivity analyses were conducted to identify sources of heterogeneity between studies. Subgroup meta-analysis was performed for nine variables and their categories planned a priori (ie, geography [SDG subregions], sample size [>500 or ≤ 500], risk of bias [low or high], studies conducted in STI clinics or equivalent

[no or yes], first year of data collection [before 2006, 2006–13, or 2014 or later], method of sampling [self-collected or clinician collected], anatomical sample site [at least the penile shaft and the glans penis or coronal sulcus sampled or did not collect data from either the shaft or the glans penis or coronal sulcus], number of HPV types tested in the assay [8–15 types, 16–26 types, or 27–50 types], and age [<30 years or ≥ 30 years]; appendix 3 p 4). The influence of study variables on the variation of the prevalence was assessed by meta-regression, including those variables that caused significant heterogeneity.

All statistical analyses were conducted in Stata (version 16). Although the review was not registered, an internal protocol was followed describing these methods.

Role of the funding source

The funders of the study had no role in study design, data collection, data analysis, data interpretation, or writing of the report.

Results

We identified 5685 publications from database searches, of which 65 studies^{26–90} comprising data from 44769 men were included in the systematic review and meta-analysis (figure 1, table 1). No additional publications were identified from the reference lists of the selected publications identified. Two studies provided data for more than one population. Authors of 49 publications were contacted to provide additional information. 40 of the authors responded and 31 provided unpublished data,^{27,28,32,35,38,39,41–43,50,51,53,55–57,59,60,62–64,66,71,73,75,80,81,83,86,87,90} including 27 authors who shared data for HPV-type distribution or age distribution.

The 65 studies^{26–90} provided data from 35 countries, with 16 countries having more than one study. One SDG region (Europe and Northern America) accounted for 31 (48%) of the studies. No prevalence data were found from three SDG regions (Northern Africa and Western Asia, Central and Southern Asia, and Oceania [excluding Australia and New Zealand]). 36 (55%) studies were from high-income countries and only six (9%) studies were from low or lower-middle-income countries (table 2).

The data included in the analysis came from prevalence surveys, case-control studies, and cohort studies conducted in a range of populations, including university students, the military, different occupational groups, participants of circumcision trials, outpatient clinics, and asymptomatic men attending STI or sexual health services (table 1). Of the 62 studies with information on date of specimen collection, 30 (48%) had samples collected before 2006, 25 (40%) between 2006 and 2013, and only seven (11%) from 2014 or later. 32 (49%) of 65 studies sampled at least the penile shaft and the glans of the penis or coronal sulcus. The most sampled genital anatomical sites were glans of the penis and corona sulcus (44 [68%] studies)

Study	Recruitment years	Study population or setting	Study design	Age range, years	Selection of study population	Specimen sample sites	HPV detection method	Risk score	Sample size	Estimated HPV prevalence		Inclusion in analyses		
										Any type	HR-HPV	Overall	Age Type	
Australia and New Zealand (Oceania)														
Australia	Machalek et al (2017) ^{35*}	2014–16	Sexual health clinics, general practice clinics, and outreach using Facebook	Cross-sectional	16 to 35	Convenience	Glans, corona, foreskin, and shaft	PCR-PGM09-PGM11, Cobas HPV test (Roche Molecular Systems, Alameda, CA, USA) and Linear Array HPV Genotyping Test (Roche Molecular Systems, Alameda, CA, USA)	High	511	28%	19%	Yes	Yes
Eastern and South-Eastern Asia														
China	Tang et al (2006) ³⁶	2003–04	STI clinic	Cross-sectional	18 to 70	Convenience	Urethra	PCR-MY09-MY11 and restriction fragment length polymorphisms	High	305	14%	NR	Yes	Yes
China	He et al (2013) ^{41*}	2007–09	Rural community	Cross-sectional	25 to 65	Cluster	Glans, corona, shaft, and scrotum	PCR-SPF1/GP6+	Low	2236	18%	6%	Yes	Yes
China	Wei et al (2016) ^{38*}	2014	Urban community	Cross-sectional	18 to 55	Convenience	Glans, corona, penile, perianal, and anal canal	PCR-GP5+/6+	Low	1509	11%	10%	Yes	Yes
China	Zhang et al (2018) ^{39**}	2013	Rural community	Cross-sectional	<30 to >50†	Convenience	Urethra	Human Papillomavirus Genotyping Kit (Gene Chips; Genetel Pharmaceuticals, Shenzhen, China)	High	104	13%	10%	Yes	No
China	Ma et al (2019) ³⁴	2016–18	STI clinic	Cross-sectional	18 to 67	Convenience	Glans, corona, shaft, scrotum, and urethra	Real-time PCR genotyping (Liferiver, Shanghai, China)	High	737	26%	19%	Yes	Yes
China	Wang et al (2021) ³⁴	2015–20	Men attending Henan Provincial People's Hospital	Cross-sectional	20 to 85	Convenience	Glans, corona, shaft; prepuce, and distal urethra	PCR-HPV genotyping kit (Gene Chips; Genetel Pharmaceuticals, Shenzhen, China)	High	3690	30%	12%	Yes	Yes
Japan	Takahashi et al (2003) ³⁴	2002	University students	Case-control	18 to 35	Convenience	Glans, corona, and foreskin	Hybrid Capture 2, for high-risk and low-risk HPV types (Digene, Gaithersburg, MD, USA)	Low	75	1%	1%	Yes	No
Japan	Takahashi et al (2005) ^{33*}	2004	University students	Cross-sectional	18 to 35	Convenience	Glans, corona, and foreskin	Hybrid Capture 2, for high-risk and low-risk HPV types (Digene, Gaithersburg, MD, USA)	Low	150	8%	8%	Yes	No
Japan	Matsuzawa et al (2020) ^{36**}	2011–15	Urology clinic	Cross-sectional	15 to 95	Convenience	Glans	PCR-GENOSEARCH-HPV31 (Medical and Biological Laboratories, Nagoya, Japan)	High	759	25%	13%	Yes	Yes

(Table 1 continues on next page)

Study	Recruitment years	Study population or setting	Study design	Age range, years	Selection of study population	Specimen sample sites	HPV detection method	Risk score	Sample size	Estimated HPV prevalence		Inclusion in analyses	
										Any type	HR-HPV	Overall	Age Type
(Continued from previous page)													
Malaysia	2014–16	Community	Cross-sectional	18 to 60	Convenience	Shaft	PCR-BGISEQ-100 (Beijing Genome Institute- assembled Ion Proton Sequencer from Life Technologies, South San Francisco, CA, USA)	Low	389	21%	19%	Yes	Yes
South Korea	2002	University students	Cross-sectional	18 to 28	Convenience	Glans, corona, foreskin, penile, and scrotum	PCR line probe assay	Low	381	9%	4%	Yes	Yes
Philippines, Taiwan, and Australia	2004–08	Community (baseline data of men participating in the Gardasil trial)	Cross-sectional	16 to 14	Convenience	Penile, scrotum, and perineal or perianal areas	PCR multiplex real-time fluorescent detection (Atia BioSystems, Mountain View, CA, USA)	Low	263	10%	9%	Yes	Yes
Europe and Northern America													
Canada	2006–07	STI clinic	Cross-sectional	16 to 69	Convenience	Glans, foreskin, penile shaft, and scrotum	PCR Linear Array HPV Genotyping Test (Roche Molecular Systems, Alameda, CA, USA)	High	261	61%	57%	Yes	Yes
Canada	2005–11	University students	Cohort	17 to 45	Convenience	Glans, corona, foreskin, shaft, and scrotum	PCR Linear Array HPV Genotyping Test (Roche Molecular Systems, Alameda, CA, USA)	Low	535	59%	42%	Yes	Yes
Canada	2011–13	Urban community	Cross-sectional	16 to 83	Convenience	Foreskin and shaft	PCR Linear Array HPV Genotyping Test (Roche Molecular Systems, Alameda, CA, USA)	High	175	43%	24%	Yes	Yes
Croatia	2009–11	STI clinic	Cross-sectional	17 to 60	Convenience	Genital	PCR-AMPLICOR HPV test (Roche Diagnostics, Mannheim, Germany)	High	330	32%	32%	Yes	No
Czechia	2013–16	Men in couples treated for infertility	Cross-sectional	22 to 57	Convenience	Glans and corona	PCR-PapilloCheck test (Greiner Bio-One, Frickenhausen, Germany)	High	195	41%	31%	Yes	No
Denmark	2006–07	Military conscripts and employees	Cross-sectional	18 to 65	Population-based	Glans, corona, foreskin, shaft, perineum	PCR-INNO-LiPA HPV Genotyping Extra II (Immogenetics, Ghent, Belgium)	Low	2436	42%	30%	Yes	Yes
Denmark	1998	Military conscripts	Cohort	18 to 29	Population-based	Glans and corona	PCR-GP5+/6+	Low	337	34%	NR	Yes	Yes
Finland	No data	Male spouses of pregnant women in their third trimester	Cohort	19 to 46	Convenience	Urethra	PCR-GP5+/6+ and MY09/11	Low	128	23%	9%	Yes	No
Italy	2005–06	STI clinic	Case-control	18 to 45	Convenience	Urethra	PCR-INNO-LiPA HPV Genotyping Extra (Immogenetics, Rome, Italy)	High	1081	27%	11%	Yes	No
Netherlands	2002	Outpatient clinic (not an STI clinic)	Cross-sectional	23 to 73	Convenience	Glans, corona, and foreskin	PCR-GP5+/6+	Low	83	25%	19%	Yes	Yes

(Table 1 continues on next page)

Study	Recruitment years	Study population or setting	Study design	Age range, years	Selection of study population	Specimen sample sites	HPV detection method	Risk score	Sample size	Estimated HPV prevalence		Inclusion in analyses		
										Any type	HR-HPV		Overall	Age Type
(Continued from previous page)														
Netherlands	Vriend et al (2013) ^{35*}	2009–11	STI clinic	Cross-sectional	16 to 24	Convenience	Glans, corona, and foreskin	PCR-SPF10-DEIA line probe assay (DDL Diagnostic Laboratory, Rijswijk, Netherlands)	High	414	54%	40%	Yes	Yes
Netherlands	Luttmer et al (2015) ^{33*}	2011–12	Healthy men	Cross-sectional	18 to 65	Convenience	Glans, corona, and foreskin	PCR-SPF10-DNA enzyme-linked immunoassay (DDL Diagnostic Laboratory, Rijswijk, Netherlands)	Low	170	34%	26%	Yes	Yes
Netherlands	Koene et al (2016) ^{36*}	2011	STI clinic	Cross-sectional	18 to 61	Convenience	Glans, corona, shaft, and urethra	PCR-RHA Kit SPF10-LIPA25 version 1 (Labo Bio-medical Products, Rijswijk, Netherlands)	High	111	65%	42%	Yes	Yes
Russia	Smelov et al (2013) ^{71*}	2006–09	STI clinic	Cross-sectional	16 to 60	Convenience	Urethra	PCR-Bioplex 200 Luminex system (Bio-Rad, Hercules, CA, USA)	High	895	25%	17%	Yes	Yes
Slovenia	Golob et al (2014) ^{39*}	2010–13	Male partners from couples attending a clinic due to inability to conceive within at least one year of unprotected regular sexual intercourse	Cross-sectional	16 to 55	Convenience	Penile surface	PCR Linear Array HPV Genotyping Test (Roche Molecular Diagnostics, Pleasanton, CA, USA)	High	299	37%	17%	Yes	Yes
Spain	Álvarez-Argüelles et al (2013) ^{38*}	2002–11	STI clinic	Cross-sectional	17 to 87	Convenience	Balanopreputial or urethral	PCR-MY11/MY09 and GP5+/GP6+	High	565	12%	3%	Yes	Yes
Sweden	Wikström et al (2000) ³⁹	No data	STI clinic	Cross-sectional	18 to 54	Convenience	Glans, corona, and foreskin	PCR reverse hybridisation DNA sequencing	High	235	13%	8%	Yes	No
Sweden	Söderlund-Strand et al (2013) ³⁹	2008	Sexual health clinic	Cross-sectional	20 to 29	Convenience	Urethra	PCR-HPV MassArray (Agena Bioscience, Hamburg, Germany)	High	597	22%	NR	Yes	No
Sweden	Söderlund-Strand et al (2015) ⁷²	No data	Sexual health clinic	Cross-sectional	21 to 56	Convenience	Shaft	PCR-HPV MassArray (Agena Bioscience, Hamburg, Germany)	High	127	49%	34%	Yes	No
UK	Jalal et al (2007) ⁴⁵	2003	STI clinic	Cross-sectional	15 to 77	Convenience	Urethra	PCR reverse blot hybridisation	High	437	21%	13%	Yes	No
UK	Cuschieri et al (2011) ^{35*}	2007–08	Youth clinic	Cross-sectional	16 to 25	Convenience	Shaft	PCR-INNO-LiPA-HPV Genotyping Extra II (Fujirebio, Gent, Belgium)	High	117	29%	20%	Yes	Yes
USA	Baldwin et al (2003) ³⁹	2000–01	STI clinic	Cross-sectional	18 to 70	Convenience	Glans and corona	PCR-PGMV09/11 and reverse line blot or PCR-L1 consensus	High	393	28%	12%	Yes	Yes
USA	Weaver et al (2004) ⁸⁵	2001–02	University students	Cross-sectional	18 to 25	Population-based	Glans, foreskin, shaft, and scrotum	PCR-MY09/MY11/HMB01	Low	317	33%	NR	Yes	No

(Table 1 continues on next page)

Study	Recruitment years	Study population or setting	Study design	Age range, years	Selection of study population	Specimen sample sites	HPV detection method	Risk score	Sample size	Estimated HPV prevalence		Inclusion in analyses		
										Any type	HR-HPV	Overall	Age Type	
(Continued from previous page)														
USA	Nielson et al (2007) ⁶⁵ 2003–06	STI clinic and the community	Cross-sectional	18 to 40	Convenience	Glans, corona, shaft, scrotum, urethra, perianal area, anal canal, and semen	PCR-PGMY09/11 and reverse line blot	High	463	65%	29%	Yes	No	Yes
USA	Partridge et al (2007) ⁶⁵ 2003–06	University students	Cohort	18 to 20	Population-based	Glans, shaft, and scrotum	PCR-based direct DNA sequencing	Low	240	26%	20%	Yes	Yes	Yes
USA	Hernandez et al (2008) ^{63*} 2004–06	University population	Cohort	18 to 79	Convenience	Glans, corona, shaft, and scrotum	PCR-PGMY09/11 and reverse line blot	Low	410	40%	24%	Yes	Yes	Yes
USA	Hernandez et al (2013) ⁶⁴ 2010–12	Community clinic and medical practices	Cross-sectional	14 to 59	Convenience	Glans, corona, foreskin, and shaft	PCR Linear Array HPV Genotyping Test (Roche Diagnostics, Indianapolis, IN, USA)	High	450	44%	16%	Yes	Yes	Yes
USA	Sudenga et al (2017) ^{62*} 2005–09	Community (HPV Infection in Men study [HIM])	Cohort	18 to 70	Baseline	Glans, corona, shaft, and scrotum	PCR-L1 consensus and Linear Array HPV Genotyping Test (Roche Diagnostics, Indianapolis, IN, USA)	Low	1274	47%	28%	Yes	Yes	Yes
USA	Gargano et al (2017) ^{68*} 2013–14	Community (NHANES)	Cross-sectional	14 to 59 [†]	Population-based	Glans	PCR Linear Array HPV Genotyping Test (Roche Molecular Systems, Alameda, CA, USA)	Low	1623	47%	26%	Yes	Yes	Yes
USA	Widdice et al (2019) ⁶⁸ 2013–14	Hospital-based adolescent primary care clinic, STI clinic, and the community	Cross-sectional	13 to 26	Sequential sampling	Glans, corona, shaft, scrotum, and perianal or anal areas	PCR Linear Array HPV Genotyping Test (Roche Molecular Systems, Alameda, CA, USA)	High	310	61%	NR	Yes	No	Yes
Croatia, Finland, Germany, Netherlands, Norway, Portugal, Spain, and Sweden	Vardas et al (2011) ⁶⁶ 2004–08	Community (baseline data of men participating in the Gardasil trial)	Cross-sectional	16 to 24	Convenience	Penile, scrotum, and perineal or perianal areas	PCR-Multiplex Real Time Fluorescent Detection (AtiaBioSystems, Mountain View, CA, USA)	Low	354	21%	20%	Yes	Yes	Yes
USA and Canada	Vardas et al (2011) ⁶⁶ 2004–08	Community (baseline data of men participating in the Gardasil trial)	Cross-sectional	16 to 24	Convenience	Penile, scrotum, and perineal or perianal areas	PCR-Multiplex Real Time Fluorescent Detection (AtiaBioSystems, Mountain View, CA, USA)	Low	712	27%	24%	Yes	Yes	Yes
Latin America and the Caribbean														
Brazil	Rosenblatt et al (2004) ⁶⁷ 1999–2001	Partners of women screened for cervical cancer	Cross-sectional	NR	Convenience	Foreskin, shaft, dorsal and ventral prebalanic area, and urethra	Hybrid Capture 2, for high-risk and low-risk HPV types (Digene, Gaithersburg, MD, USA)	Low	60	15%	15%	Yes	No	No

(Table 1 continues on next page)

Study	Recruitment years	Study population or setting	Study design	Age range, years	Selection of study population	Specimen sample sites	HPV detection method	Risk score	Sample size	Estimated HPV prevalence		Inclusion in analyses	
										Any type	HR-HPV	Overall	Age Type
(Continued from previous page)													
Brazil	2009	Community	Cross-sectional	15 to 64	Convenience	Urethra	Hybrid Capture 2, for high-risk HPV types (Digene, Gaithersburg, MD, USA)	High	278	14%	14%	Yes	No
Brazil	2000–10	Partners of women screened for cervical cancer	Cross-sectional	18 to 51	Convenience	Penile scrape	PCR-MY09/11 type-specific E6	Low	60	17%	NR	Yes	No
Brazil	2011–14	Asymptomatic men from an STI clinic, a dermatology clinic, and a metallurgical factory	Cross-sectional	18 to 65	Convenience	Glans, corona, and foreskin	PCR-restriction fragment length polymorphism	High	550	22%	10%	Yes	No
Brazil	2010–11	Asymptomatic men having laboratory tests done	Cross-sectional	1867	Convenience	Glans, corona, and frenulum	PCR-MY09/11 type-specific E6	High	110	16%	4%	Yes	No
Brazil	2005–09	Community (HPV in Men study [HIM1])	Cross-sectional	18 to 70	Baseline	Glans, corona, shaft, and scrotum	PCR-L1 consensus and Linear Array HPV Genotyping Test (Roche Diagnostics, Indianapolis, IN, USA)	Low	1398	60%	34%	Yes	Yes
Brazil	2016–17	Young people who use public health system	Cross-sectional	15 to 25	Convenience	Glans, corona, shaft, and scrotum	PCR-L1 consensus and Linear Array HPV Genotyping Test (Roche Diagnostics, Indianapolis, IN, USA)	Low	1120	53%	29%	Yes	Yes
Chile	No data	University students	Cross-sectional	20 to 51	Convenience	Corona and shaft	PCR-GP5+/6+ and reverse line blot	Low	61	84%	75%	Yes	No
Mexico	1998	University students and industry workers	Cross-sectional	14 to 55	Convenience	Corona and urethra	PCR-GP5+/6+	Low	96	43%	20%	Yes	No
Mexico	2000–01	University students	Cross-sectional	≥16	Convenience	Glans, corona, and foreskin	Hybrid Capture 2, for high-risk HPV types (Digene, Gaithersburg, MD, USA)	Low	71	9%	9%	Yes	No
Mexico	2000–03	Military	Cross-sectional	16 to 40	Convenience	Corona, shaft, scrotum, and urethra	PCR strip assay using the reverse line blot	Low	1045	43%	32%	Yes	Yes
Mexico	2003–04	Men seeking vasectomy	Cross-sectional	15 to 65	Convenience	Glans, corona, foreskin, shaft, scrotum, and urethra	PCR-L1 consensus	Low	779	9%	6%	Yes	Yes
Mexico	2002–03	Partners of women attending a primary health centre	Cross-sectional	18 to 75	Convenience	Foreskin, shaft, scrotum, and urethra	PCR-L1 consensus and reverse line blot	Low	504	20%	8%	Yes	Yes

(Table 1 continues on next page)

Study	Recruitment years	Study population or setting	Study design	Age range, years	Selection of study population	Specimen sample sites	HPV detection method	Risk score	Sample size	Estimated HPV prevalence		Inclusion in analyses
										Any type	HR-HPV	
(Continued from previous page)												
Mexico	2002–03	University students	Cross-sectional	≥18	Convenience	Penis, glans, and corona	PCR-MY09/MY11 and Linear Array HPV Genotyping Test (Roche Diagnostics, Indianapolis, IN, USA)	Low	253	19%	17%	Yes
Mexico	2005–09	Community (HPV in Men study [HIM])	Cross-sectional	18 to 70	Baseline	Glans, corona, shaft, and scrotum	PCR-L1 consensus and Linear Array HPV Genotyping Test (Roche Diagnostics, Indianapolis, IN, USA)	Low	1342	50%	27%	Yes
Brazil, Costa Rica, Mexico, Peru	2004–08	Community (baseline data of men participating in the Gardasil trial)	Cross-sectional	16 to 24	Convenience	Penile, scrotum, and perineal or perianal areas	PCR-Multiplex Real Time Fluorescent Detection (Atila BioSystems, Mountain View, CA, USA)	Low	1301	29%	26%	Yes
Sub-Saharan Africa												
Botswana	2019–21	Men without HIV infection from the University of Botswana	Cross-sectional	18 to 22	Convenience	Penile, shaft, glans, and foreskin	PCR real-time Anyplex II HPV28 assay (Seegene, Seoul, South Korea)	Low	493	31%	24%	Yes
Kenya	2005	Fishermen from the community	Cross-sectional	18 to 68	Population-based	Glans, corona, shaft, scrotum, and perianal region	PCR-MY09/MY11/HMB01 and Linear Array HPV Genotyping Test (Roche Diagnostics, Indianapolis, IN, USA)	Low	186	53%	32%	Yes
Kenya	2002–05	Community (circumcision trial)	Cross-sectional	17 to 28	Population-based	Glans, corona, foreskin, and shaft	PCR-GP5+/6+ and reverse line-blot hybridisation	Low	2702	51%	35%	Yes
Mozambique	2009–11	Young people attending a youth clinic	Cross-sectional	18 to 24	Convenience	Urethra	PCR-Clart HPV 2 (Genomica, Madrid, Spain)	High	176	10%	6%	Yes
Rwanda	2007–09	Control group in an infertility study	Case-control	21 to 57	Convenience	Glans, corona, foreskin, shaft, and scrotum	PCR Linear Array HPV Genotyping Test (Roche Diagnostics, Indianapolis, IN, USA)	Low	166	43%	27%	Yes
South Africa	2006–09	Couples studies	Cross-sectional	19 to 67	Convenience	Glans, foreskin, and shaft	PCR Linear Array HPV Genotyping Test (Roche Diagnostics, Indianapolis, IN, USA)	High	313	51%	25%	Yes
South Africa	2005–06	Community (circumcision trial)	Cross-sectional	18 to 24	Population-based	Urethra	PCR Linear Array HPV Genotyping Test (Roche Diagnostics, Indianapolis, IN, USA)	Low	1683	19%	17%	Yes

(Table 1 continues on next page)

and the penile shaft (32 [49%] studies); prepuce, foreskin, or frenulum (22 [34%] studies); the urethra or meatus (21 [32%] studies); and the scrotum (19 [29%] studies).

The estimated overall HPV prevalence (of any type) among men was 31% (95% CI 27–35) with study-specific prevalences ranging from 1% to 84% (tables 1, 2; appendix 3 p 12). The pooled prevalence estimates for any HPV, HR-HPV, HPV-16, and HPV-6 are shown in table 2; forest plots for the 56 studies with data for HR-HPV, any HPV, HPV-16, and HPV-6 are shown in appendix 3 (pp 11–14).

The overall prevalence of HR-HPV was 21% (95% CI 18–24) with study-specific prevalences ranging from 1% to 75%. Globally, HPV-16 was the most frequent HR-HPV type at 5% (95% CI 4–7) followed by types 51 (3%, 3–4), 52 (3%, 2–3), 59 (2%, 2–3), and 18 (2%, 2–3; figure 2; appendix 3 p 6). HPV-6, a non-HR-HPV type, was the second most prevalent HPV type globally (4%, 95% CI 3–5; table 2, figure 2; appendix 3 p 6). The pooled prevalence was 7% (95% CI 6–8) for the HPV types found in the two-valent vaccine, 11% (95% CI 9–13%) for the four-valent vaccine, and 16% (95% CI 14–18%) for the nine-valent vaccine (appendix 3 p 7).

47 studies (39183 individuals) had sufficient age-specific information to estimate prevalence by age (figure 3). The age-specific prevalence curves show a high prevalence of HPV in young adult men, which remains high throughout adulthood. Prevalence was highest in people aged 25–29 years for any HPV (35%, 95% CI 30–41), HR-HPV (24%, 19–29), and HPV-16 (6%, 5–9). Prevalence in people aged 15–19 years was also high (28% [95% CI 24–32] for any HPV; 20% [17–23] for HR-HPV; and 3% [2–4] for HPV-16). HPV-16 age-specific prevalence curves for HR-HPV in Eastern and South-Eastern Asia and Europe and Northern America reflect upward prevalence from ages 15 years to 20 years followed by stable prevalence in older age groups, whereas in Latin America and the Caribbean and Sub-Saharan Africa, the curves appear to trend downwards after they peak (figure 3).

There were sufficient data to generate regional estimates for five SDG regions. The pooled prevalence for any HPV was highest in Sub-Saharan Africa (37%, 95% CI 26–49), followed by Europe and Northern America (36%, 32–41; table 2). The lowest prevalence was in Eastern and South-Eastern Asia (15%, 95% CI 11–21) and was the only regional prevalence estimate that was significantly different from the others. The same pattern is true for HR-HPV; for all ten of the studies from Eastern and South-Eastern Asia, the prevalence of HR-HPV was 10% (95% CI 7–13), below the global pooled HR-HPV prevalence (21%, 18–24; table 2; appendix 3 p 11). Although there were no significant differences, the pooled prevalence for any HPV, HR-HPV, and HPV-16 was slightly higher in high-income countries than in low-income and middle-income countries; for example, the prevalence of any HPV was 34% (95% CI 29–39) in

Study	Recruitment years	Study population or setting	Study design	Age range, years	Selection of study population	Specimen sample sites	HPV detection method	Risk score	Sample size	Estimated HPV prevalence		Inclusion in analyses					
										Any type	HR-HPV	Overall	Age	Type			
(Continued from previous page)																	
South Africa	Vardas et al (2011) ⁸⁰	2004–08	Community data of men participating in the Gardasil trial	Cross-sectional	16 to 24	Convenience	Penile, scrotal, and perineal or perianal areas	PCR-Multiplex Real Time Fluorescent Detection (Atila BioSystems, Mountain View, CA, USA)	Low	518	42%	36%	Yes	Yes	Yes		
Tanzania	Olesen et al (2013) ^{65*}	2009	Urban and rural community	Cross-sectional	16 to 65	Convenience	Glans, corona, and shaft	Hybrid Capture 2 HPV DNA Test, for high-risk and low-risk HPV types (Qiagen Gaithersburg, MD, USA) and INNO-LiPA HPV Genotyping Extra II (Fujirebio, Gent, Belgium)	Low	1343	20%	15%	Yes	Yes	Yes		
Uganda	Tobian et al (2013) ⁷⁷	2003–06	Community (circumcision trial)	Cross-sectional	15 to 49	Population-based	Glans and corona	PCR Linear Array HPV Genotyping Test (Roche Diagnostics, Indianapolis, IN, USA)	Low	978	61%	39%	Yes	Yes	Yes		

HPV=human papillomavirus. HR-HPV=high-risk HPV. NR=not reported. STI=sexually transmitted infection. * Authors provided additional information. †Data were reported from men younger than 30 years, men aged 30–49 years, and men aged 50 years or older; the full range of ages included was not reported. ‡To exclude HPV-vaccinated cohorts, only data for people aged 20–59 years were considered.

Table 1: Studies included reporting prevalence of genital HPV in men by UN Sustainable Development Goals regional grouping

Region	Any type			HR-HPV			HPV-16			HPV-6		
	Number of studies	Number of men	HPV prevalence, % (95% CI)	Number of studies	Number of men	HPV prevalence, % (95% CI)	Number of studies	Number of men	HPV prevalence, % (95% CI)	Number of studies	Number of men	HPV prevalence, % (95% CI)
Global*	65	44 769	31% (27–35)	56	41 617	21% (18–24)	54	41 482	5% (4–7)	53	41 045	4% (3–5)
Australia and New Zealand (Oceania)	1	511	28% (24–32)	1	511	19% (16–23)	1	511	3% (2–5)	1	511	3% (2–5)
Eastern and South-Eastern Asia†	11	10 335	15% (11–21)	10	10 030	10% (7–13)	9	10 110	2% (1–5)	9	10 110	3% (0–10)
Eastern Asia	10	9946	15% (10–20)	9	9641	9% (6–12)	8	9721	2% (1–5)	8	9721	3% (0–11)
Europe and Northern America‡	31	16 074	36% (32–41)	26	13 947	24% (20–28)	27	13 577	7% (5–9)	26	13 142	4% (3–5)
Europe	19	8911	31% (25–37)	16	7412	22% (17–28)	16	6732	6% (4–7)	15	6296	3% (2–5)
Northern America	13	7163	45% (38–51)	11	6535	27% (21–32)	12	6845	9% (6–12)	12	6846	5% (3–7)
Latin America and the Caribbean	15	9028	30% (21–40)	12	8308	22% (16–29)	10	8463	7% (4–10)	10	8461	4% (3–6)
Central America	7	4090	26% (13–41)	7	4090	16% (8–26)	5	3923	5% (2–9)	5	3923	2% (0–4)
South America	8	3637	34% (19–50)	5	2917	31% (21–43)	5	3239	11% (5–20)	5	3239	7% (6–9)
Sub-Saharan Africa	10	8558	37% (26–49)	10	8558	25% (18–32)	10	8558	4% (3–7)	10	8558	4% (3–6)
Eastern Africa	6	5551	38% (23–55)	6	5551	24% (15–35)	6	5551	5% (2–9)	6	5551	4% (2–5)
Southern Africa	4	3007	35% (21–51)	4	3007	25% (17–34)	4	3007	4% (3–5)	4	3007	6% (3–10)
Income level												
High income	36	17 116	34% (29–39)	31	14 989	23% (19–27)	30	14 394	7% (5–9)	29	13 959	4% (3–5)
Low and middle income	31	27 390	28% (22–34)	27	26 365	19% (15–24)	26	26 825	4% (3–6)	26	26 823	4% (2–6)
Upper-middle income	25	21 839	26% (20–32)	21	20 814	18% (14–22)	20	21 274	4% (3–6)	20	21 272	4% (2–7)
Lower-middle income	3	4231	40% (18–65)	3	4231	26% (12–44)	3	4231	6% (1–13)	3	4231	4% (2–5)
Low income	3	1320	36% (9–70)	3	1320	22% (5–46)	3	1320	4% (0–9)	3	1320	3% (1–6)

UN Sustainable Development Goals regional or subregional groupings were used for regional classification and World Bank income classification was used for income level. HR-HPV=high-risk HPV. HPV=human papillomavirus. *The number of studies in each region does not add to the global number of studies because Vardas et al⁸⁰ and Sudenga et al⁷⁹ included more than one country or region. †The number of studies in Eastern Asia is different to the number of studies in Eastern and South-Eastern Asia because subregional estimates were generated only for studies in the subregions for which the total number of men was at least 500, which excluded one study in South-Eastern Asia.⁴⁸ ‡Vardas et al⁸⁰ was included in both subregions of Europe and Northern America but is counted only once for the region of Europe and Northern America.

Table 2: Meta-analyses of studies reporting prevalence of any HPV, HR-HPV, HPV-16, and HPV-6 by region and income classification

high-income countries and 28% (22–34) in low-income and middle-income countries (table 2).

Figure 2 shows 14 HPV types (ie, the 12 main HR-HPV types, HPV-6, and HPV-11) by region. HPV-16 was the most common HPV type in four of five regions. The exception was Eastern and South-Eastern Asia, where HPV-6 was the most prevalent, although the 95% CIs were wide. The second most common HPV types were HPV-51 in Europe and Northern America, HPV-6 in Sub-Saharan Africa and Latin America and the Caribbean, and HPV-16 in Eastern and South-Eastern Asia.

Studies had a median HR-HPV prevalence of 20% (IQR 12–29; appendix 3 p 8) with significant heterogeneity across the studies ($I^2=98%$, $p<0.0001$; appendix 3 p 11). No study size effects were observed (appendix 3 p 9), and an influence analysis did not show influential studies in the overall estimate. The Egger test had a p value of 0.92, and the adjusted overall HR-HPV prevalence using both the observed and imputed potentially non-published studies was 24% (95% CI 21–27) versus 21% (18–24) using observed data only (appendix 3 p 16). Similar results were

observed for any HPV ($I^2=99%$, $p<0.0001$), HPV-16 ($I^2=95%$, $p<0.0001$), and HPV-6 ($I^2=97%$, $p=0.027$; appendix 3 pp 12–14).

We performed subgroup meta-analyses for nine variables looking at the prevalence of any HPV, HR-HPV, HPV-16, and HPV-6 (appendix 3 p 9). No differences were observed by sample size, risk of bias score, inclusion of men recruited from STI or sexual health clinics, start year of data collection, method of sampling, or age. For any HPV, significant between-group heterogeneity was observed for three variables: Eastern and South-Eastern Asia compared with the other regions ($p<0.0001$), anatomic sites sampled ($p=0.001$), and number of HPV types tested in the HPV detection test ($p<0.0001$). Overall, any HPV prevalence was lower in studies from Eastern and South-Eastern Asia (15%, 95% CI 11–21%) than in studies from other regions (34%, 30–38). Prevalence was significantly greater in studies that sampled at least the penile shaft and the glans penis or coronal sulcus (37%, 95% CI 31–42) than in studies that did not (24%, 20–30). As expected, and as a proxy of the HPV detection method (table 1), the

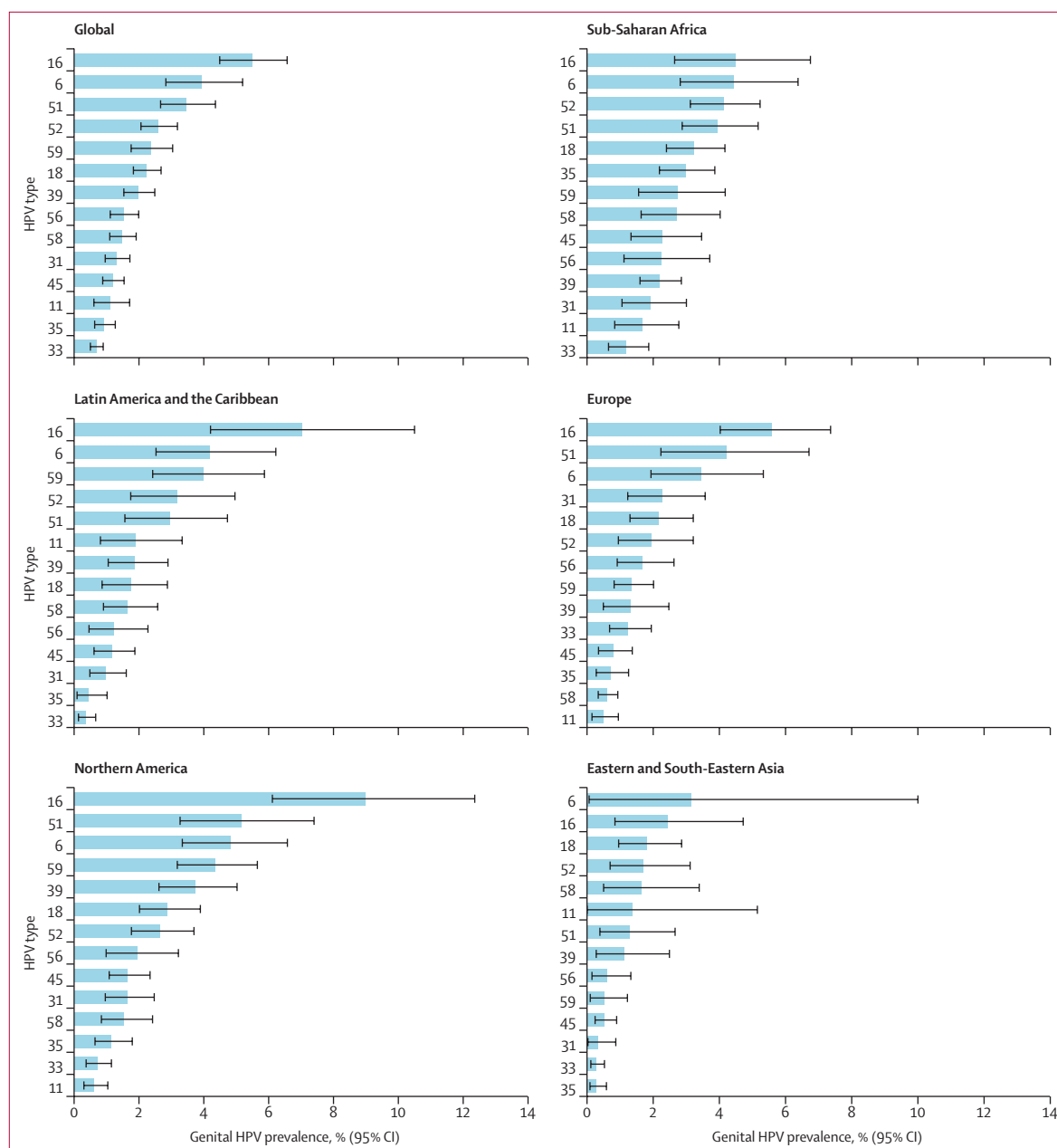


Figure 2: Pooled prevalence of HR-HPV types, HPV-6, and HPV-11 in men by region

Regions are defined by the UN Sustainable Development Goals regional or subregional grouping. Europe and Northern America are shown separately, and Central America and South America were the only subregions for Latin America and the Caribbean. HR-HPV types were defined as types 16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, and 59. HPV types are ranked by prevalence. Error bars represent the 95% CIs. Numbers of studies with available data for each HPV type and the number of men for whom data were contributed are shown in appendix 3 (p 6). HR-HPV=high-risk HPV. HPV=human papillomavirus.

prevalence of any HPV increased with the number of HPV types tested for, from 20% (95% CI 15–25) in studies that tested for eight to 15 HPV types, 25% (18–33) in those that tested for 16 to 26 HPV types, and to 38% (33–43) in those that tested for more than 26 HPV types. After adjusting for geography, anatomical sites sampled, and number of HPV types tested for, any HPV prevalence was 29% (95% CI 26–33). Similar results were observed for HR-HPV and HPV-16. For HR-HPV, after adjusting for

geography and anatomical sites sampled prevalence was 19% (95% CI 17–22). For HPV-16, after adjusting for geography, anatomical sites sampled, and number of HPV types included in the assay, prevalence was 5% (95% CI 4–6).

Discussion

We estimated the global pooled prevalence for genital HPV infection among men to be 31% (95% CI 27–35) for

any HPV and 21% (18–24) for HR-HPV on the basis of data from 65 studies (including 44769 men) conducted between Jan 1, 1995, and June 1, 2022.^{26–90} HPV-16 was the dominant HPV type (5%, 95% CI 4–7), followed by HPV-6 (4%, 3–5). The age-specific analysis showed a high prevalence of HPV in young adult men, which remained high throughout adulthood. These estimates are consistent with the hypothesis that sexually active men, regardless of age, are at risk of HPV-related morbidity and are a reservoir of sexually transmissible HPV infection.

Globally in men, as in women, the most common oncogenic and preventable HPV type is HPV-16.⁶ The roll-out of HPV vaccination in young women, and increasingly in young men, is beginning to have a beneficial effect on reducing the prevalence of the specific genotypes targeted by the different HPV vaccines and on HPV-related disease in men and women.⁹¹ Three HPV vaccine formulations are available on the market: two-valent (HPV types 16 and 18), four-valent (HPV types 6, 11, 16, and 18), and nine-valent (HPV types 6, 11, 16, 18, 31, 33, 45, 52, and 58). All three vaccine formulations target HPV-16 and HPV-18, the two HR-HPV types that are most often associated with HPV-related cancers.⁶ By 2022, 45 countries were providing HPV vaccination for boys.^{92,93} And, as a result of the synergy of the protective effects of vaccinating boys and girls, mathematical modelling studies suggest that

the HPV types targeted by the different HPV vaccines could be eliminated from circulation with gender-neutral vaccination.⁹⁴

HPV prevalence in men peaked in the group aged 25–29 years and remained high until at least age 50 years. Prevalence in the group aged 15–19 years was also high, suggesting that young men are being infected rapidly following first sexual activity. These estimates are consistent with data from studies on the natural history of HPV infection in men, which show stable rates of detection of incident genital HPV across age groups and low seroconversion rates following HPV infection, suggesting that men remain susceptible to HPV infection across the lifespan.^{95,96} This age profile of infection in men is different from the profile in women, for whom genital HPV prevalence peaks soon after first sexual activity and declines with age, with a slight rebound after age 50–55 years (ie, often after or around the time of menopause) in some populations.^{97,98}

Regional pooled prevalence estimates for the five SDG regional groupings with data were similar apart from for Eastern and South-Eastern Asia. Eastern and South-Eastern Asia had the lowest pooled prevalence for both any HPV (15%, 95% CI 11–21) and HR-HPV (10%, 7–13). These results mirror the lower HPV prevalence reported in women in Asia^{15,98} and among Asian men compared

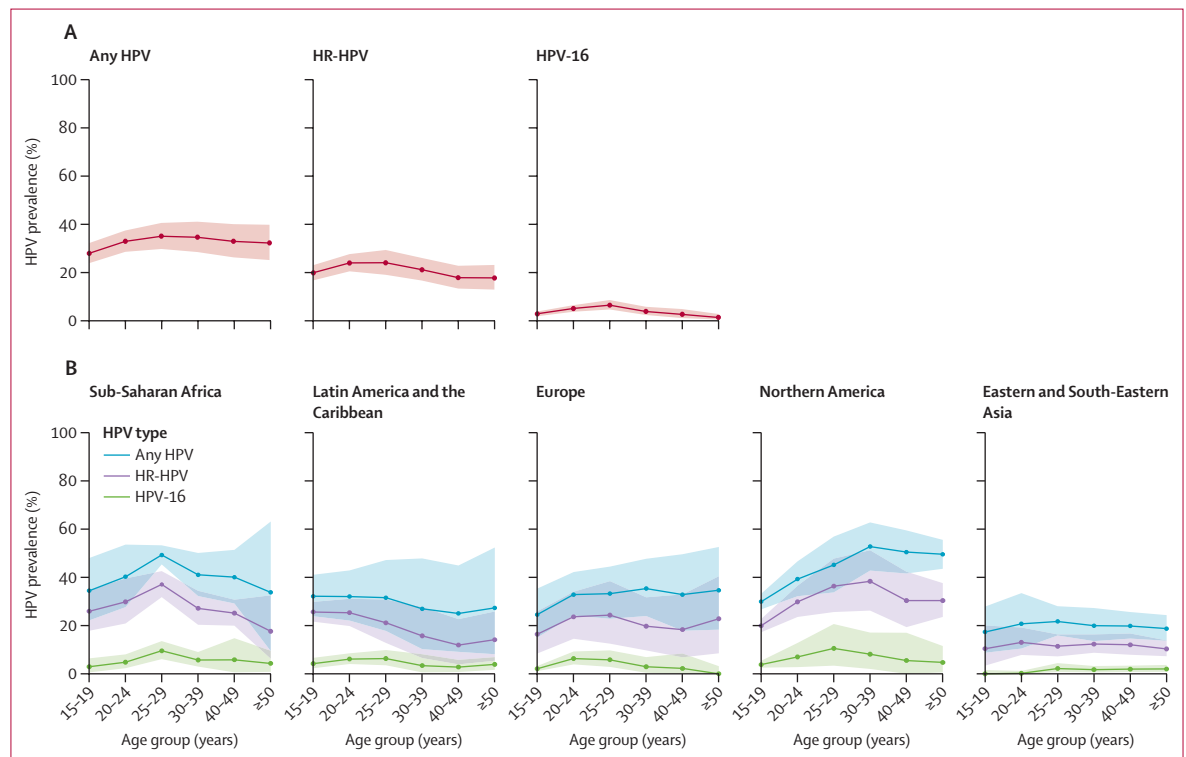


Figure 3: Age-specific prevalence of genital HPV infection in men
Global (A) and regional (B) prevalence of any HPV, HR-HPV, and HPV-16 by age group. Areas represent 95% CIs. Regions are defined by the UN Sustainable Development Goals regional or subregional grouping. Europe and Northern America are shown separately, and Central America and South America were the only subregions for Latin America and the Caribbean. The number of studies for which age-specific data were available, the number of men for whom data were contributed, and the countries included in each region are shown in appendix 3 (p 6). HR-HPV=high-risk HPV. HPV=human papillomavirus.

with other world regions and the global population.⁹⁹ A prominent presence of HPV-35 in Sub-Saharan Africa was also confirmed (figure 2). HPV-35 has been consistently identified to be more prevalent among African women or women of African descent, with a greater contribution to cancers and precancerous lesions than in women from other regions.^{15,100,101}

Our estimates are based on a systematic review of published prevalence surveys and unpublished data shared by study authors. Few studies provide data for heterosexual men (65 studies from 35 countries), whereas the amount of data available for women is much higher, and over half of the studies (55%) included were from high-income countries. To be eligible for inclusion, studies were required to have collected samples in 1995 or later, and only seven (11%) studies included specimens collected in 2014 or later. Therefore, our estimates do not reflect the effect of the roll-out of HPV vaccination in women on the prevalence of HPV in men,^{38,55,91} but the prevalence in general populations of men before HPV-vaccinated cohorts reached adult ages, either with girls-only or gender-neutral strategies.

One of the major efforts made when selecting studies was to select studies that could be viewed as representative of the general male population of the country. There was high heterogeneity observed in HR-HPV prevalence in the studies, with values ranging from 1% to 75% (appendix 3 p 9). High heterogeneity has also been noted in studies in women.¹⁵ We excluded studies done exclusively, or primarily, in men who have sex with men, men living with HIV, and men with signs or symptoms of HPV-related disease and studies conducted solely in men who were circumcised. These men, however, are included in many of the studies as part of the general population. Regarding including studies conducted in STI clinics, as long as the study population met the selection criteria (appendix 3 p 2), our sensitivity analyses (appendix 3 p 9) identified no significant differences in HPV prevalence between study settings (STI clinic *vs* others) or differences by risk of bias. Most studies combined samples from more than one anatomical location; 49% of studies included at least the penile shaft and the glans penis or coronal sulcus as recommended¹⁹ (table 1, appendix 3 p 9). We were limited in our ability to compare data across studies by differences in the numbers of HPV types tested for and specific anatomical sites sampled (appendix 3 p 9) and were not able to evaluate HPV prevalence by circumcision status, as only 26 of 65 studies provided stratified data by this variable. We could not evaluate the sensitivity of HPV sampling of abraded skin, the yield from specific genital locations, or sampling at more than one timepoint to discern contamination versus sustained infection. Despite these limitations, the pooled estimates serve to establish mean benchmark prevalences that can inform prevention strategies.

Global and regional pooled estimates provide us with mean baseline values for HPV prevalence in general populations of men. Our study draws attention to the high prevalence, ranging from 20% to 30% for HR-HPV in men across most regions, and the need for strengthening HPV prevention within overall STI control efforts. It also emphasises the scarcity of HPV data among men from some parts of the world and the importance of expanding HPV prevalence surveys in these areas to inform and measure the effects of prevention efforts. Incorporating HPV vaccination for adolescent males into national immunisation schedules can be further considered as vaccine supplies allow and single-dose strategies are assessed.¹⁰² Future epidemiological studies are needed to monitor trends in prevalence in men, especially considering the roll-out of HPV vaccination in girls and young women and that many countries are beginning to vaccinate boys.

Contributors

GA, LB, JR, and MT designed the study and did the literature searches. GA, LB, and JR designed the data-extraction form. JR extracted the data. GA, LB, and MT cross-checked the data extraction. GA did the statistical analyses. LB supervised the statistical analyses. MA conceptualised the statistical packages *metaprop* and *metapreg*. GA, LB, JR, and MT wrote the manuscript. All authors critically revised subsequent drafts and read and approved the submitted version. GA and JR accessed and verified the data. All authors had full access to all the data in the study and had final responsibility for the decision to submit for publication.

Declaration of interests

The Cancer Epidemiology Research Program (with which LB, LA, and GA are affiliated) has received sponsorship for grants from Merck and HPV test kits at no cost from Roche for research purposes. ARG reports payments from Merck to her institution, and as consulting fees to herself, and payments from Merck for participation on an advisory board. All other authors declare no competing interests.

Data sharing

All datasets generated and analysed, including the search strategy, list of the included and excluded studies, data extracted, and quality assessment, are available in the Article and on request from the corresponding author. On request, the statistical source code is available in the IDIBELL repository.

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