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EDITED BY

Leeya Pinder,
University of Cincinnati, United States

REVIEWED BY

Umamaheswaran Gurusamy,
Nationwide Children's Hospital, United States
Yara Lucia Furtado,
Federal University of Rio de Janeiro, Brazil
Kwabena Amo-Antwi,
Kwame Nkrumah University of Science and
Technology, Ghana

*CORRESPONDENCE

Solomon Demis Kebede
✉ solomondemis@gmail.com

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Prevalence and distribution of human papillomavirus genotypes in women with abnormal cervical cytology in Ethiopia: a systematic review and meta-analysis

Solomon Demis Kebede^{1*}, Shegaw Zeleke², Amare Kassaw³,
Tigabu Munye Aytenew², Demewoz Kefale³
and Worku Necho Asferie¹

¹Department of Maternity and Neonatal Nursing, College of Health Sciences, Debre Tabor University, Debre Tabor, Ethiopia, ²Department of Nursing, College of Health Sciences, Debre Tabor University, Debre Tabor, Ethiopia, ³Department of Pediatrics and Child Health Nursing, College of Health Sciences, Debre Tabor University, Debre Tabor, Ethiopia

Background: Cervical cancer is the 4th most common cancer in women globally. Determining the prevalence of the high-risk human papillomavirus (HR-HPV) and low-risk (LR-HPV) genotypes and the distribution in abnormal cervical cytology will be essential in a future population-based cervical cancer prevention program.

Method: Primary studies with women with abnormal cervical cytology were systematically searched for in Medline, CINAHL, Google Scholar, African Journal Online, and the University of Antwerp repository from 19-30 May 2023. A weighted inverse-variance random effects model was used. Variations across the studies were checked using a forest plot, I² statistics, and Egger's test. Group analysis was performed for evidence of heterogeneity.

Results: The pooled prevalence of human papillomavirus (HPV) genotypes with abnormal cervical cytology of a precancerous cervical lesion was 38.74% (95% CI: 27.56-49.93). The leading pooled prevalence estimates by subgroup analysis were 18% (95% CI: 13-26), 14% (95% CI: 11-16), and 66% (51-79) for women with retroviral infection (RVI), DNA genotyping with amplification, and central parts of Ethiopia respectively. There were 25 HPV variants identified by genotyping techniques with the five most prevalent HPV genotypes being HPV-16 and HPV-18 coexisting at 54%; HPV-16 alone at 29%; HPV-51 at 16%; HPV-52 at 13%; and HPV-31 and HPV-33 each contributing approximately 12%.

Conclusion: The pooled prevalence of HPV genotypes was higher than in other countries. HPV-51, HPV-52, HPV-31, and HPV-33 are the most prevalent genotypes. Hence, the nonavalent vaccine type would be the one that includes all the most prevalent HPV genotypes, but HPV-51 in Ethiopia. Additional data on similar DNA test techniques for comparisons with

precancerous lesions and invasive cancer are needed. Cervical cancer prevention and control programs in Ethiopia should be aligned with the most prevalent genotypes.

Systematic review registration: <https://www.crd.york.ac.uk/prospero/>, identifier CRD42023428955.

KEYWORDS

HPV genotypes, cervical lesion, abnormal cervical cytology, pap smear test, cervical cancer screening

Background

Cervical cancer is the most prevalent type of cancer affecting the reproductive organs of women and the primary cause of cancer-related deaths in low- and middle-income countries (LMICs), such as Ethiopia. For instance, the ten African countries with the highest rates of cervical cancer were all above the global average, at 13.30 per 100,000 women and 604,127 cases (1–3).

Africa has the highest incidence of cervical cancer worldwide with rates of 31.6 cases per 100,000 people which is above the global incidence of 13.3 cases per 100,000 people (2, 4).

A systematic population-based program with pap tests has been reducing the incidence of invasive cervical cancer in high-income countries by detecting and treating cervical lesions. However, screening is limited in low-income countries as it is being performed in public or private laboratories in urban areas for only approximately 5% of eligible women. In addition, the absence of a well-organized surveillance and review system results in poor screening or lack of follow-up (2, 5–7).

Evidence suggests that less than 5% of all eligible women in developing countries receive cytology-based screening within 5 years. This is because there are few healthcare providers and professionals involved in such analyses or because of the limited availability of medical facilities available to accommodate the demand for screening and treatment. Moreover, in LMICs, cytology services are limited to teaching hospitals or private clinics in larger cities and are not accessible to all eligible women (5, 6).

The Bethesda system is a standardized model for reporting cervicovaginal cytology by which there are low-grade squamous intraepithelial lesions (LSILs), high-grade squamous intraepithelial lesions (HSILs), or atypical squamous cells [of undermined significance (ASCUS) or cannot rule out HSIL (ASC-H)] (8–10). Approximately 15% of human papillomavirus (HPV) infections progress to low LSILs within 3–4 years, and 30–70% of LSILs

advance to HSILs in 10 years (11–13). The most common HPV types identified in previous studies were 16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 68, and 59, which were considered high risk. Several groups, including HPV types 53, 66, 70, 73, and 82, have been classified as potential or high-risk types. Approximately seven types of high-risk human papillomavirus (HR-HPV) are associated with approximately 87% of cervical cancer cases worldwide. Forty types of papillomaviruses, which tend to spread to the genitals, usually infect the cervix, genitals, urethra, and anus in both sexes (1, 7, 14).

According to the WHO global strategy to accelerate the elimination of cervical cancer as a public health problem by 2030, 90% of girls will be fully vaccinated against HPV by the age of 15 (5). There are currently two types of HPV vaccines licensed in many countries, and these vaccines have been proven to prevent more than 95% of HPV infections caused by HPV types 16 and 18, which cause 70% of cancer cases (15). However, there is no consistent information on which type of vaccine is better at preventing HPV-related cervical cancer in Ethiopia. This review aimed to determine the prevalence, most specific type, and distribution of HPV genotypes among women with abnormal cervical cytology.

Materials and methods

Reporting

The results of this review were reported in accordance with the MOOSE checklist for meta-analyses of observational studies (16). [Supplementary File 1](#) shows the MOOSE checklist.

The review has been registered with PROSPERO ID: CRD42023428955.

Search strategy and source of information

Data searching was conducted from 19–30 May 2023. The articles retrieved were published from 2006 to 2023, were written in English, and had cross-sectional and cohort study designs. The MEDLINE, Web of Science, Scopus, Google Scholar, Africa Online Journals, University of

Abbreviations: DNA, Deoxyribonucleic acid; HPV, human papillomavirus; RNA, Ribonucleic acid; RVI, retroviral infection; VIA, visual inspection via acetic acid.

Antwerp repository, and gray literature databases were searched. The key search terms and phrases used were “human papillomavirus”, “human papillomavirus DNA tests”, “human papillomavirus investigating”, “cervical cancer”, “precancerous cervical lesion”, “cervical tumor”, “cervical malignancy”, “reproductive women”, “adolescent girls”, “mothers”, and “Ethiopia”. The search strategy was developed using various Boolean operators. Hence, to fit the advanced PubMed database, the following search strategies were applied on 29 March 2023: [(human papillomavirus screening [MeSH Terms]) AND (human papillomavirus testing [MeSH Terms] AND (human papilloma investigating [MeSH Terms] AND (cervical neoplasms [MeSH Terms]) OR (cervical cancer [MeSH Terms]) OR (precancerous cervical lesion [MeSH Terms]) OR (cervical tumor [MeSH Terms]) AND (reproductive women [MeSH Terms]) OR (adolescent girls [MeSH Terms]) AND (Ethiopia)).

Study selection

The studies were imported into Mendeley Desktop using data management software to eliminate duplicate data. Two independent reviewers reviewed the title and abstract. Differences between reviewers were checked by article-based analysis. Abstract and full-text analyses were performed by two independent authors in three groups. All reviewers screened all studies with discussions on inconsistency amendments among the reviewers.

Eligibility criteria

Inclusion criteria

The primary studies included were those that reported both high-risk HPV (HR-HPV) and low-risk HPV (LR-HPV) genotype prevalence and distribution in women with LSILs or HSILs in Ethiopia.

Exclusion criteria

Articles without full text available and qualitative studies were excluded.

Outcome measurement

The overall HPV prevalence was defined as the number of women with positive HPV tests among all women with LSIL or HSIL cytology reports, expressed as a percentage.

Similarly, the prevalence of HPV type specificity was defined as the number of women with positive HPV type-specific tests among all women with LSIL or HSIL cytology reports, expressed as a percentage.

Quality assessment

The JBI quality appraisal criteria were used (17). The tool has nine main features. The first feature is suitability for the sample frame. The second is using the convenient sampling technique. Third, the sample size should be large enough. Fourth is a description of the research object and environment. Fifth, the

data analysis program was sufficient. The sixth is the validity of the situation analysis method. The seventh feature is being reliable for all participants. Eight is the necessity of statistical analysis. The final feature is being reasonable and cost-effective.

Studies were considered low risk when five or more were positive out of the nine criteria. Two independent authors evaluated the quality of the studies. Disputes are resolved with the intervention of a third-party moderator. [Supplementary File 2](#) shows the JBI quality assessment of the included studies.

Data extraction

The adapted PICO format was used to explicitly review the pieces of literature and clear specifications for the inclusion and exclusion criteria. The adapted PICO comprises Population (P), Exposure (E), Outcome (O), and Context (Setting) as described below.

- a. Population: women with abnormal cervical cytology
- b. Exposure: human papillomavirus (HPV)
- c. Outcome: prevalence and distribution
- d. Context (Setting): Ethiopia

Both authors (SD and TM) extracted the data using a standard method. The author, year, study area, study design, setting, sample size, and HPV type on abnormal cervical cytology were extracted. This step was repeated every time a change was found in the extracted data. If inconsistencies between the extracted data persisted, a third reviewer (SZ) was included.

Statistical analysis

Statistical pooling for the prevalence proportion of estimates was performed according to the random effects model using Statistical software for Data Science (STATA V17). The random effects model of analysis was used since the studies identified were observational and had both clinical and methodological variability. The heterogeneity of the studies was evaluated based on Cochrane’s Q and I² tests as well as the Q/df (degree of freedom) ratio. Thus, Cochrane’s Q test ($p = 0.1$), $Q/df = 1$, and $I^2 = 50\%$ were considered cutoff points for identifying heterogeneity and selecting an effective model for analysis.

Forest plots were generated to present the pooled prevalence of HPV genotypes in women with precancerous cervical lesions. In line with this, subgroup analyses were carried out to explain HPV DNA variant distributions in subgroups with the potential to account for the differences in the effect sizes of the HPV genotypes. Egger’s regression tests were performed to objectively test for the presence of a small study effect.

Results

Selection of studies for review

A total of 1,779 research citations that met the requirements of the National Institute of Health (NIH) quality assessment tool for

observational cohort and cross-sectional study guidelines were retrieved. Following the removal of duplicates and the screening of titles and abstracts, 35 studies were retrieved for full-text review. Of these, a further 17 were excluded as they were not full-length articles or did not report outcomes of interest. The remaining 18 full-text articles were assessed for eligibility and two were excluded as they did not report the outcome of interest. This left 16 studies included in the review and meta-analysis. Data were extracted by title before beginning the systematic screening using the PRISMA flow diagram for the final review of the included studies. Figure 1 shows the PRISMA flow diagram of the study selection process.

Institute, and gynecology referral hospitals in Ethiopia, respectively (4, 14, 15, 24–30). The age range of the women studied was 15–85 years (14, 19, 21, 22, 26, 27, 29, 30). The mean age of the women was 32 years in one study (18), and the mean age was 15– ≥ 44 years in another study (16).

A total of 5,276 study participants were included. Of these, 2,621 were infected with one or more HPV genotypes. Table 1 shows the characteristics of the included studies.

Regarding the type of HPV genotyping tests and techniques, two studies used DNA testing with direct genomic detection with hybrid capture (4, 24), eight used DNA testing with amplification for HR genotyping (14, 21, 22, 25–31), and RNA amplification of an E6/E7mRNA HPV assay was used in three studies (18, 19, 23).

Characteristics of the included studies

For the systematic review, 16 studies were included from which three studies were from the Oromia region (18–20), three from Addis Ababa in central Ethiopia (21–23), two studies from northwest Ethiopia (15, 24), and one in each of Amhara region, Tigray, Southern nations nationalities, south-central Ethiopia, southwest Ethiopia, eastern Ethiopia, Armauer Hansen Research

Meta-analysis

The pooled prevalence of HPV in abnormal cervical cytology. The absence of publication bias was assessed with Egger’s regression test analysis ($p = 0.125$), which showed no publication bias. Table 2 shows the Egger’s regression results.

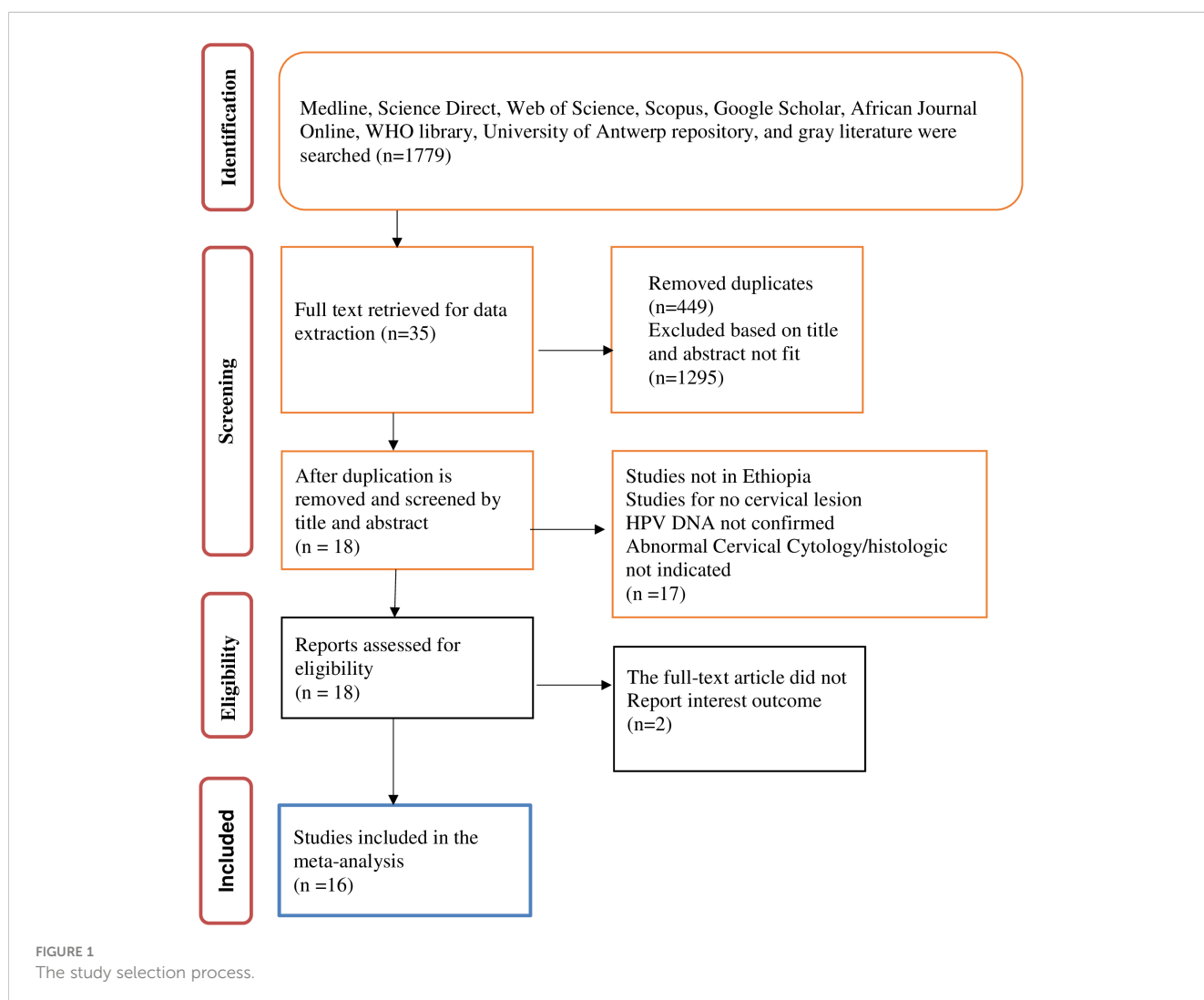


TABLE 1 Characteristics of the included studies.

First author and year	Participants age range or mean	Health facility	Study area/region	Study design	Sample size	Population outcome	Prevalence	Quality status
Ali et al. (2019) (21)	18-64	Addis Ababa	Central Ethiopia	Cross-sectional	50	38	76.00	Low risk
Bartholomeusz and Locarnini (2006) (29)	21-85	Central	Armauer Hansen Research Institute,	Cross-sectional	149	136	91.28	Low risk
Bekele et al. (2010) (27)	32-65	Jimma	Southwest Ethiopia	Cross-sectional	83	68	81.93	Low risk
Bogale et al. (2022) (22)	25-49	Addis Ababa	Central Ethiopia	Cross-sectional	130	24	18.46	Low risk
Derbies et al. (2022) (31)	—	Bahir Dar	Amhara	Cohort	3633	1950	53.67	Low risk
Derbies et al. (2023) (14)	30-67	Gynecology referral clinics	Northwest Ethiopia	Cross-sectional	154	77	50.00	Low risk
Gebremariam (2016) (25)	—	Mekele	Tigray	Cohort	86	21	24.42	Low risk
Haile et al. (2019) (18)	32	Adama	Oromia	Cross-sectional	27	6	22.22	Low risk
Kiros et al. (2021) (24)	Debre Tabor Comprehensive Hospital	Northwest	Cross-sectional	109	14	12.84	Low risk
Lemma et al. (2022) (19)	30-35	Adama	Oromia	Cross-sectional	66	6	9.09	Low risk
Leyh-Bannurah et al. (2014) (4)	15-64	gurance zone	southern nations	Cross-sectional	86	21	24.42	Low risk
Megersa et al. (2023) (20)	15-≥44	hashemite	Oromia	Cross-sectional	143	21	14.69	Low risk
Mekuria et al. (2020) (23)	18-70	Addis Ababa	Central Ethiopia	Cross-sectional	164	28	17.07	Low risk
Seyoum et al. (2023) (28)	30-60	Harara, Dire Dawa and Jigjiga	Eastern Ethiopia	Cross-sectional	152	35	23.03	Low risk
Teka et al. (2021) (26)	30-49	Butajira rural	South-central Ethiopia	Cross-sectional	205	117	57.07	Low risk
Wolday et al. (2018) (30)	40.1-43.2	Gynecology referral clinics	Ethiopia	Cross-sectional	134	59	44.03	Low risk
	Total				5276	2621		

The overall pooled prevalence of HPV genotypes among women screened and identified with precancerous cervical lesions, either LSIL or HSIL, was 38.75%, with a 95% CI of 25.69-51.8 (4, 14, 18–31). Figure 2 shows a forest plot of the pooled prevalence of HPV variants in Ethiopia.

Subgroup analysis

Subgroup analysis was performed based on the study’s geographical region, HPV genotyping testing technique, and characteristics of the women. Based on the pooled effect of two or more studies, the three most common genotyping testing techniques identified were acetowhite changes by visual

inspection with acetic acid (VIA) and HPV DNA testing for specimens in women with retrovirus infection (RVI) at 18%, all women screened for HPV at 12%, and women with RVI at 10% (4, 18, 19, 21, 23, 25, 26, 28, 29, 31). The least prevalent HPV type, at 6%, was found in two studies (24, 30). Among the genotyping test techniques used, the DNA test with amplification was the most commonly used test modality (14, 21, 22, 25–31). Central Ethiopia was the highest contributor to the HPV genotyping evidence, accounting for 66%, and the lowest were Oromia and southern Ethiopia, which accounted for 5% of the studies (4, 18–20). Table 3 shows a subgroup analysis of the characteristics of the women, HPV testing technique, and region of Ethiopia.

Among the 16 studies, there were 25 HPV variants identified by genotyping techniques in this review. The most prevalent HPV type

TABLE 2 Egger's regression results.

Std.-Eff.	Coef.	Std. Err	t	p>t	95% confidence interval	
Slope	5.022488	9.950689	0.50	0.622	-16.31962	26.36459
Bias	30.05708	18.41711	1.63	0.125	-9.443692	69.55784

was HPV-16 and HPV-18 coexisting (14) at 54%. The second most prevalent type was HPV-16 alone, accounting for 29% of the total number of studies. The third and fourth most common HPV types were HPV-51 and HPV-52, accounting for 16% and 13% (4, 14, 18, 19, 21–23, 25, 28–31) respectively. The fifth most prevalent HPV type were HPV-31 and HPV-33, each contributing approximately 12% of all HPV variant burdens in Ethiopia in previous studies (4, 14, 18, 19, 21, 22, 25–31). Table 4 shows the prevalence of HPV

DNA test results by subgroup analysis of HPV DNA genotypes in Ethiopia.

Sensitivity analysis

Two studies (27), and (29), had an impact on the overall estimation of the meta-analysis results. Supplementary File 3 shows the sensitivity analysis.

Discussion

According to our review and meta-analysis, the prevalence any HPV genotype being detected among women who had a precancerous cervical lesion in health facilities was 38.75% (25.69-

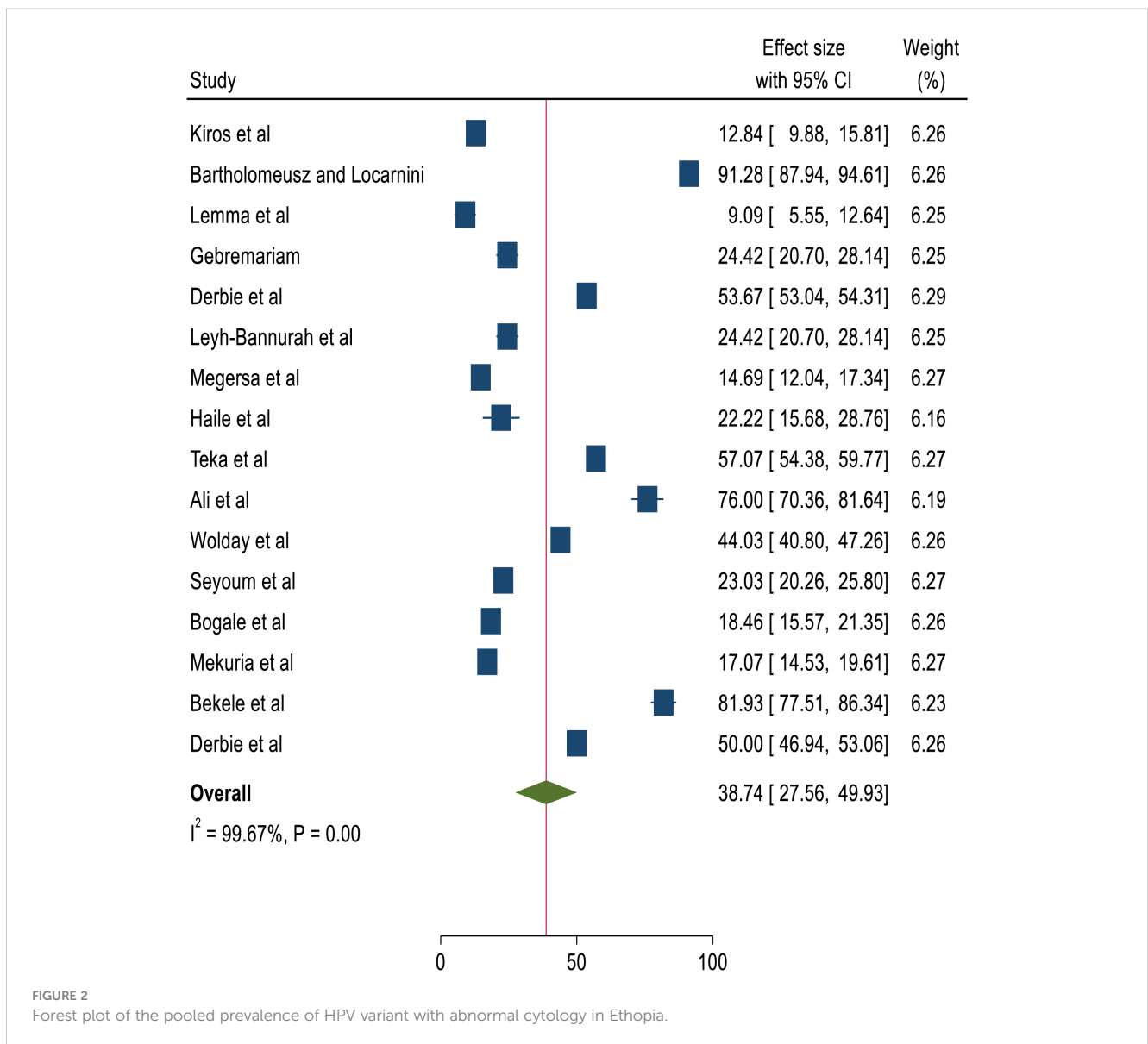


FIGURE 2 Forest plot of the pooled prevalence of HPV variant with abnormal cytology in Ethiopia.

TABLE 3 The subgroup analysis of the characteristics of the women, HPV testing technique, and region of Ethiopia.

Variable	Characteristics	Pooled prevalence (95% CI)	I ² (P value)
Characteristics of the women	With abnormal cervical cytology	6%(3-13)	-
	Women screened for HPV	12%(10-15)	98.86(0.00)
	With abnormal cervical cytology and RVI	10%(7-14)	-
	With abnormal cervical cytology, but no RVI	6%(2-12)	93.74(0.00)
	With abnormal cervical cytology and acetowhite changes	18%(13-26)	82.44(0.00)
	With abnormal cytology and other STI complaints	7%(3-12)	95.55(0.00)
	Genotyping testing techniques	Direct genome detection	5%(3-7)
DNA with amplification		14%(11-16)	98.97(0.00)
RNA amplification of E6/E7		6%(4-8)	35.29(0.02)
By region of Ethiopia	Northwest	6%(2-10)	93.99(0.00)
	Armauer Hansen Res Center	12%(4-24)	98.08(0.00)
	Oromia	5%(3-7)	43.57(0.02)
	Tigray	9%(5-14)	71.14(0.00)
	Amhara	7%(3-13)	99.84(0.00)
	Southern Ethiopia	5%(3-7)	71.87(0.00)
	Central Ethiopia	66%(51-79)	93.66(0.00)
	South-central Ethiopia	22%(11-36)	96.64(0.00)
	Gynecology referral clinics	7%(4-10)	84.93(0.00)
	Eastern Ethiopia	7%(4-9)	79.93(0.00)
	Central Ethiopia	16%(12-20)	81.20(0.00)
	Southwest Ethiopia	8%(1-20)	96.41(0.00)

51.81). A recent meta-analysis showed that the proportion of patients infected with HR-HPV was 42.2% in Eastern Africa (32). Similarly, the prevalence of HPV in women with precancerous cervical lesions and cervical cancer was between 13.7% and 93%. A globally based review showed that the prevalence of HPV genotype was between 11% and 12% (with higher rates, 24%, in sub-Saharan Africa) in women without cervical abnormalities (15, 31, 33).

The detection of HPV increases in women with abnormal cervical cytology in proportion to the severity of the lesions,

TABLE 4 The prevalence of HPV DNA test results by subgroup analysis of HPV DNA genotypes in Ethiopia.

Variable	HPV type	Pooled prevalence (95% CI)	I ² (P value)
HPV DNA genotype	16	29% (19-41)	97.69(0.00)
	18	5%(3-7)	78.72(0.00)
	31	12%(7-18)	94.75(0.00)
	33	12%(3-26)	96.12(0.00)
	35	11%(6-18)	95.20(0.00)
	39	11%(4-22)	94.69(0.00)
	45	10%(5-16)	94.16(0.00)
	52	13%(7-19)	94.98(0.00)
	58	10%(4-17)	95.90(0.00)
	66	10%(1-26)	96.67(0.00)
	68	11%(4-19)	95.86(0.00)
	39 and 68	3%(1-7)	-
	56 and 74	1%(0-4)	-
	6	5%(1-11)	86.23(0.00)
	51	16%(6-31)	94.14(0.00)
	56	10%(5-17)	94.44(0.00)
	59	7%(7-14)	94.61(0.00)
	53	2%(0-5)	-
	35 and 39	6%(3-13)	-
	45 and 68	5%(2-11)	-
	16 and 18	54%(52-55)	-
	11	7%(0-24)	-
	42	2%(1-2)	-
	70	2%(0-6)	-
	68 and 73	2%(1-8)	-

which supports our findings (33). Based on a global review, HPV was detected 90% of the time in abnormal cervical cytology, which is relatively higher than that reported in this review and meta-analysis (33). This might be because developed nations use more sophisticated DNA testing techniques than Ethiopia. In addition, a review showed that the prevalence of HPV was 84.8% among Asian patients with atypical squamous cell lesions (34).

The predominant genotypes identified in this review were HPV-16 and HPV-18, accounting for 9.52% and 8.33%, respectively; HPV-31 and HPV-48, each accounting for 7.74%; HPV-52 and HPV-56, each accounting for 7.14%; and HPV-35, HPV-58, and HPV-59 with an average of 6.55% of all HPV variant burdens in Ethiopia. These findings are essential for predicting how HPV vaccination and HPV-based screening will impact cervical cancer prevention in Ethiopia. This infers that further HPV vaccine studies in Ethiopia should mainly target the most predominant

genotypes as the current vaccine type only targets HPV-6, HPV-11, HPV-16, and HPV-18.

Based on similar review reports in different parts of the globe, the genotype distributions of HPVs in different countries from different kinds of cervical lesions were compared with this review. HPV-16 is the most common genotype consistently reported globally as an important cause of cervical abnormalities (35–37). The pooled prevalence of HPV-16 sub genotypes in this review and meta-analysis was found to be 29% which was relatively comparable with the overall incidence in Africa (35). The pooled prevalence of subgroup HPV genotypes 31 and 33 were 12% each, which was comparable to (35), which found 8.2% and 10.3%, respectively. However, HPV types 51 and 52 were not reported as prevalent genotypes, but in this study, they were the most prevalent cases, accounting for 16% (6–31) and 13% (7–19), respectively. HPV genotype 18 was among the lowest at 5% and HPV genotype 35 was among the dominant at 11% in this review.

This variation in HPV genotype distribution across the studies is likely attributable to differences in the population, severity of cervical lesions, age at screening initiation, frequency, coverage, and follow-up rates of women with cervical abnormalities (38). In addition, the difference might also be associated with ethnic differences, geographical location, and the sexual behavior of their male partners (39).

Globally, HPV type-specific prevalence varies. A study in Asia (40) indicated that HPV-16 was most prevalent at 23.9%, which was comparable with the findings of this review. In contrast, the prevalence of HPV type 52 was lower than that in this review. However, studies in North America (37) found the prevalence of HPV types 16, 31, and 51 to be 26%, 11.5%, and 10.6%, respectively. These findings are comparable to those of this review and meta-analysis. Similarly, in a study in Israel (41), the most prevalent HPV type was HPV-16 (46.5%), which is higher than that of this review and meta-analysis. However, the prevalence of HPV type 31 was comparable at 7%. These differences among the studies and this review might be due to variations in population, DNA testing technique, and sampling technique.

According to the results of this review and meta-analysis, the pooled prevalence of HPV 16/18 in the combined subgroup was 54%. Similarly, other reviews showed that 45.1% of HPV16/18 combined were from high-grade cervical lesions, while 67.7% were from abnormal cervical cytology among African women and 605 Israeli women (15, 31, 35, 41). Among HPV-positive patients, the co-existing prevalence of HPV 16/18 was reported differently in different countries, as it was 87.5% in Central and Eastern Europe (42) and 80% in India among those with high-grade cervical lesions (43).

HPV-16 was the most prevalent type in this review at 29% (19%–41%), and HPV-18 was not among the five most prevalent types at 5% (3%–7%). These findings were comparable to those of studies in Italy on HPV-18 (7%). However, HPV-16 (64%) was much more prevalent than this review finding (44). A review by Guan et al. revealed that HPV-16 positivity increased steeply from normal to high-grade cervical lesions (44). Accordingly, vaccine mixes and HPV-based screening tests should always include this genotype, although some low-grade cervical lesions associated with

certain other HPVs may preferentially progress to cervical cancer (3, 15). Our review envisages a future impact of the broadly identified subgroup pooling of the genotypes (HPV-16 and HPV-18 coexisting, HPV-16, HPV-51, HPV-52, HPV-31, and HPV-33) on vaccination and HPV-based screening in Ethiopia.

The Ethiopian Ministry of Health started vaccinating schoolchildren aged 14 years using Gardasil-4™ (HPV-6, HPV-11, HPV-16, HPV-18) in 2018. However, in this review, in addition to the genotypes covered by the current vaccine, there were other genotypes found to be prevalent in Ethiopia, such as HPV-51, HPV-52, HPV-31, and HPV-32. Hence, HPV-based screening based on the detection of HPV16/18 oncoproteins and, most recently, the use of the HPV DNA test has been employed. This finding suggests that vaccinating girls using Gardasil-4™ and screening women for cervical lesions using HPV16/18 oncoproteins significantly reduces the number of girls who might be protected.

The vaccine for girls would be more effective if the most prevalent genotype distribution was included. This is because women might be missed by screening programs for the most dominant HPV genotypes circulating in the country. For this reason, most developed countries are currently using other vaccine types of the monovalent Gardasil®9 (6, 11, 16, 18, 31, 33, 45, 52, and 58) vaccine that targets close to 90% of all HR-HPVs (45), which is essentially an ideal type of vaccine for Ethiopians based on our review findings. However, this vaccine type might not cover all the top five highly distributed HPV genotypes, except for HPV-52. Even though there is a financial limitation, the nonavalent vaccine type would be the one that includes all the most prevalent HPV genotypes, including HPV-51, for the Ethiopian setting.

Strengths and limitations

This systematic review and meta-analysis was the first to analyze results from women with abnormal cervical cytology, and important input will be obtained to revise the current vaccination and HPV-based screening program in Ethiopia. The review included studies from different health facilities and geographical areas, with a wide range of study participants and different DNA tests and techniques, which enabled us to obtain a better picture of the HPV genotype burden in Ethiopia. This review and meta-analysis result should be interpreted in light of several limitations. Because of the absence of articles on women's abnormal cervical cytology test results in some parts of the country, our findings could compromise the overall picture of the HPV genotype distribution in Ethiopia.

Conclusion

In this review and meta-analysis, HPV genotypes were predominantly identified from different kinds of cervical samples via abnormal cervical cytology. There are currently two types of HPV vaccines licensed in many countries, and these vaccines have been proven to prevent more than 95% of HPV infections caused by HPV types 16 and 18, which cause 70% of cancer cases, but the

HPV genome distribution is not uniform across the country. The pooled prevalence of HPV genotypes in Ethiopia was greater than that in the other countries. HPV-16 and HPV-18 coexist, and HPV-16, HPV-51, HPV-52, HPV-31, and HPV-33 are the most prevalent HPV genotypes which require special attention when designing vaccination and HPV-based cervical cancer screening programs. Additional data on similar DNA test techniques among women with cervical cancer are needed. It is important to place emphasis on the nationwide HPV distribution in the prevention and control strategies.

Data availability statement

The data will be available upon reasonable request to corresponding author. Requests to access these datasets should be directed to SK, solomondemis@gmail.com.

Author contributions

SK: Investigation, Supervision, Writing – original draft, Writing – review & editing. SZ: Methodology, Writing – original draft, Writing – review & editing. AK: Formal analysis, Writing – original draft, Writing – review & editing. TM: Conceptualization, Writing – original draft, Writing – review & editing. DK: Software, Writing – original draft, Writing – review & editing. WA: Formal analysis, Methodology, Writing – original draft, Writing – review & editing.

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Conflict of interest

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Supplementary material

The Supplementary Material for this article can be found online at: <https://www.frontiersin.org/articles/10.3389/fonc.2024.1384994/full#supplementary-material>

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