Integrated Health Research Journal (IHRJ)

The Official Journal of the College of Health and Allied Sciences University of Cape Coast, Ghana

RESEARCH ARTICLE

Detection of Genital Herpes Simplex Virus Type 1 And 2 among Asymptomatic Women in Ghana: Evidence From a Pilot Cervical Screening Study

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Abstract

Background: Herpes simplex virus (HSV) infections account for a large burden of disease worldwide. HSV type 1 is traditionally associated with orofacial infections, whereas HSV type 2 is commonly linked to genital infections. Recent studies suggest an increasing role of HSV- 1 in genital infections. In Ghana, In Ghana, where surveillance is limited, epidemiological data remain scarce. This pilot study aimed to detect HSV-1 and HSV-2 DNA in genital samples from asymptomatic women.

Methods: Cervical swabs from 94 asymptomatic women attending cervical screening clinics in Ghana were analyzed. HSV-1 and HSV-2 DNA were detected using polymerase chain reaction (PCR). Serological data from the parent study were used for descriptive purposes.

Results: HSV-1 DNA was detected in 12.8% of participants, while HSV-2 DNA was detected in 4.3%. Co-infection occurred in 4.3% of participants. Most HSV-1 DNA-positive individuals were also HSV-1 IgG seropositive (92%), and all HSV-2 DNA-positive individuals were HSV-2 IgG seropositive. No statistically significant associations were observed between HSV DNA detection and participant characteristics.

Conclusion: HSV-1 and HSV-2 DNA were detected in genital samples from asymptomatic women, indicating the presence of genital HSV infection in this population. Larger studies are needed to better characterize the epidemiology and public health relevance of genital HSV infection in Ghana.

Keywords: Herpes simplex virus, HSV-1, HSV-2, Genital infection, PCR, Ghana, Women

Citation: Ryabinina O, Asmah RH, Essuman GAA, Donkoh ET, Thomford NE, Boateng G, Asamani D. Detection of genital herpes simplex virus types 1 and 2 among asymptomatic women in Ghana: evidence from a pilot cervical screening study. Integrated Health Research Journal. 2026;3(2):67-75. https://doi.org/10.47963/jkpzwh81

Received 9th April 2026; **Accepted** 20th June 2026; **Published** 14th September 2026.

Introduction

Herpes Simplex Virus (HSV) is a lifelong human pathogen comprising two main types: HSV-1 and HSV-2 [1]. Globally, HSV infection remains highly prevalent, with an estimated 846.1 million people aged 15–49 years affected in 2020 [2]. HSV-1 is traditionally associated with orofacial infections, whereas HSV-2 is more commonly linked to genital herpes and remains the leading cause of genital ulcer disease worldwide [3,4]. However, recent studies indicate an increasing proportion of genital herpes cases are

attributable to HSV-1, although HSV-2 continues to predominate in most settings [5–8].

HSV establishes lifelong latency in sensory neurons and can periodically reactivate, resulting in recurrent disease and asymptomatic viral shedding, which contributes to ongoing transmission [3,8]. In addition to genital disease, HSV infection has been associated with an increased risk of acquiring other sexually transmitted infections, including HIV and human papillomavirus (HPV) [9,10]. Changes in sexual behavior, including oral–genital contact and multiple sexual partnerships, have also been implicated in the changing epidemiology of HSV infection and the emergence of genital HSV-1 in some populations [6,11].

Despite its substantial global burden, the epidemiology of HSV in Africa remains poorly documented. Evidence from Africa and other low-resource settings is limited but suggests a high burden of HSV among women, with considerable regional variation [2]. In Ghana, HSV infections are considered common. However, surveillance is not mandatory, and reliable population-based epidemiological data are lacking [12–14]. Most existing studies are hospital-based and rely primarily on serological assays, with limited use of molecular methods for direct viral detection and type differentiation [12–14].

Given the absence of an effective vaccine and the limitations of antiviral therapy in eliminating infection [3], accurate identification of HSV types is important for understanding transmission dynamics, guiding clinical management, and informing prevention strategies [15]. Molecular detection methods, such as PCR, allow for direct identification of HSV DNA in clinical specimens and provide improved specificity compared with serological testing alone.

This study therefore aimed to determine the presence of HSV-1 and HSV-2 DNA in cervical samples from asymptomatic women in Ghana and to describe their epidemiological characteristics.

Methods

Study Design and Sample Selection

This study utilized archived cervical swab samples collected during a parent cross-sectional study on the prevalence of genital HPV and seroprevalence of herpes infection among women attending cervical screening clinics at regional hospitals in Ghana [14]. The present study was designed as a pilot investigation to evaluate the feasibility of molecular detection of genital HSV infection using archived cervical samples and to generate preliminary data to inform future larger studies. A subset of 94 de-identified cervical swabs was randomly selected using computer-generated codes. Corresponding HSV serological data from the parent study were available for all selected participants, allowing comparison between PCR-based detection of HSV DNA and HSV IgG serostatus. Serological results were used to describe prior exposure to HSV-1 and HSV-2 and to provide supportive epidemiological context for the molecular findings.

Ethical consideration

Ethical approval for the parent study was obtained from the Ghana Health Service Ethics Review Committee (GHS-ERC:07/03/14). The current study, which involved secondary analysis of archived samples, was conducted under the same ethical approval framework. Additional approval was also obtained from the Ethical and Protocol Review Committee of the School of Biomedical and Allied Health Sciences, University of Ghana (SBAHS-MLS/10572569/SA/2018–2019). Written informed consent was obtained from all participants at the time of enrolment in the parent study, including consent for future research use of archived biological samples and associated de-identified data.

DNA Sample Processing

Archived DNA extracts from cervical swabs, originally prepared for HPV testing, were used as templates for HSV detection. DNA integrity was verified prior to PCR. No additional sample collection was required for this study.

PCR Amplification of HSV DNA

Detection of **HSV-1 and HSV-2 DNA** was performed by polymerase chain reaction (PCR) using primers and methods adapted from Blankson et al., 2019 [16]. In brief, the following primers were used in the work: for HSV-1: 5′-CGTACCTGCGGCTCGTGAAGT-3′ (forward) and 5′ AGCAGGGTGCTCGTGTATGGGC-3′reverse); for HSV-2: 5′-TGGTATCGCATGGGAGACAAT-3′ (forward) and 5′-CTCCGTCCAGTCGTTTATCTTG-3′. A final PCR reaction mix of 25 µl was used containing 5X PCR buffer, 5mM $MgCl_2$, 200 µM of each of the four deoxyribonucleoside triphosphates (dNTP), 10 pmols of each primer and 1.25 units of Taq polymerase enzyme (New England Biolabs Inc., UK). Five microliters (5 µl) of purified DNA extracts were used as template for the amplification reactions carried out on the MAXYGENE II Thermal Cycler (Corning Life Sciences Company, USA). The cycling parameters for PCR were as follows: 95° C for 5 minutes (initial denaturation), followed by 45 cycles of 95° C for 30sec (denaturation), 54° C for 30sec (annealing), 72° C for 30 sec (extension) and a single final elongation step of 72° C for 5 minutes.

Detection of PCR Products

The amplified PCR products were detected by agarose gel electrophoresis (2%) containing ethidium bromide. Ten microliters of each sample was added to 2 µl of 6X gel loading dye (New England BioLabs Inc. USA) for the

electrophoresis. Hundred base pair DNA molecular weight marker (New England Biolabs Inc., USA) was run alongside the PCR products. The gel was prepared and electrophoresed in 1X TAE buffer using a mini gel system at 100 volts for one hour. The gels were viewed in a benchtop UV illuminator (UVP, LLC, Upland, CA, USA) and photographed using Canon camera Sx230 HS.

Data Analysis

The presence of HSV-1 and HSV-2 DNA was recorded as positive or negative for each sample. Results were compared with serological HSV data from the parent study. Categorical variables were summarized as percentages, and associations between HSV detection and participat characteristics. Associations between HSV DNA positivity and participant characteristics were assessed using Fisher's exact test, with the Freeman–Halton extension applied where appropriate due to sparse data and small expected cell counts. Odds ratios were not estimated because the limited number of HSV-positive cases resulted in sparse data and unstable estimates. Statistical significance was set at $p < 0.05$.

Missing responses, including "not remember" categories, were treated as missing data and excluded from specific analyses. Therefore, analyses were conducted using complete-case data for each variable, resulting in variable sample sizes across different analyses. Considering the exploratory design and limited sample size, missing data were not imputed.

Results

Sociodemographic and Reproductive Characteristics of Participants

The subset of 94 women whose cervical swab samples were analyzed had a mean (SD) age of 38.45 (9.59) years (range 21–65 years). Most participants were aged 25–44 years (n=72, 76.60%), reflecting the typical screening population at the Cervicare clinics. Regarding educational attainment, most women had less or senior high school education (n=69, 73.40%), while a smaller proportion had completed senior high school or higher (n=25, 26.60%). The majority of participants were actively employed (n=88, 93.61%), and most were married or cohabited (n=69, 73.40%).

Analysis of reproductive history showed that 48.94% of the participants had three or more pregnancies. Among those who had been pregnant, the mean (SD) age at first pregnancy was 24.31 (4.63) years, with a subset reporting first pregnancies after 25 years (n=28, 38.36%). These sociodemographic and reproductive characteristics are summarized in Table 1.

Table 1. Sociodemographic and reproductive characteristics

Characteristics	Frequency, N	Prevalence, %
Age category, years		
< 25	3	3.19
25-44	72	76.60
45-64	18	19.15
> 65	1	1.06
Education		
< SHS	69	73.40
≥ SHS	25	26.60
Work status		
Active	88	93.61
Not active	6	6.39
Marital status		
Single/widowed/divorced	25	26.60
Married/ cohabiting	69	73.40
Number of pregnancies		
Never pregnant	21	22.34
1	18	19.15
2	9	9.57
> 3	46	48.94
Age of first pregnancy, years (n=73)		
≤ 17	2	2.73
18-21	15	20.55
22-25	18	24.66
>26	23	31.51
Do not remember	15	20.55
Age of coitarche, years (n=53)		
≤ 20	28	52.8
21-25	15	28.3
≥26	10	18.9
Number of sexual partners (n=53)		
1	21	39.6
≥ 2	32	60.4
Condom use (n=46)		
No	28	60.9
Yes	18	39.1
Tobacco use (n=46)		
No	46	100.0
Yes	0	0
Alcohol use (n=46)		
No	15	32.6
Yes	31	67.4

Table 2. Prevalence of Genital HSV-1 and HSV-2 DNA Detection Among Study Participants (N=94).

HSV-1 DNA Status	HSV-2 DNA Positive n (%)	HSV-2 DNA Negative n (%)	Total n (%)
Positive	4 (4.3)	8 (8.5)	12 (12.8)
Negative	0 (0.0)	82 (87.2)	82 (87.2)
Total	**4 (4.3)**	**90 (95.7)**	**94 (100)**

Table 3. Distribution of HSV DNA Detection According to HSV Serological Status.

	DNA HSV-1		DNA HSV-2		DNA HSV-1+ & HSV-2+
	Positive (n=12)	Negative (n=82)	Positive (n=4)	Negative (n=90)	(n=4)
HSV-1 IgG positive, N (%)	11 (92)	81 (99)	4 (100)	88 (98)	4 (100)
HSV-1 IgG negative/borderline, N (%)	1 (8)	1 (1)	0 (0)	2 (2)	0 (0)
HSV-2 IgG positive, N (%)	9 (75)	58 (71)	4 (100)	63 (70)	4 (100)
HSV-2 IgG negative/borderline, N (%)	3 (25)	24 (29)	0 (0)	27 (30)	0 (0)
HSV-1+ IgG & HSV-2+ IgG, N (%)	9 (75)	58 (71)	4 (100)	64 (71)	4 (100)

Molecular Detection of HSV DNA

As shown in Table 2, cervical and vaginal swabs from ninety-four women were analyzed. Twelve women, representing 12.8% (95% CI: 6.8-21.2%) tested positive for genital HSV-1, whereas 4.3% (95% CI: 1.2-10.5%) were positive for genital HSV-2. Co-infection with both HSV-1 and HSV-2 was detected in 4.3% of participants. Among twelve positive cases for HSV-1, eleven (92%) patients had confirmed seropositive HSV-1 status, and 8% (n=1) with borderline results. All PCR-positive cases for genital HSV-2 were also seropositive for HSV-2 IgG (Table 3).

HSV DNA Detection and Serological Status

The distribution of HSV DNA detection and HSV serological status is presented in Table 3. Among the 12 participants who tested positive for HSV-1 DNA, 11 (92%) were seropositive for HSV-1 IgG, while 1 (8%) had a negative or borderline HSV-1 IgG result. Among the 82 participants who were negative for HSV-1 DNA, 81 (99%) were HSV-1 IgG seropositive and 1 (1%) was seronegative or borderline. For HSV-2, all four participants (100%) who tested positive for HSV-2 DNA were also seropositive for HSV-2 IgG. Among the 90 HSV-2 DNA negative participants, 63 (70%) were HSV-2 IgG seropositive, whereas 27 (30%) were negative or borderline for HSV-2 IgG antibodies.

Dual seropositivity for both HSV-1 IgG and HSV-2 IgG was observed in 9 of the 12 HSV-1 DNA positive participants (75%), while 58 of the 82 HSV-1 DNA negative participants (71%) were also seropositive for both viruses. Similarly, all HSV-2 DNA positive participants (100%) were seropositive for both HSV-1 and HSV-2 IgG, whereas 64 of the 90 HSV-2 DNA negative participants (71%) demonstrated dual seropositivity. HSV DNA detection in cervical samples and HSV IgG seropositivity were both observed among study participants, reflecting current viral detection and prior exposure respectively.

Sociodemographic, Obstetric, and Behavioral Correlates of HSV DNA Detection

The distribution of HSV-1 and HSV-2 DNA positivity according to selected sociodemographic, obstetric, and behavioral characteristics is summarized in **Table 4**. These variables were examined because previous studies have identified factors such as age, marital status, reproductive history, sexual behavior, and condom use as potential determinants of HSV acquisition and transmission. Accordingly, they were explored in relation to HSV DNA positivity. HSV DNA positivity was observed across multiple participant categories. No statistically significant associations were observed between HSV DNA positivity and any of the examined variables (all $p > 0.05$). Most HSV-1 DNA positive participants were aged 25–44 years (75.0%, 9/12), while the remaining 25.0% (3/12) were aged 45–64 years. All HSV-2 DNA positive cases occurred in the 25–44-year age group (100%, 4/4), although age was not significantly associated with HSV-1 ($p = 0.703$) or HSV-2 DNA positivity ($p = 0.579$). Similarly, most HSV-1 (66.7%, 8/12) and HSV-2 (75.0%, 3/4) positive participants had attained senior high school education or higher, with no significant association observed for either HSV-1 ($p = 0.727$) or HSV-2 ($p = 0.941$). The majority of HSV-1 (91.7%, 11/12) and all HSV-2 (100%, 4/4) positive cases were among actively employed women, and work status was not significantly associated with infection (HSV-1 $p = 0.570$; HSV-2 $p = 0.594$). Most HSV-1 positive participants were married or cohabiting (83.3%, 10/12), and all HSV-2 positive participants were within this group, although no significant association was observed (HSV-1 $p = 0.506$; HSV-2 $p = 0.570$).

For reproductive history, most HSV-1 positive women reported three or more pregnancies (58.3%, 7/12), while 75.0% (3/4) of HSV-2 positive participants were in the

Table 3. Distribution of HSV DNA Detection According to HSV Serological Status.

Characteristics	HSV-1 DNA Positive, n (%)	HSV-1 DNA Negative, n (%)	p-value[1]	HSV-2 DNA Positive, n (%)	HSV-2 DNA Negative, n (%)	p-value[1]
Age category, years						
≤44	9 (75.0)	66 (80.5)	0.703	4 (100.0)	71 (78.9)	0.579
>44	3 (25.0)	16 (19.5)		0 (0.0)	19 (21.1)	
Education						
< SHS	4 (33.3)	21 (25.6)	0.727	1 (25.0)	24 (26.7)	0.941
≥ SHS	8 (66.7)	61 (74.4)		3 (75.0)	66 (73.3)	
Work status						
Active	11 (91.7)	77 (93.9)	0.570	4 (100.0)	84 (93.3)	0.594
Not active	1 (8.3)	5 (6.1)		0 (0.0)	6 (6.7)	
Marital status						
Single/widowed/divorced	2 (16.7)	23 (28.0)	0.506	0 (0.0)	25 (27.8)	0.570
Married/cohabiting	10 (83.3)	59 (72.0)		4 (100.0)	65 (72.2)	
Number of pregnancies[2]						
1	2 (16.7)	16 (19.5)	0.789	1 (25.0)	17 (18.9)	0.734
2	2 (16.7)	7 (8.5)		0 (0.0)	9 (10.0)	
≥3	7 (58.3)	39 (47.6)		3 (75.0)	43 (47.8)	
Age at first pregnancy, years[2]						
≤25	4 (57.1)	26 (66.7)	0.681	2 (50.0)	28 (66.7)	0.602
>25	3 (42.9)	13 (33.3)		2 (50.0)	14 (33.3)	
Age of coitarche, years[2]						
≤20	3 (37.5)	25 (48.1)	0.354	2 (50.0)	26 (48.1)	0.947
21–25	2 (25.0)	13 (25.0)		1 (25.0)	14 (25.9)	
>25	3 (37.5)	7 (26.9)		1 (25.0)	9 (16.7)	
Number of sexual partners[2]						
1	5 (62.5)	16 (40.0)	0.240	2 (50.0)	19 (38.8)	0.659
≥2	3 (37.5)	29 (60.0)		2 (50.0)	30 (61.2)	
Condom use[2]						
No	2 (28.6)	16 (41.0)	0.688	1 (25.0)	17 (40.5)	0.545
Yes	5 (71.4)	23 (59.0)		3 (75.0)	25 (59.5)	

Note 1: Fisher's exact test

Note 2: Denominators vary due to missing responses in specific variables; analyses were performed using available complete cases for each variable.

same category; however, parity was not significantly associated with infection (HSV-1 p = 0.789; HSV-2 p = 1.000). For age at first pregnancy (n = 73), HSV DNA positivity was distributed across categories of ≤25 years and >25 years with no significant associations observed (HSV-1 p = 0.681; HSV-2 p = 0.602). Similarly, age at sexual debut (n = 53) and number of sexual partners (n = 53) showed no statistically significant associations with HSV DNA positivity, although HSV-2 cases were evenly distributed across sexual partner categories. The majority of HSV-1 (71.4%) and HSV-2 (75.0%) positive participants reported no condom use, but this was also not significantly associated with infection (HSV-1 p = 0.688; HSV-2 p = 0.545).

Discussion

This study provides evidence of HSV-1 DNA detection in cervical swabs from asymptomatic women in Ghana, indicating the presence of genital HSV-1 infection in this population. These findings suggest that genital HSV-1 infection may occur in individuals without clinical symptoms and may therefore be underrecognized in routine clinical practice.

Globally, HSV-2 has traditionally been the predominant cause of genital herpes However, recent studies have reported an increasing proportion of genital herpes cases

attributed to HSV-1 in some populations [17–21]. The estimated prevalence of genital HSV-1 infection among adults aged 15-49 years was 10.2% [2]. Although, data from African settings remain limited and inconsistent [2,6], highlighting important gaps in region-specific epidemiological evidence.

HSV establishes lifelong latency in sensory neurons and is characterized by intermittent viral reactivation and asymptomatic shedding [3,8]. These features may result in low and transient viral loads, particularly in asymptomatic individuals, which can limit detection if sensitive molecular methods are not used. In this study, the detection of HSV-1 DNA in cervical specimens therefore provides direct evidence of genital viral presence and underscores the value of PCR-based diagnostic approaches in identifying infections that may otherwise go undetected.

Available data from Ghana and West Africa suggest a high burden of HSV exposure based primarily on serological studies. For example, a previous study from Ghana reported HSV-1 and HSV-2 seroprevalence of 99.2% and 78.4%, respectively, indicating widespread prior exposure [14]. Similarly, studies from Nigeria and other West African settings have reported substantial HSV seroprevalence [22–25]. However, these studies primarily provide evidence of prior HSV exposure rather than active genital infection. In contrast, the present study provides preliminary PCR-based evidence of HSV DNA detection in genital samples from asymptomatic women in Ghana, thereby contributing novel data on current infection at the genital site.

One possible explanation for genital HSV-1 infection is sexual transmission through oral-genital contact [6]. Such exposure may facilitate transmission from individuals with orolabial HSV-1 infection to the genital tract [6]. Behavioral factors, including awareness of HSV transmission routes, may influence sexual practices. However, misperceptions regarding the risks associated with oral–genital contact may persist in some populations [12,21,22]. In some contexts, oral–genital sex may be perceived as a lower-risk alternative to penetrative intercourse or as a means of preserving social or cultural norms related to virginity, potentially reducing perceived risk and contributing to engagement in practices that facilitate HSV-1 transmission [15,26].

In African settings, early-life acquisition of HSV-1 infection is common, often occurring before sexual debut [6], reflecting the high background prevalence of HSV-1 exposure in childhood [2]. This early infection may result in seropositivity prior to sexual debut and subsequently influence patterns of immunity and susceptibility to genital HSV-1 infection in later life [27].

Despite reports of relatively low genital HSV-1 prevalence in some African and Asian studies [6,28], this may reflect limited availability of molecular testing data rather than a true absence of infection. In many settings, including Ghana, diagnostic capacity and surveillance systems for HSV remain limited, and routine genotyping is not widely performed. As a result, the contribution of HSV-1 to genital herpes in the region remains incompletely understood [29,30].

The present findings highlight the importance of molecular diagnostic methods for detecting HSV in genital samples, particularly among asymptomatic individuals. Molecular testing provides direct evidence of viral DNA and may identify infections that are not apparent clinically or through serological testing alone. The observed discordance between HSV-1 DNA positivity and HSV-1 IgG seronegativity or borderline results in one participant may reflect recent infection prior to seroconversion, individual variation in immune response, or limitations in serological assay sensitivity. Similar discrepancies between molecular and serological HSV detection have been reported in previous studies [31–33].

Differentiation between HSV-1 and HSV-2 remains clinically important, due to differences in recurrence patterns, viral shedding, and transmission dynamics [3,5,8,29]. However, the PCR assay used in this study did not include sequencing or characterization of viral genetic variants, and clinical outcomes were not assessed.

The detection of HSV DNA among asymptomatic women underscores the potential for unrecognized genital infection and highlights the importance of molecular surveillance approaches.

In the absence of effective vaccines and with current antiviral therapies unable to eliminate infection [3], improved characterization of HSV epidemiology remains important. Integration of molecular diagnostic approaches into sexually transmitted infection control programs in Ghana may enhance detection and type differentiation. Further studies with larger sample sizes are needed to better define the epidemiology and determinants of genital HSV infection in this setting.

Fisher's exact test analysis showed no statistically significant associations between HSV DNA positivity and the sociodemographic, obstetric, or behavioral characteristics examined. Although descriptive patterns were observed, these findings did not reach statistical significance, likely due to the small sample size and limited statistical power. Therefore, the findings should be interpreted as exploratory, and lack of statistical significance does not imply absence of association but rather reduced ability to detect true effects.

Given the pilot nature of this study, the findings provide preliminary evidence of HSV detection in genital specimens but do not allow for inference of transmission dynamics or causal relationships. These results are intended to inform the design of larger, population-based studies rather than provide definitive prevalence estimates. The detection of HSV DNA in asymptomatic individuals suggests the possibility of unrecognized infection within the population. In Ghana, routine HSV screening is not widely implemented, and many infections

may remain undiagnosed. Strengthening diagnostic capacity and awareness may support improved detection and clinical management of HSV infections. The role of targeted screening strategies, particularly among women of reproductive age, warrants further investigation [34–36].

Genital HSV-1 and HSV-2 infections may reflect underlying patterns of sexual exposure within the population. However, the present study did not assess co-infections or long-term clinical outcomes, and further research is needed to better understand the broader clinical and epidemiological implications. Further population-based studies are needed to clarify the burden of genital HSV-1 infection in Ghana and to better characterize its epidemiological distribution. Such studies will support more informed prevention strategies, particularly among women of reproductive age.

This study has several limitations. The relatively small sample size limits the external validity of the findings, and results should therefore be interpreted as exploratory and hypothesis-generating. In addition, recruitment from cervical screening clinics may introduce selection bias, limiting representativeness of the broader population of women in Ghana. Behavioral data were self-reported and may therefore be subject to recall and social desirability bias. Finally, residual confounding from unmeasured variables, including partner infection status and other sexually transmitted infections, cannot be excluded.

Conclusion

This study provides evidence of HSV-1 DNA detection in genital swabs from asymptomatic women in Ghana, indicating that HSV-1 is present in the genital tract in this population. Further population-based studies are needed to better characterize the epidemiology and public health implications of genital HSV infection in Ghana.

Declarations

Ethical Approval and consent to participate

Ethical approval for the parent study was obtained from the Ghana Health Service Ethics Review Committee (GHS-ERC:07/03/14). The current study, which involved secondary analysis of these archived samples, was conducted under the same ethical approval framework. Additional approval was also obtained from the Ethical and Protocol Review Committee of the School of Biomedical and Allied Health Sciences, University of Ghana (SBAHS-MLS/10572569/SA/2018–2019).

Availability of data and materials

The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request.

Competing interests

The authors declare that they have no competing interests.

Funding

The research was funded by the authors.

Authors' Contributions

OR formulated the concept, carried out the implementation of the research, was involved in the recruitment of the participants and data collection, performed laboratory analysis, analyzed and interpreted the data, wrote the first draft of the manuscript with input from all authors. RHA formulated the concept, directed the implementation of research, supervised findings of this work and contributed to the final version of the manuscript. EGAA carried out the implementation of the research, performed laboratory analysis, analyzed and interpreted the data and contributed to the final version of the manuscript. ETD contributed to the analysis of the results and contributed in writing the manuscript. NET contributed to the analysis and interpretation of the results and was a major contributor in writing the manuscript. GB contributed to the final version of the manuscript. AD contributed to the final version of the manuscript.

Acknowledgements

We wish to acknowledge all the study participants.

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