Integrated Health Research Journal (IHRJ)

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

REVIEW ARTICLE

Allium sativum (Garlic) in Medicinal Chemistry: Phytochemical Constituents and Pharmacological Potential - A Review

Fakeha Mohammed Rehan Shaikh[1] & Ashish Sambhaji Uzgare[1*]

[1] Department of Chemistry, Faculty of Science, Wilson College (Autonomous), Mumbai-400007, Maharashtra, India.

*Correspondence should be addressed to Ashish Sambhaji Uzgare (email: ashish.uzgare@wilsoncollege.edu)

Abstract

Allium sativum (garlic) is widely recognized for its diverse medicinal and therapeutic properties, attributed to its rich content of bioactive compounds such as organosulfur compounds, flavonoids, polyphenols, saponins, vitamins, and minerals. This review highlights current research on *Allium sativum* pharmacological potential, emphasizing its antioxidant, anti-inflammatory, anticancer, and antimicrobial activities. Garlic exhibits strong antioxidant effects by scavenging free radicals and enhancing enzymatic defense systems, protecting cells from oxidative stress and related damage. Its anti-inflammatory properties involve modulation of cytokine production and inhibition of key pathways, offering therapeutic benefits in chronic diseases including cardiovascular disorders, metabolic syndrome, and inflammatory conditions. *Allium sativum* also demonstrates anticancer activity through apoptosis induction, cell-cycle arrest, tumor suppression, and antimutagenic effects, as observed in various cell lines and experimental models. Additionally, garlic possesses potent antimicrobial effects against bacteria, fungi, and drug-resistant pathogens, achieved via membrane disruption, biofilm inhibition, and suppression of virulence factors. These pharmacological activities validate garlic's traditional use and underscore its role as a natural, multifunctional agent and functional food. Future research should focus on standardized preparations, isolation of novel bioactive compounds, detailed mechanistic studies, clinical validation, and advanced delivery systems to enhance bioavailability, optimize therapeutic efficacy, and integrate garlic into modern preventive healthcare and treatment strategies.

Keywords: *Allium sativum* , Antioxidants, Anti-inflammatory, Anticancer, Antimicrobial, Healing, Herb

Citation: Shaikh FMR, Uzgare AS. *Allium sativum* (Garlic) in medicinal chemistry: phytochemical constituents and pharmacological potential: a review. Integrated Health Research Journal. 2026;3(2):1-10. https://doi.org/10.47963/03tmg067

Received 22nd February 2026; **Accepted** 29th May 2026; **Published** 14th September 2026.

Introduction

Herbal medicines, obtained from plant parts such as leaves, roots, and flowers, have been central to traditional healing systems for centuries. As gifts of nature, herbs have provided effective remedies, with garlic notably offering antibacterial and antiseptic health benefits [1]. *Allium sativum* , commonly known as clove garlic, is classified under the family Liliaceae and is renowned for its broad spectrum of medicinal applications [2]. *Allium sativum* is a perennial flowering bulb that has been widely consumed worldwide as a functional food and recognized for its medicinal and culinary uses for thousands of years [3]. The name *Allium sativum* is derived from the Celtic word "all" (burning or stinging) and the Latin "sativum" (cultivated). The term "garlic" comes from the Anglo-Saxon "gar-leac", meaning spear plant. Garlic has been traditionally used as a dietary supplement for diabetes in Asia, Europe, and the Middle East and exhibits broad pharmacological activities, including antiviral, antibacterial, antifungal, antioxidant, anti-atherosclerotic, and anticancer effects [4]. It also contains bioactive compounds such as organosulfur compounds, saponins, flavonoids, phenolic acids, and polysaccharides [5]. It is rich in over 30 sulfur compounds, enzymes, minerals (calcium, iron, potassium, magnesium, selenium, zinc, germanium), vitamins A, B1, C, fiber, water, and 17 amino acids including lysine, histidine, arginine, threonine, serine, glutamine, proline, glycine, alanine, cysteine, valine, methionine, isoleucine, leucine, tryptophan, and phenylalanine [6,7]. Numerous clinical studies have evaluated the wide-ranging therapeutic effects of garlic. Ongoing research continues to validate traditional claims, uncover its mechanisms of action, and

investigate its potential for disease prevention and treatment [8].

This review objective is to summarize current research on *Allium sativum* (Garlic), as a natural source of antioxidants, anti-inflammatory, anticancer, and antimicrobial agents, highlighting its medicinal and therapeutic potential.

Literature review strategy

The information included in this review was gathered from several well-established scientific databases, including Google Scholar, ScienceDirect, and PubMed, to ensure broad and reliable coverage of relevant literature. Greater emphasis was placed on systematic reviews and meta-analyses, as these provide strong, evidence-based conclusions. In addition, original research articles, including in vitro, in vivo, and clinical studies, were also examined to gain deeper insight into the underlying mechanisms and experimental findings.

The literature search included both experimental and observational studies published between 1996 to 2026. Keywords such as *Allium sativum* , garlic, pharmacological activities, antioxidant, anti-inflammatory, antimicrobial, and anticancer were used to identify relevant publications. Furthermore, the reference lists of selected articles were carefully reviewed to locate additional relevant studies. This comprehensive search strategy ensured a thorough, balanced, and reliable evaluation of the available scientific evidence.

Data extraction

The studies identified through the selected search engines were first screened by reviewing their titles and abstracts to determine their relevance to the topic. Articles that met the initial inclusion criteria were then retrieved in full and organized using Microsoft Excel for systematic data handling. Each selected study was carefully reviewed and categorized based on its objectives, methodology, key findings, and overall conclusions.

This structured approach made it easier to compare findings across studies and synthesize the available evidence while reducing the risk of duplication and bias. Studies that lacked sufficient data, showed methodological weaknesses, or were not directly relevant to the scope of this review were excluded at this stage. By following this careful and organized selection process, we ensured that only high-quality and scientifically relevant literature was included, thereby strengthening the credibility and reliability of the review findings.

Literature review

Antioxidant and Phytochemical Insights from *B. cereus*

Phytochemicals are plant-derived bioactive compounds responsible for the flavor, color, and aroma of foods. Major groups include polyphenols, terpenes, and sulfur- or nitrogen-containing compounds. These molecules exhibit important biological activities such as antioxidant, anti-inflammatory, antiviral, and anticancer effects, thereby contributing to disease prevention and overall health [9,10]. *Allium sativum* (garlic) is particularly rich in antioxidant compounds that help neutralize free radicals unstable molecules that can damage cells and DNA, leading to aging, cardiovascular diseases, and cancer [11]. Studies have shown that garlic exhibits significant antioxidant activity, measured using assays such as ABTS (1.97–4.42 mmol TE/kg DM) and FRAP (1.12–2.64 mmol TE/kg DM). Among different cultivars, Garpel demonstrated the highest antioxidant capacity, which strongly correlated with total phenolic content (TPC) and total flavonoid content (TFC) ($p < 0.001$), confirming garlic as a potent natural source of polyphenols and flavonoids [12]. Garlic essential oil, rich in organosulfur compounds such as diallyl trisulfide and diallyl disulfide, also shows strong antioxidant activity in DPPH and β-carotene assays. Computational studies suggest that certain volatile compounds, including α-bisabolol, may inhibit NADPH oxidase, further contributing to antioxidant effects [13]. Although allicin levels in raw garlic are difficult to quantify using High-Performance Liquid Chromatography (HPLC), DPPH assays confirm its substantial antioxidant potential [14]. Garlic by-products, such as garlic peel, also possess notable antioxidant properties. These properties can be enhanced through fermentation with Lactobacillus plantarum or mild heat treatment. In particular, a 48-hour fermented ethanolic extract exhibited the highest phenolic and flavonoid content along with strong antioxidant activity, indicating its potential use as a natural antioxidant in food applications [15]. Garlic contains a wide range of secondary metabolites, including alkaloids, flavonoids, glycosides, tannins, saponins, triterpenoids, and phenolics, which contribute to its antioxidant and cardioprotective effects. The phytochemical composition varies depending on the plant part (leaves, roots, bulbs) and extraction method (aqueous vs. methanolic) [16]. For example, the Hisar garlic 17 (HG17) variety demonstrated higher antioxidant activity than Snow Mountain garlic (SMG), with its dry methanolic extract showing the highest phenolic and flavonoid content. LC-MS analysis identified unique polyphenols likely responsible for its enhanced activity, highlighting its potential for functional food and therapeutic applications [17]. Comparative studies between fresh and black garlic indicate that both contain flavonoids, alkaloids, and saponins, with black garlic showing slightly higher concentrations. However, DPPH assays revealed relatively weak antioxidant activity in both (IC50: garlic 670.03 mg/mL; black garlic 637.80 mg/mL), despite significant differences in certain phytochemical contents [18]. Garlic is also a rich source of organosulfur compounds, selenium, and flavonoids, all contributing to its antioxidant properties. Extraction methods, particularly ethanol extraction, and cooking processes such as boiling or frying can significantly influence the levels of these compounds and, consequently, antioxidant activity [19]. Additionally, analytical techniques like Fourier Transform Infrared (FT-IR) spectroscopy combined with chemometric models (PLSR) have demonstrated strong

correlations between phenolic functional groups and antioxidant activity across garlic samples from different geographic locations [20]. Beyond food applications, garlic extracts also show potential in animal science. Ethanolic *Allium sativum* extract (EASE), when added to boar semen stored at 17°C, improved sperm viability, membrane integrity, and reduced lipid peroxidation, with the most effective concentration observed at 100 µg/mL [21].

Overall, garlic is confirmed as a rich source of natural antioxidants, particularly polyphenols, flavonoids, and organosulfur compounds. Among extraction methods, methanolic and ethanolic extracts are consistently more effective than aqueous extracts, as they yield higher concentrations of bioactive compounds and stronger antioxidant activity. Variations in reported results across studies are primarily explained by differences in extraction techniques, plant material, processing methods, and analytical assays rather than contradictions in the inherent antioxidant potential of garlic.

B. cereus as a Natural Anti-Inflammatory Agent

Phytochemicals from plants act as important anti-inflammatory agents, with both crude extracts and isolated compounds shown to effectively modulate inflammatory responses [22]. *Allium sativum* enhances immune function by stimulating key immune cells and modulating cytokine secretion, immunoglobulin production, and phagocytosis. These effects may underlie its therapeutic potential in managing obesity, metabolic syndrome, cardiovascular disorders, gastric ulcers, and cancer [23]. The anti-inflammatory effects of ethanol extract of *Allium sativum* were assessed in a smoker rat model. Treatment markedly reduced inflammatory cell infiltration, improved alveolar integrity, and lessened alveolar dilation. These results suggest that *Allium sativum* can protect against smoke-induced lung inflammation [24]. Aqueous *Allium sativum* extract demonstrated strong antioxidant, anti-inflammatory, and anticoagulant activities. It effectively scavenged free radicals, inhibited hemolysis and 15-lipoxygenase, and reduced serine protease activity. Molecular docking identified Rhamnetin as a stable 15-LOX1/2 inhibitor, highlighting garlic's anti-inflammatory potential [25]. Garlic sulfur compounds, including Z- and E-ajoene and their sulfonyl derivatives, showed potent anti-inflammatory effects by inhibiting nitric oxide, prostaglandin E2, and pro-inflammatory cytokines (TNF-α, IL-1β, IL-6) in LPS-activated macrophages. They also suppressed iNOS and COX-2 expression through inhibition of NF-κB activation and p38/ERK phosphorylation, indicating strong therapeutic potential [26]. The 14-kDa protein from *Allium sativum* exhibited anti-inflammatory effects in LPS-stimulated macrophages by lowering nitric oxide, PGE2, TNF-α, and IL-1β levels. It suppressed iNOS and COX-2 expression and inhibited NF-κB signaling, suggesting its potential as a natural agent for controlling inflammation [27]. Garlic (*Allium sativum*) extract modulates immune responses in vitro by inhibiting pro-inflammatory Th1 cytokines (IL-12, TNF-α, IL-1α, IL-6, IL-8, IFN-γ, IL-2) and enhancing anti-inflammatory IL-10 production in monocytes and T-cells. Its effects were partly acid-labile and additive with methylprednisolone, suggesting garlic may help reduce inflammation in inflammatory bowel disease, pending in vivo validation [28]. Garlic (*Allium sativum*) compound allicin is rapidly metabolized in the liver, exhibiting a strong first-pass effect and remaining unchanged only at toxic levels. It is mainly converted into diallyl disulfide (DADS) and allyl mercaptan, with DADS acting as a precursor. These metabolites were detected in the liver, bile, and perfusion fluid, while other garlic-derived compounds such as ajoenes and vinyldithiins passed through without identifiable metabolites [29]. Garlic's therapeutic effects are largely attributed to allicin, which has shown benefits in reducing cholesterol and improving oral health conditions. However, its usefulness is limited due to instability and low bioavailability, particularly in rapidly disintegrating tablet forms [30]. Allicin is the main bioactive compound in raw garlic, but its bioavailability varies widely across supplements and foods due to gastrointestinal conditions affecting its formation. Non-enteric tablets and some garlic products showed high bioavailability, while enteric tablets performed poorly, especially with protein-rich meals; unexpectedly, certain cooked garlic foods still provided moderate allicin-related activity [31]. Allicin, the key active compound in fresh garlic, shows dose- and time-dependent inhibition of colon cancer cell growth. It induces apoptosis by regulating proteins like Bcl-2 and Bax and activating the Nrf2 pathway, which plays a central role in its anticancer effects [32].

Anticancer Potential of *B. cereus*

Table1 shows Comparative IC_{50} / Dose-Dependent Anticancer Effects of Garlic Across Cell Lines.

Cancer remains a major global health challenge, affecting populations across all economic backgrounds. Medicinal plants offer potential for cancer prevention and treatment due to their antioxidant properties and tumor-suppressing effects [33]. Garlic (*Allium sativum* L.) is recognized for its cancer-preventive potential. Fresh garlic, powders, oils, and organosulfur compounds particularly allyl sulfides exert anticancer effects by promoting apoptosis, inhibiting the cell cycle, enhancing detoxification enzymes, and providing anticarcinogenic and antimutagenic protection [34]. Studies suggest garlic's chemopreventive effects stem from organosulfur compounds in fresh, aged, or oil forms. Mechanisms include antioxidant activity, enzyme modulation, tumor inhibition, and antimutagenesis. Aged garlic extract, particularly S-allylcysteine, demonstrates strong radical scavenging and tumor-suppressing activity in experimental models, highlighting its potential in cancer prevention [35]. *Allium sativum* (garlic) exhibits significant anticancer effects on human breast cancer cell lines MCF-7 and MDA-MB-231. The extract induced cytotoxicity and apoptosis via caspase-9 activation, inhibited cell proliferation, and reduced cell motility. GC-MS analysis revealed numerous bioactive compounds likely responsible for these antitumoral and antimotility effects [36]. Garlic fractions, especially the ethyl acetate extract, show significant anticancer activity against MCF7 and HepG2 cells by inducing apoptosis and arresting cells in the G2/M phase. HPLC analysis identified linoleic acid and S-allylthiocysteine as major constituents, indicating the

Table1. Comparative IC_{50} / Dose-Dependent Anticancer Effects of Garlic Across Cell Lines

Garlic Preparation	Cell Line (Cancer Type)	Assay Used	IC_{50} / Effective Dose	Dose-Response Observation	Effects
Garlic extract	MCF-7, MDA-MB-231 (Breast)	Not specified	Not reported	Dose-dependent cytotoxicity and apoptosis	Quantitative IC_{50} missing [36]
Ethyl acetate fraction	MCF-7 (Breast), HepG2 (Liver)	Not specified	Not reported	Dose-dependent apoptosis and G2/M arrest	Needs IC_{50} for comparison [37]
Garlic extract vs 5-FU	KB (Oral cancer)	MTT assay	Not reported	Significant dose-dependent reduction ($p = 0.0027$)	Comparative potency unclear [38]
Garlic peel methanol extract (GpMet)	HeLa (Cervical)	MTT assay	IC_{50} = 763 µg/mL	Clear dose-dependent cytotoxicity	Only study with IC_{50} value [39]
Garlic-derived SEVs	A498 (Kidney), A549 (Lung)	Not specified	Not reported	Selective, dose-dependent apoptosis	No IC_{50} reported [40]
Aqueous garlic extract (AGE)	HeLa (Cervical)	In vitro cytotoxicity	~500 µL/5 mL (95% cell death)	Strong dose-dependent effect	Semi-quantitative, not IC_{50} [41]

therapeutic potential of this fraction as an adjuvant or lead for anticancer drug development [37]. Garlic (*Allium sativum*), rich in organosulfur compounds, exhibits anticancer activity against various cancer cells. This study evaluated its cytotoxic effect on KB cell lines and compared it with 5-fluorouracil (5-FU) using MTT assays, showing a significant, dose-dependent reduction in cell viability ($p = 0.0027$). These findings support garlic's potential as an adjuvant or source for developing new anticancer therapies [38]. Garlic (*Allium sativum*) peel methanol extract (GpMet) exhibits significant antioxidant and anticancer activity against HeLa cervical cancer cells. Phytochemical analysis showed flavonoids, alkaloids, and glycosides, while ABTS and FRAP assays confirmed free radical scavenging. MTT assay revealed dose-dependent cytotoxicity (IC50 = 763 µg/ml), suggesting GpMet's potential as a natural, cost-effective therapeutic agent [39]. Garlic-derived small extracellular vesicles (SEVs) were studied for anticancer effects. They triggered intrinsic apoptosis, reduced VEGF levels, and selectively killed A498 kidney and A549 lung cancer cells while sparing normal fibroblasts, suggesting SEVs as a novel cancer therapy [40]. Garlic (*Allium sativum*) has long been used for its medicinal properties, including immune enhancement and anticancer effects. In this study, aqueous garlic extract (AGE) was applied to HeLa cells in vitro at concentrations of 100–500 µL/5 mL medium. Results showed a dose-dependent cytotoxicity, with 95% of cancer cells destroyed at 500 µL and decreasing destruction at lower concentrations [41].

Exploring the Antimicrobial Potential of *B. cereus*

Compounds derived from plants with potent antimicrobial activity are increasingly investigated as potential treatments for bacterial, fungal, viral, and parasitic infections. Plant extracts continue to serve as important sources for developing effective antimicrobial agents [42]. Garlic (*Allium sativum*), a traditional remedy for infections, owes its antibacterial power to organosulfur compounds such as allicin and ajoenes. These compounds act against bacteria through bactericidal, antibiofilm, antitoxin, and anti-quorum sensing mechanisms, targeting even multi-drug resistant strains [43]. To address bacterial resistance in oral health, the antimicrobial potential of aqueous garlic extract (*Allium sativum*) against Porphyromonas gingivalis was assessed. The extract exhibited notable inhibitory and bactericidal activity, though chlorhexidine remained more potent. This suggests that garlic extract could serve as a natural alternative or supplement in managing periodontal infections [44]. Ultrasonicated garlic extract demonstrated significant antibacterial activity against multiple pathogens, including *E. coli*, *S. aureus*, *S. mutans*, and *P. gingivalis*, with *S. mutans* showing the highest susceptibility. FTIR, TEM, and spectrophotometry confirmed bioactive organosulfur and phenolic compounds, highlighting its potential as an alternative strategy against resistant bacteria45. Hydroalcoholic extracts of six 14th September 2026 species showed that *Allium sativum* and 14th September 2026 ursinum contained high levels of thiosulfinates, with garlic being richer in allicin. These extracts exhibited strong antimicrobial effects, particularly against Candida species and *Allium sativum* , indicating their potential as effective adjuncts in the treatment of microbial infections [46]. Aqueous *Allium sativum* extract exhibited potent antibacterial effects against both Gram-positive (*Allium sativum*) and Gram-negative (Salmonella spp.) pathogens.

Table 2. Summary of Pharmacological Activities of *Allium sativum* With Herb Drug Interactions

Activity	Pharmacological Potential	Mechanism / Target	Key Compounds	Herb–Drug Interactions / Safety
Antioxidant	Protects cells from oxidative stress; supports cardiovascular and reproductive health	Scavenges free radicals; inhibits lipid peroxidation; enhances antioxidant enzymes (SOD, CAT, GPx)	Polyphenols, flavonoids, organosulfur compounds, selenium	May potentiate effects of antihypertensive and antidiabetic drugs due to additive antioxidant and metabolic effects[11,21].
Anti-inflammatory	Reduces inflammation in chronic diseases (lung disorders, IBD, obesity)	Inhibits NF-κB, iNOS, COX-2; suppresses TNF-α, IL-1β, IL-6; modulates cytokines	Ajoenes, Z/E-sulfonyl derivatives, rhamnetin, 14-kDa protein	May enhance effects of NSAIDs; increased risk of gastrointestinal irritation or bleeding when combined[22,28]
Anticancer	Chemopreventive and cytotoxic effects against multiple cancer types	Induces apoptosis (caspase-9), cell-cycle arrest; inhibits tumor growth and mutagenesis	Allyl sulfides, S-allylcysteine, linoleic acid, SEVs	Possible interaction with chemotherapeutic agents via antioxidant or CYP modulation; requires clinical caution[30,34-37].
Antimicrobial	Inhibits bacteria, fungi, and resistant pathogens; supports oral/systemic health	Disrupts microbial membranes; inhibits biofilm formation; suppresses virulence genes	Allicin, ajoenes, thiosulfinates, garlic lectin (ASA)	May alter gut microbiota affecting drug absorption; limited clinical interaction data[39-48].
Antithrombotic / Cardioprotective	Reduces platelet aggregation; supports cardiovascular health	Inhibits platelet aggregation; decreases thromboxane synthesis	Ajoene, allicin, diallyl disulfide	Significant interaction with anticoagulants (e.g., Warfarin) and antiplatelets → increased bleeding risk[49-52] .
Anticoagulative	Prolongs blood clotting time; potential preventive and supportive role in thromboembolic disorders	Increases prothrombin time (PT) and activated partial thromboplastin time (aPTT); interferes with coagulation cascade pathways	Isoflavones, organosulfur compounds, polyphenols, steroid glycosides	May enhance effects of anticoagulant drugs (e.g., Warfarin), increasing bleeding risk; caution advised in patients with bleeding disorders or those on blood thinners[53]

Beyond growth inhibition, garlic extract effectively suppressed the expression of critical virulence genes in Salmonella, demonstrating its dual antimicrobial and antivirulence activity and supporting its therapeutic potential against resistant bacteria [47]. An ethanolic garlic extract demonstrated bactericidal effects against both Streptococcus pyogenes and Pseudomonas aeruginosa, with lower bactericidal concentrations required for P. aeruginosa. This highlights garlic's effectiveness against both Gram-positive and Gram-negative bacteria and its promise as an alternative antibacterial agent [48]. *Allium sativum* shows potent antibacterial activity against a wide range of clinical pathogens, including multidrug-resistant strains. Garlic extract alone displays bactericidal and bacteriostatic effects similar to standard antibiotics. When combined with antibiotics, it enhances antimicrobial efficacy and may help combat resistance [49]. Garlic (*Allium sativum* L.) and holy basil (*Allium sativum* L.) essential oils exhibited notable antimicrobial activity in both liquid and vapor phases. Garlic oil, rich in diallyl disulfide and diallyl trisulfide, showed strong vapor-phase inhibition, completely suppressing *Bacillus cereus* and *Allium sativum* . When combined with holy basil oil (1:1), the formulation inhibited all tested bacteria, with complete bactericidal effects against *Allium sativum* and S. aureus at low concentrations (MBC < 0.4% v/v). These findings highlight the potential of garlic–basil essential oil combinations for natural food preservation applications [50]. Aeromonas hydrophila is an antibiotic-resistant pathogen in aquatic environments, necessitating alternative antimicrobials. Uiseong garlic, a Korean variety rich in bioactive compounds, was tested for antibacterial activity

Table 3. Phytochemical Profile of *Allium sativum* and Associated Biological Activities

Phytochemical Class	Key Compounds	Major Sources (Garlic Part/ Type)	Reported Biological Activities
Organosulfur Compounds	Allicin, Ajoene (E/Z), DAS, DADS, DATS, S-allylcysteine	Fresh garlic, aged extract, garlic oil	Antioxidant, anti-inflammatory, antimicrobial, anticoagulant anticancer[13,19,26,30,31,39,53]
Polyphenols	Phenolic acids, gallic acid, caffeic acid	Bulb, peel, fermented extracts	Antioxidant, anti-inflammatory[12,15,17,20].
Flavonoids	Quercetin, Rhamnetin, Kaempferol	Peel, leaves, extracts	Antioxidant, anti-inflammatory, antiviral[12,15,16,25].
Saponins	Steroidal saponins	Bulb, methanolic extracts	Antimicrobial, immune-modulating[16,18].
Alkaloids	Nitrogen-containing compounds	Aqueous and ethanolic extracts	Antioxidant, antimicrobial[16,18].
Tannins	Hydrolyzable and condensed tannins	Peel, outer layers	Antioxidant, antimicrobial[16].
Terpenoids	α-bisabolol, volatile compounds	Essential oil	Antioxidant, anti-inflammatory[13].
Glycosides	Various glycosidic compounds	Whole plant extracts	Antioxidant, cardioprotective[16]
Proteins & Lectins	ASA, 14-kDa protein	Bulb	Antimicrobial, antifungal, anti-inflammatory[27,47].
Selenium Compounds	Selenium-containing amino acids	Whole garlic	Antioxidant, anticancer[19].

and cell-wall disruption. Water and ethanol extracts at 22 °C and 90 °C were evaluated for antimicrobial effects, protein leakage, and morphological changes. Extracts at 22 °C, especially ethanol, showed strong activity against nine A. hydrophila strains, causing significant protein leakage (92.87 ± 0.46 µg/mL) and membrane damage, as confirmed by electron microscopy. Ethanol extract of Uiseong garlic is a promising antibiotic alternative [51]. *Allium sativum* agglutinin (ASA), a garlic lectin, exhibits antifungal and antimicrobial activity. ASA inhibited Candida auris and C. glabrata growth (MIC_{50} 30–70 µg/mL), induced hydrogen peroxide production, and disrupted cell morphology. It also showed anti-biofilm effects against Candida and bacteria, with the strongest activity against Klebsiella pneumoniae, highlighting its potential as a novel antimicrobial agent [52].

Despite its promising results as seen in preclinical and experimental studies, there is inadequate human clinical evidence for validation of many claims of therapeutic effectiveness associated with *Allium sativum* . Most of the clinical trials that have assessed garlic's medicinal value are limited by low sample size, a short period of intervention, and heterogeneity between study populations, dosage levels, and outcomes studied. Also, variability between the form of preparation used, which may include raw garlic, garlic powder, aged garlic extract, and garlic oil, leads to differences in the bioavailability of allicin and other compounds with medicinal activity due to different concentrations. Even where some benefits have been observed from human studies, for example, in the management of heart disease and blood metabolism, the evidence for the effectiveness of garlic in fighting cancer, infections, and immunological disorders lacks and mainly depends on laboratory findings. Thus, further research involving randomized controlled trials among larger human subjects would be important in determining garlic's effectiveness, recommended dosages, and possible adverse reactions.

Pharmacological Activities of *B. cereus*

Allium sativum (garlic) exhibits a wide range of pharmacological activities, including antimicrobial, antioxidant, anti-inflammatory, and cardioprotective effects. Its bioactive compounds, especially allicin, contribute to cholesterol-lowering, antihypertensive, and antithrombotic actions. Garlic has also shown potential anticancer and immunomodulatory properties, supporting its traditional and therapeutic use [30,48,52].

Table 2 indicates the major pharmacological activities of *Allium sativum* , highlighting the key bioactive compounds responsible and their observed therapeutic effects. The table summarizes antioxidant, anti-inflammatory, antimicrobial, and anticancer activities.

Table 3 Shows Phytochemical Profile of *Allium sativum* and Associated Biological Activities.

The antioxidant and anti-inflammatory properties of garlic play a significant role in mitigating oxidative damage and

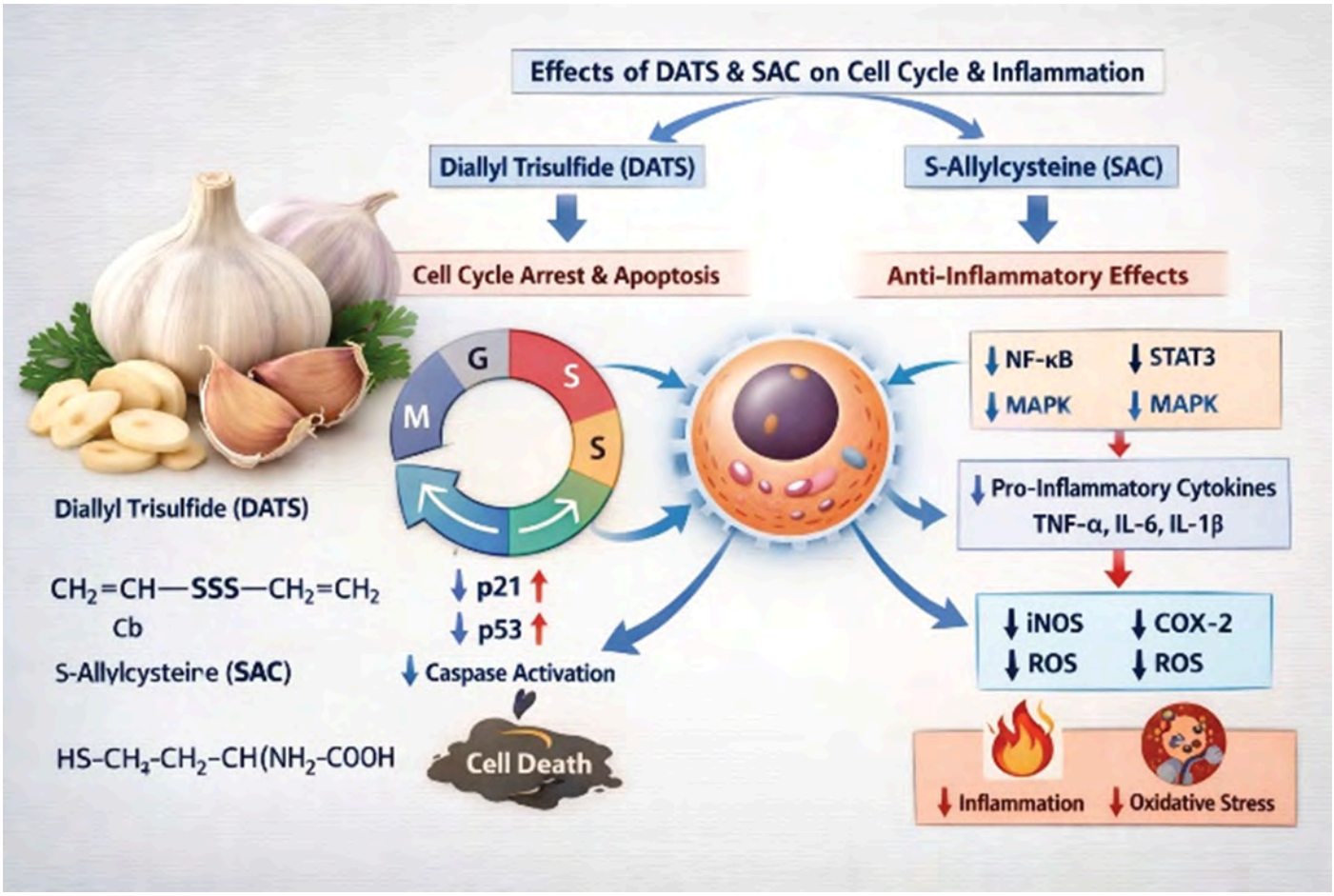

Figure 1. Garlic's Diallyl trisulfide or S-allylcysteine affects the cell cycle or inflammation process

regulating inflammatory signaling pathways involved in chronic disease progression. Additionally, its antimicrobial and anticancer effects, largely driven by organosulfur compounds such as allicin and allyl sulfides, contribute to pathogen inhibition and cancer cell apoptosis. These collective pharmacological actions validate the traditional medicinal use of *Allium sativum* and suggest its potential as a supportive therapeutic agent, warranting further clinical investigation to confirm efficacy and safety [20,48,53].

Toxicology effects of *B. cereus*

Allium sativum possesses numerous therapeutic properties; however, it may also exhibit certain toxic or adverse effects under specific conditions [54]. *Allium sativum* exhibits significant therapeutic potential; however, its toxicological effects at higher doses require careful evaluation. In Wistar rats, intraperitoneal administration of 250–500 mg/kg garlic extract over 38 days resulted in dose-dependent elevations in hepatic enzymes and serum creatinine, indicating hepatorenal stress. Histopathological analysis further confirmed progressive, dose-related damage to liver, kidney, and cardiac tissues [55]. Garlic essential oil (GEO) from *Allium sativum* L. has therapeutic potential but requires safety evaluation due to possible adverse effects at high intake. Genotoxicity assessments, including Ames test, CHO–K1 cell assay, and micronucleus test, showed no mutagenic or clastogenic effects with or without metabolic activation. Additionally, a 28-day oral toxicity study in ICR mice indicated no adverse effects, establishing a no-observed-adverse-effect level (NOAEL) greater than 50 mg/kg body weight/day, demonstrating a favorable toxicological safety profile under the tested conditions [56]. Aqueous extract of *Allium sativum* bulbs was evaluated for antimicrobial and toxicological effects in Wistar rats using biochemical and hematological parameters. The extract showed significant antibacterial activity, but toxicological findings indicated dose-dependent alterations in certain parameters, particularly at 600 and 1,200 mg/kg, suggesting physiological stress. However, at 300 mg/kg, only mild changes were observed, indicating that garlic extract is relatively safe at lower doses for potential therapeutic use [57]. Heavy consumption of *Allium sativum* during pregnancy was associated with nephro- and pulmonary toxicity in albino rats. Treated animals showed elevated serum urea and lipid levels, along with histopathological damage such as kidney necrosis, lung hemorrhage, and fibrosis in maternal and fetal tissues. These findings indicate that high doses of garlic may induce significant renal and pulmonary toxicity, particularly during developmental stages [58].

Figure 1 illustrates Garlic's Diallyl trisulfide or S-allylcysteine affects the cell cycle or inflammation process.

The antioxidant and anti-inflammatory properties of garlic play a significant role in mitigating oxidative damage and regulating inflammatory signaling pathways involved in chronic disease progression. Additionally, its antimicrobial and anticancer effects, largely driven by organosulfur

compounds such as allicin and allyl sulfides, contribute to pathogen inhibition and cancer cell apoptosis. These collective pharmacological actions validate the traditional medicinal use of *Allium sativum* and suggest its potential as a supportive therapeutic agent, warranting further clinical investigation to confirm efficacy and safety [20,48,53].

Toxicology effects of *B. cereus*

Allium sativum possesses numerous therapeutic properties; however, it may also exhibit certain toxic or adverse effects under specific conditions [54]. *Allium sativum* exhibits significant therapeutic potential; however, its toxicological effects at higher doses require careful evaluation. In Wistar rats, intraperitoneal administration of 250–500 mg/kg garlic extract over 38 days resulted in dose-dependent elevations in hepatic enzymes and serum creatinine, indicating hepatorenal stress. Histopathological analysis further confirmed progressive, dose-related damage to liver, kidney, and cardiac tissues [55]. Garlic essential oil (GEO) from *Allium sativum* L. has therapeutic potential but requires safety evaluation due to possible adverse effects at high intake. Genotoxicity assessments, including Ames test, CHO–K1 cell assay, and micronucleus test, showed no mutagenic or clastogenic effects with or without metabolic activation. Additionally, a 28-day oral toxicity study in ICR mice indicated no adverse effects, establishing a no-observed-adverse-effect level (NOAEL) greater than 50 mg/kg body weight/day, demonstrating a favorable toxicological safety profile under the tested conditions [56]. Aqueous extract of *Allium sativum* bulbs was evaluated for antimicrobial and toxicological effects in Wistar rats using biochemical and hematological parameters. The extract showed significant antibacterial activity, but toxicological findings indicated dose-dependent alterations in certain parameters, particularly at 600 and 1,200 mg/kg, suggesting physiological stress. However, at 300 mg/kg, only mild changes were observed, indicating that garlic extract is relatively safe at lower doses for potential therapeutic use [57].Heavy consumption of *Allium sativum* during pregnancy was associated with nephro- and pulmonary toxicity in albino rats. Treated animals showed elevated serum urea and lipid levels, along with histopathological damage such as kidney necrosis, lung hemorrhage, and fibrosis in maternal and fetal tissues. These findings indicate that high doses of garlic may induce significant renal and pulmonary toxicity, particularly during developmental stages [58].

Conclusion

Garlic, scientifically known as *Allium sativum* , possesses substantial therapeutic potential with regard to its composition of bioactive compounds, which include organosulfur compounds, flavonoids, and polyphenolic compounds. The antioxidant, anti-inflammatory, anti-cancer, and antimicrobial properties of garlic, as indicated by the ever-expanding volume of scientific evidence, justify the use of this plant in the prevention and promotion of health. However, despite these benefits, garlic may exhibit dose-dependent toxicological effects, with higher doses associated with hepatorenal stress and histopathological alterations in vital organs, highlighting the importance of safe dosage evaluation. The antioxidant, anti-inflammatory, anti-cancer, and antimicrobial properties of garlic enhance the immune system, protect the body from oxidative stress, and reduce the risk of cancer, respectively. In addition, the beneficial effects of garlic on the metabolic system, cardiovascular system, and gut microbiota justify the importance of this plant as a multifunctional functional food. The synergistic effects of the bioactive compounds present in garlic enhance the pharmacological potential of this plant, justifying the use of this plant in the promotion of health.

It is imperative that future studies be conducted to standardize the preparations of garlic, optimize the extraction methods, and isolate new bioactive compounds of interest for specific drug targets. Moreover, detailed mechanistic investigations are required to understand the molecular mechanisms of action of garlic and its effects on cellular signaling, gene expression, and microbiome modulation. Furthermore, well-designed clinical trials involving large and diverse populations are required to evaluate the effective dosage and possible drug interactions of garlic preparations. Recent advances in drug delivery systems such as nano-technology-based drug delivery systems and small extracellular vesicles may improve the efficacy of garlic preparations. It is also important to evaluate the effects of garlic in combination with conventional drugs or other herbal preparations to achieve synergistic effects, which may open new avenues for the management of various types of cancer, infections, metabolic syndrome, and inflammatory conditions. Functional food products and nutraceuticals are a promising area for the effective utilization of the medicinal properties of garlic for the prevention and treatment of various diseases.

Conflict of Interest

The authors declare no conflict of interest.

Authors' Contributions

The manuscript was drafted and written by Fakeha Mohammed Rehan Shaikh. The work was reviewed, and edited by Ashish Sambhaji Uzgare. Both authors reviewed and approved the final version of the manuscript.

Data Availability

Data is available upon request from the authors.

Funding

The study was fully sponsored by the authors.

References

1. Shaikh FMR, Uzgare AS. Recent advances in extraction and analytical techniques for herbal medicine characterization. Anal Bioanal Chem Res. 2026;13(1):1–12.
2. Kumar KPS, Bhowmik D, Chiranjib T, Tiwari P, Kharel R. Allium sativum and its health benefits: An overview. J Chem Pharm Res. 2010;2(1):135–146.
3. Gudalwar BR, Nimbalwar MG, Panchale WA, Wadekar AB, Manwar JV, Bakal RL. Allium sativum, a potential phytopharmacological source of natural medicine for better health. GSC Adv Res Rev. 2021;6(3):220–232.
4. Wilson A, Pandya D, Mankad AU, Solanki HA. A review on Allium sativum (L.) as a medicinal plant. J Med Plants Stud. 2019;7(2):45–52.
5. Diretto G, Rubio-Moraga A, Argandona J, Castillo P, Gomez-Gomez L, Ahrazem O. Tissue-specific accumulation of sulfur compounds and saponins in garlic cloves. Molecules. 2017;22:1359.
6. Bradley JM, Organ CL, Lefer DJ. Garlic-derived organic polysulfides and myocardial protection. J Nutr. 2016;146:403S–409S.
7. Wang YC, Guan M, Zhao X, Li XL. Effects of garlic polysaccharide on alcoholic liver fibrosis and intestinal microflora in mice. Pharm Biol. 2018;56:325–332.
8. Tudu CK, Dutta T, Ghorai M, Biswas P, Samanta D, Oleksak P, et al. Traditional uses, phytochemistry, pharmacology and toxicology of garlic. Front Nutr. 2022;9:949554.
9. Shaikh FMR, Uzgare AS. A review on Terminalia catappa: A natural source of bioactive compounds. Int J Sci Res Biol Sci. 2025;12(6):56–62.
10. Podder MK, Hossain MM, Kabir SR, Asaduzzaman AKM, Hasan I. Antimicrobial, antioxidant and antiproliferative activities of a galactose-binding seed lectin from Manilkara zapota. Heliyon. 2024;2:e24592.
11. Capasso A. Antioxidant action and therapeutic efficacy of Allium sativum L. Molecules. 2013;18(1):690–700.
12. Čeryová N, Lidiková J, Pintér E, Šnirc M, Franková H, Ňorbová M, et al. Polyphenol and flavonoid content and antioxidant activity of garlic cultivars. J Microbiol Biotechnol Food Sci. 2023;13(1):e9668.
13. Herrera-Calderon O, Chacaltana-Ramos LJ, Huayanca-Gutiérrez IC, Algarni MA, Alqarni M, Batiha GE. Chemical constituents and antioxidant activity of garlic essential oil. Antioxidants. 2021;10(11):1844.
14. Rahman MM, Fazlic V, Saad NW. Antioxidant properties of raw garlic extract. Int Food Res J. 2012;19(2):589–591.
15. Hernández-Montesinos IY, Carreón-Delgado DF, Ocaranza-Sánchez E, Ochoa-Velasco CE, Suárez-Jacobo Á, Ramírez-López C. Garlic peel extracts as antioxidant and antimicrobial agents. Int J Food Sci Technol. 2023;58(12):6794–6805.
16. Singh V, Kumar R. Phytochemical analysis and antioxidant activity of Allium sativum. Int J Life Sci Sci Res. 2017;3(6):1451–1458.
17. Monika M, Dua A, Sharma S, Gupta S, Mittal A. Comparative antioxidant activities of Allium sativum and 14th September 2026 ampeloprasum. J Food Sci. 2024;89:4250–4260.
18. Azizah Z, Yani P, Yett RD. Antioxidant activity ethanol extract of garlic and black garlic. Int J Res Rev. 2020;7(9):94.
19. Subroto E, Cahyana Y, Tensiska M, Filianty F, Lembong E, Wulandari E, et al. Bioactive compounds in garlic as antioxidants. Food Res. 2021;5(6):1–11.
20. Lu X, Ross CF, Powers JR, Aston DE, Rasco BA. Determination of phenolic content and antioxidant activity of garlic. J Agric Food Chem. 2011;59(10):5215–5221.
21. Iruo T. Antioxidative effects of garlic extract. Glob J Biotechnol Biol Res. 2025;1(1):1–5.
22. Shaikh FMR, Uzgare AS. Antimicrobial spectrum of lectins. Int J Sci Res Biol Sci. 2025;12(6):40–47.
23. Arreola R, Quintero-Fabián S, López-Roa RI, Flores-Gutiérrez EO, Reyes-Grajeda JP, Carrera-Quintanar L, et al. Immunomodulation and anti-inflammatory effects of garlic compounds. J Immunol Res. 2015;2015:401630.
24. Savira M, Sari DK, Machrina Y, Widjaja SS, Unitly AJA, Ilyas S, et al. Anti-inflammatory action of garlic extract in smoker rat model. Med Arch. 2023;77(3):178–182.
25. Khan AM, Sharif MA, Salekeen R, Rahman MH, Mahmud S, Biswas P, et al. Garlic bioactivity against inflammopathies. J Herb Med Pharmacol. 2023;12(2):283–298.
26. Lee DY, Li H, Ryu JH. Anti-inflammatory activity of sulfur compounds from garlic. J Med Food. 2012;15(11).
27. Taghizadeh Rabe SZ, Ghazanfari T, Siadat Z, Rastin M, Taghizadeh Rabe SZ, Mahmoudi M. Anti-inflammatory effect of garlic protein. Immunopharmacol Immunotoxicol. 2015;37(2):158–164.
28. Hodge G, Hodge S, Han P. Garlic suppresses leukocyte inflammatory cytokine production. Cytometry. 2002;48(4):209–215.
29. Egen-Schwind CE, Eckard R, Kemper FH. Metabolism of garlic constituents in the isolated perfused rat liver. Planta Med. 1992 Aug;58(4):301–305. doi:10.1055/s-2006-961471. PMID: 1438588.
30. Sharifi-Rad J, Silva NCC, Jantwal A, Bhatt ID, Sharopov F, Cho WC, et al. Therapeutic potential of allicin-rich garlic preparations: Emphasis on clinical evidence toward upcoming drugs formulation. Appl Sci. 2019;9(24):5555. doi:10.3390/app9245555.
31. Lawson LD, Hunsaker SM. Allicin bioavailability and bioequivalence from garlic supplements and garlic foods. Nutrients. 2018;10(7):812. doi:10.3390/nu10070812. PMID: 29937536; PMCID: PMC6073756.
32. Bat-Chen W, Golan T, Peri I, Ludmer Z, Schwartz B. Allicin purified from fresh garlic cloves induces

apoptosis in colon cancer cells via Nrf2. Nutr Cancer. 2010;62(7):947–957. doi:10.1080/01635581.2010.509837. PMID: 20924970.
33. Mandour YM, Refaat E, Hassanein HD. Anticancer activity and phytochemical investigation of Citrullus colocynthis. Sci Rep. 2023;13:20038.
34. Seki T, Hosono T, Suda S, Kimura K, Ariga T. Anticancer property of allyl sulfides from garlic. J Food Drug Anal. 2012;20:49.
35. Thomson M, Ali M. Garlic as an anticancer agent. Curr Cancer Drug Targets. 2003;3(1):67–81.
36. Isbilen O, Volkan E. Anticancer activities of garlic against breast cancer cell lines. Cyprus J Med Sci. 2020;5(4):305–312.
37. Shaban AM, Hammouda O, Abou Ghazala L, Raslan M, El-Magd MA. Garlic extract inhibits cancer cell viability. Res Article. 2018;8(9).
38. Babu BC, Sunil A, Mukunda A, Pynadath MK, Mohan A, Aswathy A. Anti-cancer potency of garlic extract. Oral Maxillofac Pathol J. 2020;11(1):11–15.
39. Chepuri K, Bhukya L, Chittepu P, Vadakavila G, Kathuroju H. Phytochemical characterization and anticancer potential of garlic extract. South Asian J Environ Biol Sci. 2023;14(5):220–225.
40. Özkan İ, Koçak P, Yıldırım M, Ünsal N, Yılmaz H, Telci D, et al. Garlic-derived vesicles inhibit cancer cell proliferation. Sci Rep. 2021;11:14773.
41. Islam MS, Kusumoto Y, Al-Mamun MA. Cytotoxicity and cancer cell killing efficacy of garlic extract. J Sci Res. 2011;3(2):375–382.
42. Shaikh FMR, Uzgare AS. Antimicrobial efficacy of Eleusine coracana. J Adv Acad Funct Res. 2025;3(12):468–474.
43. Bhatwalkar SB, Mondal R, Krishna SBN, Adam JK, Govender P, Anupam R. Antibacterial properties of garlic organosulfur compounds. Front Microbiol. 2021;12:613077.
44. Alirezaei S, Godarzi H, Moezi Ghadim N, Maheri A. Antimicrobial activity of garlic extract against oral bteria. J Res Dent Maxillofac Sci. 2019;4(4):17–22.
45. Tuyishime G, Abimana V, Ki DK, Seong JK, Iyyakkannu S, Se Chul C. Antibacterial activity of garlic nanoparticles. Appl Sci. 2022;12(7):3491.
46. Barbu IA, Ciorîță A, Carpa R, Moț AC, Butiuc-Keul A, Pârvu M. Phytochemical characterization and antimicrobial activity of 14th September 2026 extracts. Molecules. 2023;28(10):3980.
47. El-Azzouny MM, El-Demerdash AS, Seadawy HG, Abou-Khadra SH. Antimicrobial effect of garlic extract onpathogens. Cell Mol Biol. 2018;64(10):13.
48. Savitri NH, Indiastuti DN, Wahyunitasari MR. Inhibitory activity of garlic extract against bacteria. J Voc Health Stud. 2019;3(2):72–77.
49. Magryś A, Olender A, Tchórzewska D. Antibacterial properties of garlic against multidrug-resistant bacteria. Arch Microbiol. 2021;203(5):2257–2268.
50. Torpol K, Wiriyacharee P, Sriwattana S, Sangsuwan J, Prinyawiwatkul W. Antimicrobial activity of garlic essential oils. Int J Food Sci Technol. 2018;53(9):2119–2128.
51. Artawinata PC, Kim Y, Choi IY, Park MK. Antibacterial activity and mechanism of garlic extracts. J Microbiol Biotechnol. 2025;e2410035.
52. Sharma S, Raj K, Riyaz M, Singh DD. Antimicrobial studies on garlic lectin. Probiotics Antimicrob Proteins. 2023;15(6):1501–1512.
53. Clark-Montoya I, Terán-Figueroa Y, de Loera D, Gaytán-Hernández D, Alegría-Torres JA, Milán-Segovia RC. Anticoagulant effect of snow mountain garlic: In vitro evaluation of aqueous extract. Molecules. 2024;29(20):4958. doi:10.3390/molecules29204958.
54. Martins N, Petropoulos S, Ferreira ICFR. Chemical composition and bioactive compounds of garlic (Allium sativum L.) as affected by pre- and post-harvest conditions: A review. Food Chem. 2016 Nov 15;211:41–50. doi:10.1016/j.foodchem.2016.05.029.
55. Fowotade AA, Fowotade A, Enaibe BU, Avwioro GO. Evaluating toxicity profile of garlic (Allium sativum) on the liver, kidney and heart using Wistar rat model. Int J Trop Dis Health. 2017;26(2):1–12. doi:10.9734/IJTDH/2017/36282.
56. Lin YE, Lin MH, Yeh TY, Lai YS, Lu KH, Huang HS, et al. Genotoxicity and 28-day repeated dose oral toxicity study of garlic essential oil in mice. J Tradit Complement Med. 2022;12(6):536–544. doi:10.1016/j.jtcme.2022.05.001. PMID: 36325240; PMCID: PMC9618392.
57. Lawal, B., Shittu, O. K., Oibiokpa, F. I., Mohammed, H., Umar, S. I., & Haruna, G. M. (2016). Antimicrobial evaluation, acute and sub-acute toxicity studies of Allium sativum. Journal of Acute Disease, 5(4), 296–301.
58. Kamal Z, Al-Amgad Z, Zigo F, Farkašová Z, Zigová M, Ahmad AM, et al. Heavy consumption of garlic (Allium sativum) exerts nephro- and pulmonary toxicity at maternal and embryonic level in albino rats. J Environ Sci Health B. 2023:776–788. doi:10.1080/09712119.2023.2282518.

Integrated Health Research Journal (IHRJ)

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

RESEARCH ARTICLE

Admission Morbidity Characteristics as Predictors of Hospital Length of Stay in Diabetic Patients: A Retrospective Study from Ghana

Kasim Abdulai[1]*, Ivan Addae-Mensah[1,2], Nathan Kumasenu Mensah[2], Sylvester Ofosu-Gyeabour[3], Nana Adjoa Sarkwa[1], Theodora Egbenya[1]

[1] Translational Nutrition Research Group, Department of Clinical Nutrition and Dietetics, University of Cape Coast, Cape Coast, Ghana | [2] Department of Population and Health, Faculty of Social Sciences, University of Cape Coast, Cape Coast, Ghana | [3] Department of Health Information Management, School of Allied Health Sciences, University of Cape Coast, Cape Coast, Ghana | [4] Faculty of Allied Health Sciences, KAAF University College, Kasoa, Ghana

*Correspondence should be addressed to Kasim Abdulai (email: kasim.abdulai@ucc.edu.gh)

Abstract

Background: Length of hospital stay (LOS) is a critical indicator of healthcare quality, and predicting it can help identify high-risk patients and inform early interventions to improve outcomes and reduce costs.

Objective: This study aimed to investigate the relationship between admission morbidity characteristics and LOS in diabetic patients.

Methods: A retrospective analysis of medical records from January 2022 to January 2023 was conducted at the Cape Coast Teaching Hospital. A sampling method was employed to select 247 diabetic patient records, which were included in the final analysis. Quantitative data analysis was performed using SPSS version 25.

Results: The study included 247 diabetic patients, with 56.2% males and a mean age of 50.89 ± 5.09 years. The average length of stay (LOS) was 3.34 ± 0.5 days. Bivariate analysis showed that HbA1C levels ($r = 0.320$, $p < 0.001$) and the presence of Diabetes Mellitus (DM) complications ($r = 0.253$, $p < 0.001$) were significant positive predictors of LOS. A multiple linear regression model confirmed that HbA1C ($r = 0.320$, $p < 0.001$) and DM complications (Standardized beta = 0.215, $p < 0.001$) were the only independent predictors of LOS, explaining 18.5% of the variance. Other factors, including gender, age, type of diabetes, BMI, and comorbidities, showed no significant impact on LOS.

Conclusion: These findings suggest that healthcare providers can use admission morbidity characteristics to identify high-risk diabetic patients and allocate resources effectively to improve patient care and hospital management. Further research is needed to validate these findings across diverse patient populations and healthcare settings.

Keywords: Electronic Health Record, Data Quality, eHealth, Health Data, Quality Healthcare

Citation: Abdulai K, Mensah IAA, Mensah NK, Ofosu-Gyeabour S, Sarkwa NA, Egbenya T. Admission morbidity characteristics as predictors of hospital length of stay in diabetic patients: a retrospective study from Ghana. Integrated Health Research Journal. 2026;3(2):11-21. https://doi.org/10.47963/42saq518

Received 29th October 2025; **Accepted** 12th May 2026; **Published** 14th September 2026.

Introduction

Hospital length of stay (LOS) and morbidity are key indicators of patient experience and healthcare system performance worldwide. Globally, patients with chronic conditions face varied hospital stays that can affect both their quality of life and overall healthcare costs [1,2]. For instance, among OECD nations, average LOS differs substantially, from less than five days in countries such as Mexico and Turkey to as high as 18.5 days in Japan, reflecting variations in surgical techniques, discharge

policies, and healthcare system structures [3,4]. These disparities emphasize the importance of correlating morbidity with LOS, as prolonged stays often signal higher patient risk, greater resource use, and potential gaps in care.

Diabetes, particularly in its hypoglycemic state, is a significant metabolic condition linked to high morbidity, mortality, and healthcare resource use [5]. The prevalence of diabetes continues to rise, exacerbated by fast food consumption and demanding lifestyles, which hinder healthy food choices [6]. According to the International Diabetes Federation (IDF) Diabetes Atlas, 11th edition (2025), approximately 24.6 million adults aged 20-79 years in Africa are living with diabetes, representing a continued upward trajectory in disease burden across the continent. An additional 56 million adults in the same age bracket have impaired glucose tolerance (IGT), placing them at high risk for future diabetes development. Notably, approximately 15 million people with diabetes remain undiagnosed in Africa, with diabetes-related deaths estimated at 450,000 annually [7]. The annual healthcare expenditure for people with diabetes in Africa has risen to approximately 15 billion USD. In West Africa specifically, an estimated 135 million adults are living with diabetes [7]. In Ghana, national estimates suggest that over 4.5 million adults have been diagnosed with diabetes as of 2024, reflecting a steady increase over recent years [7,8]. A systematic review and meta-analysis conducted in the Ashanti region reported a diabetes prevalence of 3.8% (163,000 individuals) among adults as of 2021 [9]. Because diabetes is a chronic condition, it requires regular follow-up and can necessitate prolonged hospital stays, particularly when suboptimal management leads to associated complications.

Hospital stays vary in duration; any stay exceeding thirty days is classified as long and is a significant factor in the cost of healthcare, and it can also have a negative impact on the patient's quality of life [10]. A shorter stay typically reduces discharge expenses and sends patients to outpatient treatment status, which is typically less expensive than inpatient care, although this can diminish the patient's comfort and recovery, ultimately contributing to negative health outcomes [11]. In 2009, OECD countries saw average hospital stays under five days in Mexico (3.9), Turkey (4.3), Israel (4.5), Denmark (4.8), and Norway (4.6), while Japan recorded the longest at 18.5 days and Korea 14.6 days, against an OECD mean of seven days, a decrease from 8.2 days in 2000 to 7.2 days in 2009. The decrease can be attributed to a number of variables, such as the use of less invasive surgical techniques, modifications to hospital payment policies, and an expansion of early discharge programs that allow patients to receive follow-up treatment in the comfort of their own homes [11,12]. The average length of stay was 3.6 days; however, there were variations depending on the patient's age, sex, the hospital's geographic location, and the payer of their medical costs [13–15]. Most admissions were medically driven, reflecting a high burden of chronic illnesses, particularly among older adults, who not only had the longest average stay (5.2 days) but also comprised 26.7% of all admissions [14].

Managing the onset and progression of Type 1 diabetes and its related complications, like neuropathy, blindness, and cardiovascular and kidney diseases is essential despite the fact that treating the condition can be expensive, complicated, and time-consuming [16,17]. Ramchandani et al. (2000) argued that adhering to a demanding treatment regimen and managing the disease can disrupt patients' financial, social, and emotional well-being, ultimately lowering their quality of life [18]. Therefore, it is essential to investigate the length of stay in hospital for patients with type 1 diabetes, as it can have a significant impact on their overall well-being and quality of life.

Several factors contribute to the length of hospital stay (LOS), including patients' socio-demographic characteristics such as age, gender, living conditions, income level, health issues, and systemic factors. Patients who require intensive levels of care are more likely to experience extended hospitalizations [19,20]. In the Ghanaian context, common reasons for admission include conditions including diabetes mellitus, hypertension, pneumonia, stroke, sepsis, chronic kidney and liver diseases, and immunosuppression from causes such as HIV infection [21-24]. These conditions can influence LOS based on their pathophysiology and severity, potentially increasing or decreasing the duration of hospitalization. Diabetes, in particular, is associated with both acute and chronic complications, leading to frequent hospital admissions [25]. A review in Australia found that diabetes accounted for one out of every 25 hospitalizations between 2009 and 2010, with diabetic patients experiencing longer average LOS compared to non-diabetic patients [26,27]. Additionally, Chakraborty et al. asserted that comprehensive in-hospital interventions for individuals with type 2 diabetes mellitus have been effective in reducing LOS. Therefore, this study aimed to investigate the relationship between admission morbidity characteristics (including glycemic control, complications, comorbidities, and laboratory parameters) and length of hospital stay among diabetic patients at the Cape Coast Teaching Hospital, Ghana.

Materials and Methods

Study Design

This is a retrospective cross-sectional study assessing people living with diabetes who have attended the Cape Coast Teaching Hospital. This method was employed because it allows for a cost-effective and efficient analysis of existing clinical data, which is crucial given the limited resources and the availability of detailed hospital records. Data was obtained using a standardized data extraction sheet from the immediate past year (January 2022 to January 2023) to make the study more viable and current.

Study Site

The Cape Coast Teaching Hospital (CCTH), formerly the Central Regional Hospital, serves as the referral center for Ghana's Central Region. We chose this site due to its role as a major referral center in Ghana, which provides a representative sample of diabetic patients in the region. CCTH's Medical Department comprises separate male and female wards for patients admitted with medical illnesses, comorbidities, and related needs. Participants were people living with diabetes aged between 18 years and above.

Study Population

People with diabetes aged greater than 18 years who have attended the diabetic clinic at the Cape Coast Teaching Hospital make up the study population. To be included in the study, participants had to be in-patients. The age range was selected to accurately represent people with both types of diabetes i.e., Type 1 diabetes (T1DM) and Type 2 diabetes (T2DM). This study did not include pregnant women with gestational diabetes because of the uncertainty that the condition will progress and become chronic even after pregnancy.

Sample and Sampling Procedure

A two-stage sampling method was employed. First, purposive sampling was used to identify eligible diabetic patient records from the hospital database for the period January 2022 to January 2023 based on inclusion criteria. Second, from this eligible pool, records were randomly selected using a computer-generated random number sequence until the target sample size was achieved. The sample size was determined using $n = (Z^2 \times p \times (1-p)) / d^2$, where Z (1.96) corresponds to a 95% confidence level, p is the estimated risk proportion, and d is the margin of error [28]. Given the unknown prevalence of diabetes among adults (≥18 years) in Cape Coast, we conservatively estimated the population proportion (p) at 0.5. By setting the margin of error at 6.25% (d = 0.0625), the calculation resulted in a required sample size of $n = (1.96^2 \times 0.5 \times 0.5) / (0.0625)^2 \approx 245.8624$, which was rounded up to 246 participants, ensuring the desired level of precision at a 95% confidence interval [29]. The sample size also satisfies the minimum requirement for multiple linear regression, which recommends 10-15 events per predictor variable. With 10 predictor variables in our final model, the required minimum sample size is 100-150, which our sample of 247 exceeds.

Data Collection Instrument

The data extraction sheet was used as the research instrument. The extraction form was modified based on literature review and with the research objectives in mind. The adapted structured extraction sheet includes information on both sociodemographic data and characteristics listed below that have been established by research to be diagnostic characteristics of diabetes. This data extraction form was used to collect data on a variety of admission morbidity characteristics that may be associated with length of hospital stay in diabetic patients at Cape Coast Teaching Hospital. It was in six sections: 1. Sociodemographic characteristics 2. Type of diabetes 3. Admission clinical characteristics 4. Length of stay 5. Disease characteristics and 6. Anthropometric data. The data obtained included the patients' sociodemographic data, such as nutritional status (BMI) at the time of admission, comorbidities, blood glucose level, and duration of diabetes. The data was then analyzed to identify any associations between these characteristics and length of hospital stay. The data extraction sheet was pilot-tested on 20 randomly selected patient records (not included in the final analysis) to ensure completeness and clarity. Content validity was established through review by three senior researchers in clinical nutrition and health information management. Inter-rater reliability was assessed by having two independent extractors collect data from 30 records (kappa = 0.87, indicating strong agreement).

Data Collection Procedures

Adults with diabetes aged 18 years and above were eligible to participate in the study as per the inclusion criteria. Eligible participants were randomly selected from the hospital record list and enrolled in the study. Data was obtained from the hospital records of patients, specifically diabetic patients, using the current LHMS software and medical records.

The adapted extraction form was then applied to obtain the data needed. The extraction form was in 6 sections: a) the sociodemographic characteristics that included age, gender, and occupation; b) anthropometric assessment data that included height, weight, and BMI; c) clinical data from laboratory results such as blood glucose levels, serum creatinine, and serum urea nitrogen; d) length of stay; e) disease characteristics such as comorbidities and Diabetes Mellitus complications; and f) type of Diabetes Mellitus.

Data Analysis

The data was analyzed based on the objectives identified in the study. Data was entered and cleaned using Microsoft Excel 2019. IBM SPSS Version 25 was used to analyze the data obtained. For the purpose of determining a correlation between the morbidity characteristics and length of hospital stay, Pearson's correlation formula and a multiple linear regression model replicated from a previously conducted study were used. Categorical data were summarized by frequency and percentage; continuous data by mean and standard deviation ($x \pm SD$). Tables were used to present data. A significance level of 5% was employed to evaluate the level of significance of association among the categorical variables. The average length of stay was calculated on the entire population and on subgroups based on age, gender, type of diabetes, and presence of complications.

Data Management

After the data was obtained, it was proofread to ensure there was no missing data and that all necessary data had been obtained. This proofreading was repeated by all researchers to ensure a high degree of accuracy or minimize errors. The data was then cleaned, entered, and analyzed using SPSS. The data was transformed into a soft copy and protected with a password on the principal and co-investigator's personal computers. Hard copies were submitted and kept in a safely locked cabinet at the Department of Clinical Nutrition and Dietetics, University of Cape Coast. Only researchers and supervisors involved in this study had access to the stored data. The data gathered will be kept for as long as the researchers deem necessary; this will be determined by the number of studies similar to our study conducted in the Cape Coast Metropolis. Possible disposal methods will include incinerating the hard copies and archiving the soft copies on the principal investigator's Google account and deleting the soft copies from the personal computers of the researchers in this study.

Ethical Considerations

Ethical approval for this study was granted by the Ethical Review Committee (ERC) of the Cape Coast Teaching Hospital (Reference/Identification: CCTHERC/EC/2022/194). In accordance with the Declaration of Helsinki, prospective authorities were informed about the study's objectives and significance. To ensure confidentiality and anonymity, each participant was assigned an ID number instead of their names to reduce the chances of tracing the participants. Data was also presented as aggregate data. The data collection process began after ethical clearance was sought. Authorities were informed of their right to withdraw data at any stage of the study if any violations of privacy are encountered. Consent was sought from the staff and authorities pending their approval to be part of the study.

Results

Descriptive Data

Socio-demographic information on the study participants is presented in Table 1. The study included 247 participants who were admitted as diabetic patients at the ward in the Cape Coast Teaching Hospital. Out of the 247 participants, 56.2% (138) were male and 43.8% (109) were female. The mean age of the participants was 50.89 ± 5.09 years, with 18 as the minimum and 65 as the maximum. The majority of the participants (35.6%) fell within the 50-59 age group, with the fewest (3.2%) coming from the 18-29 age group. With regards to their occupation status, 74.1 % (183) of the participants were in the working class or were employed, 23.9 % (59) were retired and 2% (5) were students.

Predictive Factors of Hospital Length of Stay

The maximum stay was 14 days, while the minimum stay was 0. For the study participants, the average stay was 3.34 ± 0.5 days. A stay of more than 30 days is typically considered to be a long length of stay. A short stay was defined in this study as a stay of less than a week, and a long stay was defined as more than a week because none of the study participants stayed for more than 15 days, and the average length of stay was roughly 3 days. This was done for the use of easier analysis, grouping, and to comply with the chi square assumption rule.

Although hospital stays exceeding 30 days are conventionally classified as prolonged hospitalization in the broader literature, this threshold is primarily derived from studies in high-income settings with different patient populations and healthcare delivery models [10]. In the context of the Cape Coast Teaching Hospital and similar resource-limited settings, where average LOS for uncomplicated diabetic admissions typically ranges from 2 to 5 days, a 7-day threshold represents a more clinically meaningful cutoff. This threshold is approximately double the mean LOS observed in our cohort (3.34 days) and aligns with local clinical consensus that stays beyond one week warrant case review for potential barriers to discharge, including poor glycemic response, development of nosocomial complications, or inadequate social support. Furthermore, the 7-day cutoff ensured adequate cell sizes for statistical comparisons, as only 12.6% (31/247) of patients had LOS exceeding 7 days, whereas applying a 30-day threshold would have resulted in zero patients meeting the criteria (maximum LOS = 14 days). This pragmatic approach has precedent in similar studies of diabetic patient outcomes in sub-Saharan African settings [30,31].

The results of our analysis revealed that age was not a significant predictor of LOS, with a correlation coefficient of 0.038 and a p-value of 0.554. This suggests that the age

Table 1: Socio-Demographic Characteristics of Diabetic Patients at the Cape Coast Teaching Hospital

Category	Frequency (n)	Percentage (%)
Age		
18–29	8	3.2%
30–39	27	11.6%
40–49	63	25.3%
50–59	88	35.6%
60–69	61	24.3%
Gender		
Male	138	56.2%
Female	109	43.8%
Occupation		
Unemployed	-	
Student	5	2.0%
Employed	183	74.1%
Retired	59	23.9%

Source: Field work (2023)

Table 2: Admission Morbidity Characteristics of the Study Participants

Category	Frequency (n)	Percentage (%)	Mean LOS	Standard Deviation
Type of DM				
T1DM	29	11.7	3.41	2.81
T2DM	218	88.3	3.33	2.16
HbA1c (%)				
5.7–6.4	135	54.7	4.45	2.18
6.5–7.9	101	40.8	3.27	2.19
>7.9	11	4.5	3.24	1.57
BMI (kg/m²)				
<18.5	5	2.0	2.10	1.43
18.5–24.9	20	8.1	2.95	1.79
25.0–29.9	183	74.1	3.27	1.50
≥30	39	15.8	3.91	2.34
Comorbidities				
Yes	142	57.4	3.41	2.20
No	105	42.6	3.26	2.31
BUN (mmol/L)				
<2.1	72	29.3	3.56	1.26
2.1–8.5	54	21.8	8.50	1.82
>8.5	121	48.9	6.00	1.21
SCL (µmol/L)				
<0.6	201	81.4	3.70	2.10
0.6–12	31	12.6	3.81	2.59
>12	15	6.0	4.10	2.14
DM Complications				
Yes	16	6.5	5.50	1.89
No	231	93.5	3.19	2.19

SCL, Serum Creatinine Level; BUN, Blood Urea Nitrogen; HBA1C, Glycated Hemoglobin; BMI, Body Mass Index; T1DM, Type 1 Diabetes Mellitus; T2DM, Type 2 Diabetes Mellitus. The low documented prevalence of DM complications (6.5%) likely reflects under-ascertainment in medical records rather than true population characteristics, as discussed in the limitations section. This figure should be interpreted as the rate of recorded complications at admission, recognizing potential documentation gaps.
Source: Field work (2023)

of patients does not have a significant impact on their length of stay in hospital.

In contrast, gender was not found to have a statistically significant correlation with LOS, with a correlation coefficient of 0.613 and a p-value of 0.283. This p-value indicates that no statistically significant difference in LOS between males and females was detected in this study. While some previous studies have reported gender disparities in healthcare outcomes, our findings did not support this.

The type of diabetes mellitus (DM) was also investigated as a potential predictor of LOS. However, our analysis revealed that the type of Diabetes Mellitus was not significantly correlated with LOS, with a correlation coefficient of -0.011 and a p-value of 0.859. This suggests that the type of Diabetes Mellitus does not have a significant impact on LOS.

On the other hand, HbA1C levels were found to have a significant positive correlation with LOS, with a correlation coefficient of 0.320 and a p-value of <0.001. This indicates that patients with higher HbA1C levels tend to have longer stays in hospitals. This finding is consistent with previous studies that have reported a positive correlation between HbA1C levels and hospitalization rates.

Body mass index (BMI) was also investigated as a potential predictor of LOS. Our analysis revealed a weak positive correlation between BMI and LOS, with a correlation coefficient of 0.122 and a p-value of 0.055. Although this correlation was not statistically significant, it suggests that patients with higher BMIs may tend to have longer stays in hospitals.

Occupation was also examined as a potential predictor of LOS. Our analysis revealed a weak positive correlation between occupation and LOS, with a correlation coefficient of 0.061 and a p-value of 0.343. This correlation was not statistically significant, suggesting that occupation does not have a significant impact on LOS.

Comorbidities, which are the presence of one or more additional diseases or conditions, were also investigated as a potential predictor of LOS. Our analysis revealed that comorbidities were not significantly correlated with LOS, with a correlation coefficient of -0.033 and a p-value of 0.602. This suggests that the presence of comorbidities does not have a significant impact on LOS.

Blood urea nitrogen (BUN) levels were also examined as a potential predictor of LOS. Our analysis revealed a weak negative correlation between BUN levels and LOS, with a correlation coefficient of -0.028 and a p-value of 0.663. This correlation was not statistically significant,

Table 3: Association between Length of Hospital Stay and Other Variables

Variable	Coefficient (r)	Pearson Chi Square p-value
Age	0.038.	0.554
Gender	0.061	0.283
Occupation	-0.061	0.343
Type of DM	-0.011	0.859
HbA1c	0.320	0.000
BMI	0.122	0.055
BUN	-0.028	0.663
SCL	-0.048	0.454
Comorbidities	-0.033	0.602
DM Complications	-0.253	0.000

Source: Field work (2023)

suggesting that BUN levels do not have a significant impact on LOS.

Creatinine levels were also investigated as a potential predictor of LOS. Our analysis revealed a weak negative correlation between creatinine levels and LOS, with a correlation coefficient of -0.048 and a p-value of 0.454. This correlation was not statistically significant, suggesting that creatinine levels do not have a significant impact on LOS.

Finally, Diabetes Mellitus complications were examined as a potential predictor of LOS. Our analysis revealed a significant positive correlation between Diabetes Mellitus complications and LOS, with a correlation coefficient of 0.253 and a p-value of < 0.001 (Table 3). This suggests that patients with more recorded Diabetes Mellitus complications tend to have longer stays in the hospital. This finding is clinically expected and is supported by our descriptive data (Table 2), which shows that patients with complications had a longer mean LOS (5.50 days) compared to those without (3.19 days).

Our bivariate analysis found that HbA1C levels and Diabetes Mellitus complications are significant predictors of Length of Stay in hospitals.

Comparison of LOS between diabetes types revealed no statistically significant difference. Patients with Type 1 Diabetes Mellitus (n=29, 11.7%) had a mean LOS of 3.41 ± 2.81 days, while those with Type 2 Diabetes Mellitus (n=218, 88.3%) had a mean LOS of 3.33 ± 2.16 days (t = 0.174, p = 0.862). Among the 16 patients (6.5%) with documented DM complications, the distribution and associated LOS were as follows: neuropathy (n=7, mean LOS 4.9 days), nephropathy (n=5, mean LOS 6.2 days), retinopathy (n=3, mean LOS 5.0 days), and multiple complications (n=1, LOS 8.0 days).

Table 3 shows the association from the Pearson correlation calculation. Multivariate regression analysis is also shown in this table.

Multiple Linear Regression Analysis

To identify the independent predictors of LOS and control for confounding variables, a multiple linear regression analysis was performed, as stated in the methods [8]. The model included all variables from the bivariate analysis (Age, Gender, Occupation, Type of DM, HbA1C, BMI, BUN, SCL, Comorbidities, and DM Complications) as predictors for the continuous LOS variable.

The overall model was statistically significant ($F(10, 236) = 5.34$, $p < 0.001$) and explained 18.5% of the total variance in LOS ($R^2 = 0.185$, Adjusted $R^2 = 0.150$). This modest explanatory power suggests that while HbA1c and DM complications are significant predictors, the majority of variance in LOS is attributable to other unmeasured factors.

As shown in Table 4, only two variables emerged as independent predictors of LOS: HbA1C levels (Standardized beta = 0.289, $p < 0.001$) and the presence of DM complications (Standardized beta = 0.215, $p < 0.001$). This indicates that even after controlling for all other factors, poorer glycemic control and the presence of complications at admission are significantly associated with a longer hospital stay. The other variables, including BMI (which was borderline in the bivariate analysis), age, gender, and comorbidities, were not significant predictors in the multivariate model.

Discussion

In our study admissions of patients with diabetes revealed that males constituted a higher proportion at 56.2%, in contrast to females, who represented 43.8%. This observation is consistent with various studies highlighting a greater prevalence of diabetes among men. For instance, research by Elisabetta et al. reported that roughly 73% of hospital admissions for diabetes were males, while females accounted for only 27% [32]. Similarly, a study by Blandine et al. found that male patients with diabetes had a higher admission rate at 63.5% compared to their female counterparts [33]. One possible explanation is that men may have a higher risk of developing diabetes due to differences in body composition, hormone levels, and lifestyle factors such as smoking and alcohol consumption, which are more prevalent among men. Moreover, a substantial portion of the participants (74.1%) belonged to the working class. This trend may be attributed to the fact that working-class individuals, especially those in high-stress jobs with long hours, often have limited opportunities for physical activity and may adopt unhealthy eating habits, both of which are risk factors for diabetes. According to Surabhi et al., heightened work stress, as evidenced by an effort-reward imbalance, is linked to increased diabetes distress in employed individuals with type 2 diabetes mellitus, adversely affecting their diabetes management [34].

The highest prevalence of diabetic patients was observed in the 50-59 age group, accounting for 35.6%. This aligns with the established understanding that the risk of developing type 2 diabetes rises with age, particularly after

Table 4: Multiple Linear Regression Predicting Hospital Length of Stay

Variable	Unstandardized Coefficient (B)	95% CI for B	Std. Error	Standardized Coefficient (β)	t	p-value
(Constant)	1.104	-0.54 to 2.749	0.835		1.322	0.187
Age	0.021	-0.016 to 0.058	0.019	0.071	1.109	0.269
Gender	0.098	-0.434 to 0.630	0.270	0.023	0.363	0.717
Occupation	-0.045	-0.323 to 0.233	0.141	-0.020	-0.319	0.750
Type of DM	-0.153	-1.014 to 0.708	0.439	-0.022	-0.349	0.727
HbA1c	0.402	0.199 to 0.605	0.103	0.289	3.901	<0.001
BMI	0.068	-0.009 to 0.145	0.039	0.111	1.745	0.082
BUN	0.008	-0.022 to 0.038	0.015	0.034	0.530	0.596
SCL	-0.019	-0.074 to 0.036	0.028	-0.043	-0.671	0.503
Comorbidities	-0.031	-0.571 to 0.509	0.274	-0.007	-0.113	0.910
DM Complications	1.216	0.468 to 1.964	0.380	0.215	3.198	0.001

$R^2 = 0.185$; Adjusted $R^2 = 0.150$; $F(10, 236) = 5.34$, $p < 0.001$.

45, as a result of diminished insulin sensitivity and heightened insulin resistance. Palak et al. further supports this, noting that the study confirms an increased risk with advancing age, highlighting those males aged 55–59 and females aged 65–69 exhibit the greatest likelihood of progression [35].

The average length of stay (LOS) among the study participants was 3.34 ± 0.5 days, with none of the participants staying longer than 15 days. This relatively short LOS could be attributed to the early discharge protocols or the management strategies employed at the hospital. However, it is important to note that the LOS is a critical factor in healthcare outcomes, as longer hospital stays are often associated with higher healthcare costs and an increased risk of hospital-acquired infections. Our study also investigated the relationship between length of stay (LOS) and various socio-demographic and clinical factors. Notably, while age did not emerge as a significant predictor of LOS, gender also did not show a statistically significant correlation with LOS ($p = 0.283$). This finding indicates no statistical difference in hospital stay between males and females in our cohort. Furthermore, HbA1C levels demonstrated a significant positive correlation with LOS ($r=0.320$, $p<0.001$), indicating that poor glycemic control on admission is a strong predictor of extended hospitalization. This is the most clinically significant finding of our study. It aligns with extensive research showing that hyperglycemia is linked to increased risk of infection, slower wound healing, and other complications that prolong hospital stays. Our finding that HbA1c levels predict LOS is consistent with studies from other African settings. For instance, a study in Ethiopia found a significant association between poor glycemic control and hospital outcomes in type 2 diabetes patients [30]. Similarly, a systematic review and meta-analysis of low- and middle-income countries, including those in West Africa, reported that poor glycemic control is a key predictor of increased morbidity and healthcare utilization [36]. Globally, these findings align with meta-analyses demonstrating that hyperglycemia on admission is a consistent predictor of longer hospital stays [37].

A key finding of this study, confirmed by both bivariate ($r = 0.253$) and multivariate (Standardized beta = 0.215) analyses, was the significant positive association between the presence of recorded DM complications and LOS. Patients with complications on admission had a mean stay of 5.50 days, compared to 3.19 days for those without. This finding is clinically intuitive and aligns with a large body of research. Complications such as diabetic ketoacidosis, severe infections, or renal impairment (indicated by the 48.9% of patients with high BUN levels) inherently require more intensive medical management, longer observation periods, and more complex interventions, all of which directly contribute to a longer hospital stay. This underscores that the presence of complications on admission is a robust marker for increased resource utilization and patient acuity.

Although our study did not find a significant statistical difference in LOS between genders, this contrasts with some existing literature. For instance, some studies suggest male patients may have worse glycemic control or a higher prevalence of complications, leading to longer stays [31]. Conversely, other research has found that the impact of diabetes on hospital outcomes may be more detrimental for women [Published 14th September 2026]. The lack of a significant finding in our cohort may be due to the relatively short average LOS (3.34 days) or other unmeasured confounding factors specific to our study population. This discrepancy highlights the need for further research into gender-specific healthcare needs among diabetic patients in Ghana.

The majority of our study participants (88.3%) were living with type 2 diabetes mellitus (T2DM), which is in line with global statistics showing that T2DM accounts for approximately 90-95% of all diabetes cases [39]. This high prevalence can be attributed to factors such as obesity, physical inactivity, and unhealthy diets. Furthermore, a significant proportion (74.1%) of the participants were overweight, which is a well-established risk factor for T2DM. Misma et al. reported similar findings, revealing that the prevalence of obesity among diabetic patients is significantly high, with 89.4% surpassing normal BMI standards, underscoring the elevated obesity rate in this population [40]. Obesity contributes to insulin resistance, leading to the development and progression of diabetes. Additionally, nearly half (48.9%) of our participants had blood urea nitrogen (BUN) levels greater than 8.5, indicating renal impairment which is a common complication of diabetes. This finding is supported by Mahmood et al. stating elevated BUN levels are indicative

of disrupted protein metabolism in renal failure, emphasizing their potential as a marker for renal dysfunction in diabetic patients [41].

Lastly, while the majority of our participants (93.5%) did not present with recorded DM complications on admission, 6.5% did have complications noted. This relatively low reported prevalence of complications warrants further investigation. It may reflect the study's focus on admission characteristics rather than lifetime prevalence, or it could indicate gaps in clinical documentation. Despite this low prevalence, the presence of complications was a significant predictor of LOS in our analysis.

Our analysis revealed no significant difference in LOS between T1DM and T2DM patients, a finding that contrasts with some studies suggesting longer stays for T1DM due to higher complication rates [42]. However, this may reflect the relatively small proportion of T1DM patients in our sample (11.7%) and the generally short overall LOS in our cohort. Sarfo-Kantanka et al. [29] similarly found no significant difference in hospitalization duration by diabetes type in their Ghanaian cohort [31], suggesting that local management protocols may attenuate type-specific differences.

The findings of our study have important implications for healthcare policy. The significant independent predictors of LOS, specifically HbA1C levels and DM complications, highlight the need for targeted interventions to improve diabetes management and reduce the burden on healthcare facilities. Policymakers should consider implementing programs that focus on early detection, effective glycemic control, and patient education to minimize complications and reduce hospitalization rates. Additionally, the gender disparities observed in our study suggest that gender-specific strategies may be necessary to address the unique needs of male and female diabetic patients.

Our study contributes to the existing body of research on diabetes and its complications by identifying key predictors of hospital length of stay. The significant correlation between HbA1C levels and LOS underscores the importance of glycemic control in managing diabetes. Future studies should investigate the factors driving these relationships and evaluate interventions to enhance outcomes for patients with diabetes. Moreover, the high prevalence of type 2 diabetes and obesity among our participants suggests that further studies are needed to explore the interplay between lifestyle factors, genetic predisposition, and diabetes risk in different populations [21-24].

A critical limitation of our study is the modest explanatory power of the regression model ($R^2 = 0.185$), indicating that 81.5% of the variance in LOS remains unaccounted for by unmeasured confounders such as diabetes duration, pre-admission glycemic control, illness severity at admission, primary admission diagnosis, and socioeconomic factors, all of which were inconsistently available in-patient records. The absence of these variables suggests that our identified predictors (HbA1c and complications) may be overestimates if correlated with unmeasured confounders or underestimates if measurement error attenuated the observed effects. Additionally, the documented complication rate in our cohort (6.5%) is substantially lower than the 30–65% reported in comparable sub-Saharan African studies [30,31], likely reflecting systematic under-ascertainment in medical records due to incomplete documentation, reliance on inpatient notes only, or variable coding practices. This under-ascertainment has two opposing implications: if the true complication rate is much higher, the observed effect size ($\beta = 0.215$) may be a conservative estimate because random under-reporting biases toward the null; conversely, the 16 identified patients may represent a higher-acuity subgroup, potentially inflating the mean LOS difference (5.50 vs. 3.19 days) if milder complications were preferentially missed. Future prospective studies should employ standardized complication screening protocols (e.g., foot examination, retinal screening, urine albumin) rather than relying solely on medical record documentation. A retrospective medical record audit with standardized chart abstraction guidelines would also help quantify the extent of under-documentation at CCTH and inform quality improvement efforts. These steps would more precisely quantify the independent contributions of glycemic control and complications to LOS.

Conclusion

This study identified poor glycemic control (as measured by HbA1c) and the presence of diabetes-related complications as independent predictors of hospital length of stay among diabetic patients at the Cape Coast Teaching Hospital. These findings provide actionable evidence for identifying high-risk patients upon admission. Healthcare providers can use admission HbA1c levels and complication status to stratify patients, allocate resources efficiently, and implement targeted early interventions for those at highest risk of prolonged hospitalization. The modest explanatory power of our model (18.5%) underscores that length of stay is multifactorial, highlighting the need for prospective studies incorporating broader clinical and social determinants of hospitalization outcomes.

Recommendations

Based on the study's findings, we recommend that CCTH implement a targeted glycemic control protocol, including mandatory diabetes educator consultations and structured follow-up for patients with high HbA1C levels (e.g., >7.9%), to address its strong correlation with longer LOS[19]. The finding that DM complications are a strong predictor of *longer* stays (mean LOS 5.50 days) warrants a review of care pathways for these high-risk patients. The

hospital should prioritize early and aggressive protocol-driven management of common complications to standardize treatment and potentially reduce LOS. Furthermore, the low documented prevalence (6.5%) of complications warrants an audit of clinical documentation practices to ensure all complications are accurately captured, as this figure seems low and may be impacting risk stratification[20]. Finally, patient education on glycemic self-management should be intensified, and the records department should implement regular staff training to ensure data accuracy and accessibility.

Declarations

Ethical Approval and Consent to Participate

Ethical approval was granted by the Ethical Review Committee (ERC) of the Cape Coast Teaching Hospital (Reference number: CCTHERC/EC/2022/194). Written informed consent was sought from all participants.

Competing interests

The authors declare that they have no competing interests.

Funding

No external funding was received for this study.

Consent for Publication

Not Applicable

Authors' contributions

Conceptualization– KA and IAM; Data Curation– SOG, IAM, KA, and TE; Formal Analysis– KA, IAM, NKM; Methodology- KA, IAM, NKM, NAS and TE; Project Administration– IAM, KA; Supervision– KA; Validation– KA, NKM, IAM and NAS; Visualization– KA, IAM, and SOG; Resources- KA, NAS, TE and IAM; Writing - original draft- KA, NAS, TE, and IAM; Writing-review and editing- KA, IAM, SOG, NKM, and NAS; Investigation- IAM, KA, TE, and NAS; Software- KA, IAM, SOG and NAS.

Authors' Information

KA is a Registered Dietitian, Senior Lecturer, and Researcher, serving as the Director of the Translational Nutrition Research Group, Department of Clinical Nutrition and Dietetics, University of Cape Coast. IAM is a Registered and Licensed Dietitian, Public Health Researcher, and Research Assistant with the Translational Nutrition Research Group at the Department of Clinical Nutrition and Dietetics, University of Cape Coast. NKM is a Senior Lecturer and Researcher with the Department of Health Information Management, University of Cape Coast. NAS is a Dietitian and Research Assistant at the Translational Nutrition Research Group, Department of Clinical Nutrition and Dietetics, University of Cape Coast. TE is a Dietitian affiliated with the Department of Clinical Nutrition and Dietetics, University of Cape Coast.

Acknowledgements

We thank the management of Cape Coast Teaching Hospital and Cape Coast Metropolitan Hospital for the support during data collection. We are grateful to all patients who participated in the study.

Data Availability Statement

The patient information data used to support the findings of this study are not publicly available due to restrictions imposed by the Ethics Review Committee of the Cape Coast Teaching Hospital to protect the privacy and confidentiality of study participants. Data may be made available upon reasonable request to the corresponding author, subject to approval by the Ethics Review Committee and in accordance with applicable data protection laws. Requests for data access should be directed to Dr. Kasim Abdulai at kasim.abdulai@ucc.edu.gh.

Disclosure

None of the article contents are under consideration for publication in any other journal or have been published in any journal. No portion of the text has been copied from other material in the literature (unless in quotation marks, with citation). We are aware that it is the author's responsibility to obtain permission for any figures or tables reproduced from any prior publications and to cover fully any costs involved. Such permission must be obtained prior to final acceptance.

Abbreviations

BMI: Body Mass Index, BUN: Blood Urea Nitrogen, CCTH: Cape Coast Teaching Hospital, DM: Diabetes Mellitus, ERC: Ethical Review Committee, HbA1c: Glycated Hemoglobin, IGT: Impaired Glucose Tolerance, LOS: Length of Stay, OECD: Organisation for Economic Co-operation and Development, SCL: Serum Creatinine Level, T1DM: Type 1 Diabetes Mellitus, T2DM: Type 2 Diabetes Mellitus

References

1. Lingsma HF, Bottle A, Middleton S, Kievit J, Steyerberg EW, Marang-van de Mheen PJ. Evaluation of hospital outcomes: the relation between length-of-stay, readmission, and mortality in a large international administrative database. BMC Health Serv Res. 2018;18(1):116. doi:10.1186/s12913-018-2916-1

2. Awad A, Bader–El–Den M, McNicholas J. Patient length of stay and mortality prediction: A survey.

Health Serv Manage Res. 2017;30(2):105-120. doi:10.1177/0951484817696212

3. Marfil-Garza BA, Belaunzarán-Zamudio PF, Gulias-Herrero A, et al. Risk factors associated with prolonged hospital length-of-stay: 18-year retrospective study of hospitalizations in a tertiary healthcare center in Mexico. PLOS ONE. 2018;13(11):e0207203. doi:10.1371/journal.pone.0207203

4. Rice T, Rosenau P, Unruh LY, Barnes AJ. Health Systems in Transition: USA, Second Edition. University of Toronto Press; 2021.

5. Pawaskar M, Iglay K, Witt EA, Engel SS, Rajpathak S. Impact of the severity of hypoglycemia on health - Related quality of life, productivity, resource use, and costs among US patients with type 2 diabetes. Journal of Diabetes and its Complications. 2018;32(5):451-457. doi:10.1016/j.jdiacomp.2018.01.012

6. Mozaffarian D. Dietary and policy priorities to reduce the global crises of obesity and diabetes. Nat Food. 2020;1(1):38-50. doi:10.1038/s43016-019-0013-1

7. IDF. IDF Diabetes Atlas 2025. Diabetes Atlas. 2025. Accessed May 3, 2026. https://diabetesatlas.org/resources/idf-diabetes-atlas-2025/

8. Kazibwe J, Gad M, Abassah-Konadu E, et al. The epidemiological and economic burden of diabetes in Ghana: A scoping review to inform health technology assessment. PLOS One Global Public Health. Published online 2024. doi:10.1371/journal.pgph.0001904

9. Katey D, Addo AA, Abass K, Morgan AK. Prevalence study of type 2 diabetes mellitus in the Ashanti region of Ghana: a systematic review of risk factors. Journal of Endocrinology, Metabolism and Diabetes of South Africa. 2022;27(3):3. Accessed March 29, 2025. https://www.ajol.info/index.php/jemdsa/article/view/245401

10. Kozyrskyj A, De Coster C, John PS. Long Stay Patients In Winnipeg Acute Care Hospitals. Healthcare Management Forum. 2002;15(4, Supplement):15-20. doi:10.1016/S0840-4704(10)60177-9

11. Kamoun M, Abdelkafi I, Ghorbel A. The Impact of Renewable Energy on Sustainable Growth: Evidence from a Panel of OECD Countries. J Knowl Econ. 2019;10(1):221-237. doi:10.1007/s13132-016-0440-2

12. Sharma GD, Tiwari AK, Erkut B, Mundi HS. Exploring the nexus between non-renewable and renewable energy consumptions and economic development: Evidence from panel estimations. Renewable and Sustainable Energy Reviews. 2021;146:111152. doi:10.1016/j.rser.2021.111152

13. Healthcare Cost and Utilization Project (HCUP). HCUP Facts and Figures: Statistics on Hospital-Based Care in the United States, 2009. Agency for Healthcare Research and Quality (US); 2011. Accessed March 29, 2025. http://www.ncbi.nlm.nih.gov/books/NBK91984/

14. Weiss AJ, Elixhauser A. Overview of Hospital Stays in the United States, 2012. In: Healthcare Cost and Utilization Project (HCUP) Statistical Briefs. Agency for Healthcare Research and Quality (US); 2006. Accessed March 29, 2025. http://www.ncbi.nlm.nih.gov/books/NBK259100/

15. Liang L, Moore B, Soni A. National Inpatient Hospital Costs: The Most Expensive Conditions by Payer, 2017. In: Healthcare Cost and Utilization Project (HCUP) Statistical Briefs. Agency for Healthcare Research and Quality (US); 2006. Accessed March 29, 2025. http://www.ncbi.nlm.nih.gov/books/NBK561141/

16. Nathan DM, Buse JB, Davidson MB, et al. Management of hyperglycaemia in type 2 diabetes: a consensus algorithm for the initiation and adjustment of therapy. Diabetologia. 2006;49(8):1711-1721. doi:10.1007/s00125-006-0316-2

17. Buse JB, Wexler DJ, Tsapas A, et al. 2019 Update to: Management of Hyperglycemia in Type 2 Diabetes, 2018. A Consensus Report by the American Diabetes Association (ADA) and the European Association for the Study of Diabetes (EASD). Diabetes Care. 2019;43(2):487-493. doi:10.2337/dci19-0066

18. Ramchandani P, Wiggs L, Webb V, Stores G. A systematic review of treatments for settling problems and night waking in young children. BMJ. 2000;320(7229):209-213. doi:10.1136/bmj.320.7229.209

19. Styrborn K, Thorslund M. 'Bed-blockers': Delayed discharge of hospital patients in a nationwide perspective in Sweden. Health Policy. 1993;26(2):155-170. doi:10.1016/0168-8510(93)90116-7

20. Holmås TH, Kamrul Islam M, Kjerstad E. Between two beds: inappropriately delayed discharges from hospitals. Int J Health Care Finance Econ. 2013;13(3):201-217. doi:10.1007/s10754-013-9135-4

21. Sarfo P, Keney G, Achampong EK. A Retrospective Study of the Average Length of Hospital Stay of Patients on the Medical Wards in the Cape Coast Teaching Hospital. Published online June 2017. Accessed March 30, 2025. http://ir.ucc.edu.gh/jspui/handle/123456789/5200

22. Cromarty J, Parikh S, Lim WK, Acharya S, Jackson TJ. Effects of hospital-acquired conditions on length of stay for patients with diabetes. Internal Medicine Journal. 2014;44(11):1109-1116. doi:10.1111/imj.12538

23. Comino EJ, Harris MF, Islam MF, et al. Impact of diabetes on hospital admission and length of stay among a general population aged 45 year or more: a record linkage study. BMC Health Serv Res. 2015;15(1):12. doi:10.1186/s12913-014-0666-2

24. Gemeda TT, Gandile AU, Bikamo DS. HIV/AIDS knowledge, attitude and practice among Dilla University Students, Ethiopia. African Journal of Reproductive Health. 2017;21(3):3. doi:10.29063/ajrh2017/v21i3.4

25. Verma JP, Verma P. Introduction to Sample Size Determination. In: Verma JP, Verma P, eds. Determining Sample Size and Power in Research Studies: A Manual for Researchers. Springer; 2020:1-7. doi:10.1007/978-981-15-5204-5_1

26. Gebeyaw ED, Lema GD. Gender based difference in glycemic control and diabetes related chronic complications among type 2 diabetic patients in Debre Berhan city public hospitals. Metabol Open. 2025;25:100349. doi:10.1016/j.metop.2025.100349

27. Sarfo-Kantanka O, Sarfo FS, Ansah EO, Eghan B, Ayisi-Boateng NK, Acheamfour-Akowuah E. Secular Trends in Admissions and Mortality Rates from Diabetes Mellitus in the Central Belt of Ghana: A 31-Year Review. PLOS ONE. 2016;11(11):e0165905. doi:10.1371/journal.pone.0165905

28. Iacopi E, Pieruzzi L, Riitano N, Abbruzzese L, Goretti C, Piaggesi A. The Weakness of the Strong Sex: Differences Between Men and Women Affected by Diabetic Foot Disease. The International Journal of Lower Extremity Wounds. 2023;22(1):19-26. doi:10.1177/1534734620984604

29. Tramunt B, Smati S, Coudol S, et al. Sex disparities in COVID-19 outcomes of inpatients with diabetes: insights from the CORONADO study. European Journal of Endocrinology. 2021;185(2):299-311. doi:10.1530/EJE-21-0068

30. Gupta S, Solomon L, Jacob JJ. Diabetic distress and work-related stress among individuals with type 2 diabetes mellitus. | EBSCOhost. January 1, 2022. doi:10.5603/DK.a2022.0005

31. Sharma P, Dilip TR, Kulkarni A, Mishra US, Shejul Y. Risk of diabetes and expected years in life without diabetes among adults from an urban community in India: findings from a retrospective cohort. BMC Public Health. 2024;24(1):1048. doi:10.1186/s12889-024-18465-2

32. Azagew AW, Mekonnen CK, Lambie M, Shepherd T, Babatunde OO. Poor glycemic control and its predictors among people living with diabetes in low- and middle-income countries: a systematic review and meta-analysis. BMC Public Health. 2025;25(1). doi:10.1186/s12889-025-21828-y

33. Christensen MB, Gotfredsen A, Nørgaard K. Efficacy of basal-bolus insulin regimens in the inpatient management of non-critically ill patients with type 2 diabetes: A systematic review and meta-analysis. Diabetes Metabolism Research Review. Published online 2017. doi:10.1002/dmrr.2885

34. Narh CT, Der JB, Ofosu A, Blettner M, Wollschlaeger D. Trends in hospitalization of patients with diabetes mellitus in Ghana from 2012 to 2017 with predictions to 2032. Int Health. 2022;14(6):588-596. doi:10.1093/inthealth/ihab076

35. Sun H, Saeedi P, Karuranga S, et al. IDF Diabetes Atlas: Global, regional and country-level diabetes prevalence estimates for 2021 and projections for 2045. Diabetes Research and Clinical Practice. 2022;183:109119. doi:10.1016/j.diabres.2021.109119

36. Cruz MS, Silva ICF da, Miguez JSG, Machado MPR. Prevalence of hypertension and obesity in patients with type 2 Diabetes Mellitus. Braz J Pharm Sci. 2022;58:e20497. doi:https://doi.org/10.1590/s2175-97902022e20497

37. Mahmood R, Batool M, Majeed N, Shoukat Z, Qureshi AM, Shoaib M. Blood Urea Nitrogen (BUN) levels in renal failure: Unraveling the complex interplay of protein metabolism and kidney health. The Professional Medical Journal. 2024;31(03):03. doi:10.29309/TPMJ/2024.31.03.7908

38. Portillo-Canales S, Peters J, Francis-Morel G, Dhindsa S. Disparities in Outcomes and Health Care Utilization for Diabetic Ketoacidosis Among Patients With Type 1 and Type 2 Diabetes Mellitus: A 6-Year National Retrospective Cohort Study. Endocrine Practice. 2025;31(6):784-789. doi:10.1016/j.eprac.2025.04.002

Integrated Health Research Journal (IHRJ)

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

RESEARCH ARTICLE

Effect of Milk Fat Replacement with Sunflower, Corn, and Olive Oils on the Physicochemical, Microbiological, Energy, and Sensory Properties of Sudanese Braided Cheese

Khalid A. Gadein[1]*, Mariam Y. Eljak[1], Zoalnorien, H. Adam[1], Mohaned Abadallh sahl[1], Umsalama B. Eissa[2], Fatma H. Hamed[2], Emtithal Alamen Mahadi[2] and Fatima abdelhameed Hussein[3].

[1] Department of Nutrition and Food Technology, Faculty of Science and Technology, Omdurman Islamic University, Omdurman, Sudan. | [2] International university of Africa. Faculty of Productional Technology and Agricultural Processing. Khartoum State. Sudan. | [3] Department of Dairy Production, Faculty of Animal Production, University of Khartoum, PO Box 32, Khartoum North 13314, Sudan

*Correspondence should be addressed to Khalid A. Gadein (email: moroco254@gmail.com)

Abstract

Background: Rising consumer demand for reduced-fat, lower-calorie dairy products has intensified interest in replacing milk fat with vegetable oils that simultaneously maintain nutritional quality and sensory acceptance. This study investigated the influence of partial milk-fat replacement on Sudanese braided cheese.

Methods: Full-fat cow milk was mechanically separated to produce skim milk, which was reconstituted with 2, 3 or 4 % (w/w) sunflower (SO), corn (CO) or olive (OO) oil as a partial milk-fat replacer; an emulsifier (0.5 % Lacta 815) and standard starter culture were added. Cheeses were produced and analysed in triplicate for physicochemical (moisture, protein, fat, ash, acidity, total soluble solids), energy value, microbiological (total bacterial count, yeast/mould), and sensory properties using standard AOAC and ISO methods. Data were analysed by two-way ANOVA with Tukey's HSD post-hoc test ($P < 0.05$).

Results: Vegetable-oil cheeses exhibited significantly lower fat (24 → 9–15 %) and acidity (1.20 → 0.40–0.72 %) but higher ash and protein than full-fat control ($P < 0.05$). Calculated energy value dropped from 295 kcal 100 g^{-1} (control) to 215 kcal 100 g^{-1} (2 % OO), meeting the Codex Alimentarius criterion for 'reduced-energy' claims (≥ 25 % reduction, CXS 1-1985). Total bacterial counts were generally lower in treated samples at 2–3 % oil, while yeasts and moulds remained undetected. Sensory panellists awarded the highest flavour, colour and overall-acceptance scores to 2 % OO cheese ($P < 0.05$).

Conclusion: Cheese formulated with 2 % olive oil achieved lower calculated energy value, relatively high protein content, and favourable sensory acceptability compared with other reformulated samples. Further studies including fatty acid profiling, instrumental texture analysis, and shelf-life assessment are needed before commercial application.

Keywords: braided cheese; vegetable oil; fat replacement; bacterial load; sensory evaluation.

Citation: Gadein, KA, Eljak, MY, Adam, ZH, Abadallh sahl, M, Eissa, UB, Hamed, FH, Mahadi, EA, Hussein, FA. Effect of milk fat replacement with sunflower, corn, and olive oils on the physicochemical, microbiological, energy, and sensory properties of Sudanese braided cheese. Integrated Health Research Journal. 2026;3(2): 22-30. https://doi.org/10.47963/d5dxnn25

Received 16th January 2026 ; **Accepted** 25th July 2026; **Published** 14th September 2026.

Introduction

Fats and oils contribute to around 42% of the daily energy intake for most individuals. Lipids supply 9 kcal (37 kJ) of energy per gram, nearly double the amount provided by proteins and carbohydrates. Epidemiological studies have indicated that excessive consumption of fatty substances increases the risk of developing atherosclerosis,

cardiovascular diseases, and obesity. Saturated fatty acids, in particular, are associated with hypercholesterolemia and coronary heart disease [1]. Health experts and nutritionists recommend a diet focused on foods with lower energy density.

Saturated fat intake significantly increases the risk of obesity, atherosclerosis, coronary artery disease, and hypertension. This association has resulted in heightened consumer awareness and an increasing demand for low-fat food items, including cheese. Multiple authorities oversee the manufacturing of low-fat cheeses [2, 3].

Two kinds of low-fat cheese have been defined: less-fat cheese, containing 25% less fat than standard cheese, and reduced-fat cheese, which includes 50% less fat. Variations in composition have been noted among full-fat, reduced-fat, and low-fat Halloumi cheeses derived from bovine milk [3].

Recently, various fat substitutes have been developed to mitigate the risk of diet-related illnesses. However, many of these substitutes are incompatible with certain food systems[4].Research has demonstrated that using fat substitutes and replacers providing approximately 5 kcal/g can help lower overall calorie consumption by at least 10% [5].

Mudaffara cheese is a braided, semi-hard, and unripened cheese that hails from the Mediterranean region. It possesses a solid texture, a yellowish hue, and a somewhat acidic and saline taste, rendering it a favoured option among rural populations in Sudan. Globally comparable cheeses encompass Roumi and Rass cheese from Egypt, Romia cheese from the Middle East, and Mozzarella cheese [6].

The production of mudaffara cheese requires highly skilled and experienced artisans, and the process typically takes longer than that of soft white cheese. It is traditionally made from unpasteurized milk, either partially skimmed or a blend of skim milk with whole milk from cows, sheep, or goats [7].

While vegetable oil replacement has been demonstrated in soft and semi-hard cheeses such as Domiati, Halloumi, and Mozzarella, its application to Sudanese braided cheese (Mudaffara) remains unexplored, despite this cheese's distinct solid texture, unripened nature, and traditional unpasteurised milk base that preclude direct extrapolation from other systems. Furthermore, no study has directly compared sunflower, corn, and olive oils—which differ fundamentally in fatty acid profile (sunflower and corn are n-6 PUFA-rich; olive is MUFA- and polyphenol-dominant)—within a single cheese model, or defined the optimal concentration threshold (2–4% bracketing the minimum effective dose versus matrix disruption point). This gap is particularly acute for Sudan, where cardiovascular disease rates and saturated fat intake exceed WHO recommendations, yet no culturally appropriate, reduced-fat dairy alternative exists. This study therefore systematically evaluates oil type (SO, CO, and OO) and its concentration (2, 3, and 4%) effects on physicochemical, microbiological, energy, and sensory properties to identify an optimal formulation balancing nutritional improvement with quality retention.

Methods

Vegetable Oil

Virgin olive oil and corn oil were kindly supplied by the National Research Centre, Khartoum, Sudan. Refined, bleached, and deodorized sunflower oil (free from additives) was provided by Bitar Company for Oil, Khartoum Bahri, Sudan. A commercial stabilizer/emulsifier blend called Lacta 815, composed of gelatin, carrageenan, and diglycerides, was acquired from the National Research Centre in Khartoum, Sudan.

Milk

The full-cream milk (control sample) and skimmed cow's milk (treated samples) were obtained from Al Ghota Dairy Factory, Khartoum, Sudan. The baseline compositional profile of the raw full-fat milk was: fat 3.85 ± 0.12%, protein 3.42 ± 0.08%, lactose 4.65 ± 0.10%, ash 0.72 ± 0.03%, total solids 12.64 ± 0.15%, and pH 6.62 ± 0.04 (mean ± SD, n = 3). Skim milk was produced by mechanical separation of this same batch of full-fat milk, yielding skim milk with approximately 0.10 ± 0.02% fat.

Rennet sticks from Christen Hansen's laboratories in Copenhagen, Denmark, were obtained from the Ministry of Animal Resources, with one stick capable of coagulating 50 kg of milk. The starting culture was provided by Premier Food Product, Khartoum North, Sudan. Finely powdered sodium chloride (NaCl) was procured from the Omdurman Islamic University Laboratory.

Braided Cheese Manufacture

"Full-fat cow milk was mechanically separated using a laboratory separator to produce skim milk (~0.1% fat). The skim milk was divided into three separate groups and reconstituted with 2, 3, or 4% (w/w) vegetable oil (sunflower, corn, or olive) as a partial milk-fat replacer. A fourth group of unseparated full-fat milk served as control groups. Lacta 815 was used as an emulsifier at a concentration of 0.5%."

The milk (full cream for the control sample and fat-free with added oil for the treated samples) was heated to 40°C. An active starter culture (2% v/v) was incorporated into the milk and allowed to incubate for 15 minutes to facilitate acidity development (milk ripening period). The braided cheese was then produced using the methodology outlined by [8].

Chemical analysis of braided cheese types

All the fresh cheese samples were analyzed for acidity, TSS, protein, fat, and ash using standard [9].

Calculation of energy value

The gross energy content of each fresh cheese sample was estimated from the analytical composition by means of the Atwater general factors [10]:

- Protein = 4 kcal g^{-1}
- Fat (total) = 9 kcal g^{-1}
- Carbohydrate (by difference) = 4 kcal g^{-1}

Total carbohydrate was calculated as:
Carbohydrate (g 100 g^{-1}) = 100 – [moisture + protein + fat + ash].

Energy (kcal 100 g^{-1}) = (g protein × 4) + (g fat × 9) + (g carbohydrate × 4).

The experiment followed a 2 × 3 factorial arrangement with three independent replications (batches). Each batch represented an independent cheese-making run on a separate day. Data were analysed using two-way ANOVA with batch as a random blocking factor, followed by Tukey's HSD for pairwise comparisons.

Microbiological analysis

Total bacterial counts and yeast and mold counts were enumerated as described by [11].

Sensory evaluation

The sensory quality of braided cheese was evaluated by the ranking method described by [12].

Sensory evaluation was conducted by a panel of 25 trained judges from the Department of Nutrition and Food Technology, Omdurman Islamic University. Panellists underwent a standardized calibration session prior to the study and were required to achieve ≥ 80% concordance with reference scores to participate. A 5-point hedonic scale (1 = dislike extremely; 5 = like extremely) was used to evaluate four attributes: flavour, taste, colour, and overall acceptance. Samples were coded with three-digit random numbers and presented in a randomized order following a Williams Latin square design to balance carry-over effects. All evaluations were performed under blinded conditions; panellists were unaware of treatment identity. Samples were served at room temperature (22 ± 2°C) in identical opaque containers under neutral white lighting, with a 15-second palate-cleansing interval (distilled water, unsalted crackers) between samples. Each panellist evaluated all samples once per session across three independent sessions on separate days. The mean score for each attribute was calculated per treatment and subjected to statistical analysis.

Statistical Analysis

The experiment followed a completely randomized design (CRD) with a 2 × 3 factorial arrangement of treatments, comprising two independent variables: oil type (sunflower, corn, olive) at three levels and oil concentration (2%, 3%, 4%) at three levels, plus a full-fat control group. The experimental unit was explicitly defined as an independent cheese-making batch (n = 3 batches, each conducted on a separate day). We have also clarified that analytical determinations within each batch were performed in duplicate, with the mean used for statistical analysis. Data were analysed using two-way ANOVA (PROC GLM, SAS 9.4; SAS Institute, Inc., 2011) to evaluate main effects of oil type and concentration, and their interaction. Where significant interactions were detected ($P < 0.05$), simple effects were examined.

Tukey's Honestly Significant Difference (HSD) test was applied for pairwise mean comparisons to control the family-wise error rate. All analyses were performed at $\alpha = 0.05$. Assumptions of normality (Shapiro-Wilk test) and homogeneity of variances (Levene's test) were verified prior to ANOVA. The complete ANOVA summary, including F-values, degrees of freedom, and P-values for all main effects and interactions, is presented in Table S1 (Supplementary Material).

Results

Physicochemical characteristics of braided cheese

Table 1 illustrates the impact of substituting milk fat with vegetable oil on the physicochemical properties of braided cheese. The analysis revealed that all physicochemical characteristics of the cheese were significantly influenced ($P < 0.05$).

The findings showed significant differences ($P < 0.05$) in the total soluble solids (**TSS**) among the samples. Specifically, TSS decreased significantly ($P \leq 0.05$) as the oil content increased. The addition of 2% oil resulted in the highest TSS values, recorded as 70.0%, 66.15%, and 63.35% for (SO), (CO), and (OO), respectively. The control sample recorded a lower value (62.80) than treated samples in conc 2%.

These findings are consistent with [17], who noted that cheeses made with fat replacers, like whey protein concentrate (WPC), contained more moisture. This decrease in TSS indicated a reduction in curd syneresis during cheese production. It was proposed that fat replacers can directly bind water and disrupt the contraction of the casein matrix, thereby diminishing the impetus for water extraction from curd particles.

The reduction in total soluble solids (TSS) with increased oil concentration indicates better moisture retention, attributed to the hydrophilic and steric properties of the

emulsifier system and modified casein matrix. Carrageenan, present in Lacta 815, binds water through hydrogen bonding with casein micelles [15], forming a gel network that reduces syneresis. Replacing fat with vegetable oil disrupts casein–fat interactions, altering curd permeability. While full-fat cheeses form tighter gels, emulsified oils lead to a less contractile matrix with higher porosity. The study indicates a saturation threshold for emulsifiers: beyond 4% oil, excess can cause coalescence and phase separation, paradoxically increasing free moisture and reducing TSS further [16].

The study also observed a significant ($P \leq 0.05$) reduction in the **acidity** of cheese made with different types of vegetable oils compared to the control samples

In contrast, full-fat cheese exhibited increased acidity levels of 1.2%. The acidity levels of cheese containing 2% and 4% (SO), (CO), and (OO) ranged from 0.40 to 0.60%, 0.60 to 0.72%, and 0.44 to 0.60%, respectively. The control sample (full-fat control), however, recorded the highest acidity at 1.20%. These findings suggest that acidity levels are influenced by fat concentration, perhaps attributable to diminished lipolysis in defatted cheese and the resultant generation of free fatty acids. The These findings are consistent with [17], who determined that the acidity of low-fat cheese was inferior to that of full-fat cheese; however the difference lacked statistical significance. A reduction in the acid-degree value corresponding to diminished fat content has been noted in Cheddar cheese [18].

The reduction in titratable acidity in vegetable oil-treated cheeses, from 1.20% in control samples to 0.40–0.72% in treated cheeses, is attributed to various factors. The higher moisture content in treated cheeses dilutes lactic acid concentration [22], while reduced lipolytic activity in defatted systems limits the generation of free fatty acids that contribute to acidity. Furthermore, the buffering capacity is affected as vegetable oil emulsions alter casein micelle structures, leading to changes in pH buffering around the isoelectric point. Slightly higher acidity in corn oil samples may be due to their phospholipid content, which can foster minimal microbial lipolytic activity, although overall effects are minimal due to the refined oil used [23].

Furthermore, a significant ($P \leq 0.05$) decline in **protein** content was noted with increased oil content. The addition of 2% oil resulted in the highest protein values of 24.60%, 27.39%, and 27.39% for (SO), (CO), and (OO), respectively, higher than the value recorded by control sample 23.8%. These findings are consistent with [19], who observed that diminished moisture content and restricted physical alterations in proteins may influence the texture and flavour of cheese. Conversely, [20] indicated that elevated protein levels in low-fat cheese could improve the water-binding capacity of the cheese matrix and affect the rate of protein degradation, as evidenced by the concentrations of water-soluble nitrogen. Additionally, [21] noted that the reduction of fat content resulted in increased protein and decreased dry matter levels in low-fat cheeses. Adding fat substitutes to low-fat cheese makes it hold more water and taste better overall.

The study also showed that when oil levels went up, fat levels went down significantly ($P \leq 0.05$). The control sample had 24% fat, while the (SO), (CO), and (OO) samples had 15%, 13%, and 14.67% fat, respectively. The concentration of vegetable oils in the milk lowers the milk fat concentration, which in turn lowers the fat content in braided cheese.

The noted rise in protein levels in cheeses treated with vegetable oil (Table 1) is not only a result of fat reduction, but indicates significant changes in the structure of the casein matrix. Milk fat globules in full-fat cheese serve as structural fillers in the para-casein network, mechanically interfering with protein–protein interactions and forming a more porous, permeable matrix [24]. The substitution of milk fat with vegetable oils diminishes the presence of native fat globules, thereby alleviating steric hindrance and facilitating closer aggregation of casein micelles, resulting in a more compact protein network. The addition of vegetable oil droplets, stabilized by the emulsifier Lacta 815 (gelatin, carrageenan, diglycerides), creates heterogeneous inclusions in the casein matrix. These oil droplets, in contrast to the indigenous milk fat globules

Table 1: Physicochemical characteristics of Sudanese braided cheese formulated with different vegetable oils

	Oil %	Acidity (Mean ± SD)	Ash (Mean ± SD)	TSS (Mean ± SD)	Protein (Mean ± SD)	Fat (Mean ± SD)
Control (Full fat)	0%	$1.20^{c} \pm 0.200$	$2.35^{c} \pm 0.212$	$62.80^{c} \pm 1.979$	$23.80^{c} \pm 4.000$	$24.00^{a} \pm 1.000$
Sunflower oil	2%	$0.40^{d} \pm 0.100$	$2.50^{bc} \pm 0.070$	$70.00^{a} \pm 2.262$	$24.60^{bc} \pm 1.607$	$8.00^{d} \pm 1.000$
	3%	$0.60^{cd} \pm 0.200$	$2.50^{bc} \pm 0.424$	$55.40^{e} \pm 0.565$	$23.80^{c} \pm 2.000$	$10.67^{cd} \pm 0.577$
	4%	$0.60^{cd} \pm 0.300$	$2.55^{bc} \pm 0.070$	$64.50^{b} \pm 0.001$	$22.00^{c} \pm 2.000$	$15.00^{b} \pm 1.000$
Corn oil	2%	$0.60^{cd} \pm 0.200$	$2.60^{bc} \pm 0.001$	$66.15^{ab} \pm 1.060$	$27.39^{a} \pm 4.000$	$10.33^{cd} \pm 1.528$
	3%	$0.24^{e} \pm 0.040$	$2.65^{ab} \pm 0.212$	$48.65^{f} \pm 0.070$	$24.97^{bc} \pm 2.000$	$11.33^{cd} \pm 0.577$
	4%	$0.72^{bc} \pm 0.020$	$2.65^{ab} \pm 0.494$	$44.05^{f} \pm 1.202$	$21.40^{c} \pm 1.000$	$13.00^{bc} \pm 1.000$
Olive oil	2%	$0.44^{de} \pm 0.220$	$2.75^{a} \pm 0.070$	$63.35^{bc} \pm 0.784$	$27.39^{a} \pm 2.000$	$9.00^{d} \pm 1.000$
	3%	$0.40^{e} \pm 0.200$	$2.65^{ab} \pm 0.212$	$42.70^{f} \pm 1.555$	$19.00^{c} \pm 2.000$	$11.33^{cd} \pm 0.577$
	4%	$0.60^{cd} \pm 0.300$	$2.85^{a} \pm 0.070$	$44.95^{f} \pm 0.636$	$21.40^{c} \pm 1.000$	$14.67^{bc} \pm 0.577$

Two-way ANOVA: Oil type ($P < 0.001$), Oil concentration ($P < 0.001$), Type × Concentration interaction ($P < 0.01$) for all parameters. Mean values within each column with different superscript letters are significantly different by Tukey's HSD ($P < 0.05$). TSS=Total Soluble Solids

encased by the native milk fat globule membrane (MFGM), exhibit a deficiency in interfacial compatibility with casein, potentially undermining protein–fat interactions and resulting in localized matrix discontinuities [25].

The varying impacts of sunflower, corn, and olive oils on protein retention probably stem from differences in oil droplet size distribution and interfacial protein load, influenced by oil viscosity and fatty acid composition. Olive oil, possessing an elevated concentration of monounsaturated oleic acid (C18:1) and lesser amounts of surface-active polar lipids, is likely to create more stable emulsions with reduced droplet dimensions, hence enhancing incorporation into the casein matrix and minimizing serum protein loss during syneresis. In contrast, the increased presence of polyunsaturated sunflower and corn oils, abundant in linoleic acid (C18:2), tends to yield less stable emulsions characterized by larger droplets that are more susceptible to coalescence and phase separation during curd processing, which accounts for the marginally reduced protein values noted at elevated concentrations (4%) for these oils [26].

Finally, a slight but significant ($P \leq 0.05$) increase in ash content was observed with higher oil content. The control sample recorded the lowest ash content at 2.35%, while the addition of 4% oil resulted in the highest values of 2.55%, 2.65%, and 2.85% for (SO), (CO), and (OO), respectively. This increase in ash is unlikely to reflect direct mineral contribution from the vegetable oils, as refined sunflower, corn, and olive oils contain negligible ash (<0.01%). Instead, the observed differences in ash content may be related to variation in salt (NaCl) retention during brining, moisture content, or concentration of solids during cheese manufacture. Higher oil concentrations may alter the protein matrix structure, affecting salt penetration and water expulsion (syneresis), thereby concentrating the mineral fraction. Additionally, the emulsifier system (Lacta 815, containing carrageenan and diglycerides) may interact with cations, influencing ash distribution. These results are consistent with [27] who reported similar ash variations in soft cheese with fat replacers.

Similarly, [14] observed slight but significant differences ($P \leq 0.05$) in the ash content of soft cheese where fat was replaced with vegetable oils.

Energy value

Replacement of milk fat with vegetable oil produced a marked reduction in calculated energy content (Table 2). The full-fat control cheese had 295 kcal per 100 g, but the 2% olive oil and 2% sunflower oil treatments brought that down to 215 and 219 kcal per 100 g, respectively, a drop of 27%. The 3% and 4% oil levels only made small changes (208–212 kcal 100 g^{-1}) because the extra oil

Table 2. Calculated energy content of Sudanese braided cheese (mean ± SD, n = 3)

Treatment	Oil %	Protein (Mean ± SD)	Fat (Mean ± SD)	CHO (Mean ± SD)	Energy (kcal 100 g^{-1})	% Reduction vs. Control
Control (Full fat)	0%	$23.80^{c} \pm 4.000$	$24.00^{a} \pm 1.000$	12.65 ± 2.15^{a}	$295^{a} \pm 4.70$	–
Sunflower oil – 2%	2%	$24.60^{bc} \pm 1.607$	$8.00^{d} \pm 1.000$	34.90 ± 2.89^{b}	$219^{b} \pm 3.00$	25.8%
Sunflower oil – 3%	3%	$23.80^{c} \pm 2.000$	$10.67^{cd} \pm 0.577$	18.43 ± 1.85^{c}	$214^{b} \pm 6.00$	27.5%
Sunflower oil – 4%	4%	$22.00^{c} \pm 2.000$	$15.00^{b} \pm 1.000$	24.95 ± 1.85^{d}	$212^{b} \pm 8.05$	28.1%
Corn oil – 2%	2%	$27.39^{a} \pm 4.000$	$10.33^{cd} \pm 1.528$	25.73 ± 3.85^{d}	$218^{b} \pm 6.20$	26.1%
Corn oil – 3%	3%	$24.97^{b} \pm 2.000$	$11.33^{bc} \pm 0.577$	9.70 ± 1.85^{e}	$213^{b} \pm 3.40$	27.8%
Corn oil – 4%	4%	$21.40^{c} \pm 1.000$	$13.00^{bc} \pm 1.000$	7.00 ± 1.85^{e}	$211^{b} \pm 9.02$	28.5%
Olive oil – 2%	2%	$27.39^{a} \pm 2.000$	$9.00^{d} \pm 1.000$	23.21 ± 1.85^{d}	$215^{b} \pm 7.22$	27.1%
Olive oil – 3%	3%	$19.00^{d} \pm 2.000$	$11.33^{c} \pm 0.577$	9.72 ± 1.85^{e}	$210^{b} \pm 9.20$	28.8%

Two-way ANOVA: Oil type ($P < 0.001$), Oil concentration ($P < 0.001$), Type × Concentration interaction ($P < 0.01$) for all parameters. Mean values within each column with different superscript letters are significantly different by Tukey's HSD ($P < 0.05$).; CHO by diff = carbohydrate by difference [100 – (moisture + protein + fat + ash)].

Table 3. Microbial loads of defatted braided cheese with different vegetable oils (log^{10} CFU/g)

Treatment	Oil %	Total Bacterial Count	Mold and Yeast
Control	0%	5.23	ND
Sunflower oil	2%	1.21	ND
	3%	1.01	ND
	4%	1.15	ND
Corn oil	2%	4.30	ND
	3%	2.30	ND
	4%	4.13	ND
	2%	1.23	ND
	3%	3.18	ND
	4%	4.48	ND

ND = Not Detected. Detection limit: < 10 CFU/g (< 1.00 log_{10} CFU/g)

Table 4. Sensory evaluation of defatted braided cheese with differences vegetable oil

Treatment	Oil %	Flavor (Mean ± SD)	Taste (Mean ± SD)	Color (Mean ± SD)	Overall Acceptance (Mean ± SD)
Control (Full fat)	0%	$4.04^{ab} \pm 1.207$	$4.20^{ab} \pm 0.816$	$4.28^{ab} \pm 0.936$	$3.88^{ab} \pm 0.927$
Sunflower oil	2%	$3.92^{ab} \pm 0.997$	$3.52^{bc} \pm 1.122$	$4.60^{a} \pm 0.707$	$4.00^{ab} \pm 3.491$
Sunflower oil	3%	$3.92^{ab} \pm 1.274$	$4.12^{ab} \pm 1.121$	$4.20^{ab} \pm 1.331$	$4.12^{a} \pm 1.258$
Sunflower oil	4%	$3.00^{c} \pm 1.115$	$3.44^{c} \pm 1.092$	$3.20^{c} \pm 0.913$	$3.40^{bc} \pm 1.092$
Corn oil	2%	$3.24^{bc} \pm 0.663$	$3.08^{c} \pm 0.812$	$3.96^{bc} \pm 1.098$	$3.56^{bc} \pm 0.768$
Corn oil	3%	$3.64^{bc} \pm 1.128$	$3.76^{bc} \pm 1.320$	$3.04^{c} \pm 1.331$	$3.67^{bc} \pm 1.429$
Corn oil	4%	$3.24^{bc} \pm 1.319$	$3.08^{c} \pm 1.164$	$3.20^{c} \pm 1.136$	$3.28^{c} \pm 1.164$
Olive oil	2%	$4.20^{a} \pm 0.734$	$4.00^{ab} \pm 1.000$	$4.60^{a} \pm 0.707$	$4.24^{a} \pm 0.831$
Olive oil	3%	$3.28^{bc} \pm 1.424$	$3.44^{c} \pm 1.338$	$2.76^{d} \pm 1.491$	$3.68^{bc} \pm 1.224$
Olive oil	4%	$2.88^{c} \pm 1.242$	$2.96^{c} \pm 0.1293$	$2.84^{cd} \pm 1.200$	$2.80^{d} \pm 1.356$

Two-way ANOVA (Type I, sequential): Oil type × Concentration. Mean values within each column with different superscript letters are significantly different by Tukey's HSD ($P < 0.05$). n = 3 replicates.

pushed out more moisture instead of protein or available carbohydrates. The 2% olive-oil cheese meets the Codex Alimentarius standard for nutrient claims (CXS 1-1985, amended 2021), which defines 'reduced energy' as a minimum 25% reduction in energy value compared to the reference product (full-fat braided cheese), while the overall nutrient content remains equivalent or enhanced (higher protein density: 27.4 g 100 g^{-1}). These numbers back up what the consumer said in the Conclusion: braided cheese with 2% olive oil is a cheaper, lower-calorie option than the traditional full-fat version.

The 295 kcal 100 g^{-1} we got for full-fat braided cheese is the same as the 294–297 kcal 100 g^{-1} we found for full-fat Halloumi [3] and a little lower than the 310 kcal 100 g^{-1} we found for Iranian UF-feta [23]. This is because braided cheese has about 5% less fat and 2% more moisture than those types. After reducing the fat content by 25% with vegetable oil, our 215 kcal 100 g^{-1} is very close to the 210–220 kcal 100 g^{-1} found by [5] in Domiati cheese made with 2% jojoba oil. It is only slightly higher than the 205 kcal 100 g^{-1} predicted by the [18] model for Cheddar with a similar fat-to-dry-matter ratio.

When the oil content was raised from 2% to 4%, the energy drop was about 3% more, which is similar to the plateau that [17] found in Macedonian white-brined cheese. This is because adding more oil also decrease in the TSS content.

Microbiological analysis

The results indicate that total viable bacterial counts varied significantly cross treatments. At 2% and 3% oil concentrations, all vegetable oil treatments substantially reduced bacterial loads compared to the control (1.01–4.30 vs. 5.23 $\log_{10}$ CFU/g). The microbial loads of the treated cheese samples were slightly lower than those of the control samples. This reduction in bacterial counts may be attributed to antimicrobial properties and concentration-dependent lipid-matrix interactions. Vegetable oils, particularly sunflower and olive oils, contain bioactive compounds such as polyphenols, tocopherols, and free fatty acids that exhibit direct antimicrobial activity against common dairy spoilage and pathogenic bacteria. A similar trend was reported by [29] vegetable Oils which suppresses bacterial growth. These findings are consistent with the observations made by [29].

Furthermore, yeast and mold counts were not detected in any of the cheese types, including both the control and treated samples.

The sensory evaluation

The sensory evaluation (flavour, taste, colour, and overall acceptance) of fat-substituted braided cheese with different vegetable oils (SO), (CO), and (OO) at levels of 2%, 3%, and 4% is illustrated in Table 4.

A significant ($P \leq 0.05$) decrease in flavour score was observed with increasing oil content. The control sample, along with 2% (OO), 2% (SO), and 3% (SO), recorded high flavour scores of 4.04, 4.2, 3.24, and 3.64, respectively. These variations in flavour could be attributed to differences in the panellists' acceptance of the types and levels of oils added to the braided cheese.

Significant ($P \leq 0.05$) differences in taste were also noted among the cheese samples. The control sample had the best taste (4.2), followed by the cheese sample with 2% (OO), which had scores of 4.0 and 4.2, respectively.

Similarly, significant ($P \leq 0.05$) differences in colour scores were observed among the cheese samples. The control sample achieved the highest colour score of 4.2, followed by cheese samples supplemented with 2% (SO), (CO), and (OO), which scored 4.2, 3.52, 3.08, and 4.0, respectively.

These changes in colour may be due to the removal of milk fat, which contains the β-carotene pigment responsible for the characteristic colour of braided cheese. Replacing milk fat with vegetable oils altered the colour, but the change was minimal at 2% supplementation and not noticeable to most panelists.

However, at higher oil concentrations (3% and 4%), the colour differences became more pronounced.[30] indicated that the reduction of fat in mozzarella cheese resulted in diminished whiteness and increased translucency, whereas [31] noted that fat reduction imparted a greenish hue to unmelted low-fat mozzarella cheese. The hue of low-fat

fresh Kashar cheeses with fat replacers varied from that of the low-fat control cheese.

Overall acceptance scores also differed significantly ($P \leq 0.05$) among the cheese samples. Samples with 2% (SO) and (OO) achieved the highest scores of 4.00 and 4.24, respectively. Panelists preferred those cheese samples due to their superior taste, texture, flavour, and appearance. Despite these differences, all cheese samples were deemed acceptable by the sensory panellists.

The superior sensory performance of 2% olive oil cheese is attributed to its unique flavor chemistry and texture perception. Oleocanthal and oleacein in olive oil activate TRPV1, adding a mild pungency that enhances dairy flavours [32]. In contrast, sunflower and corn oils lack bioactive components and can produce off-flavors due to oxidation of linoleic acid (Frankel, 2005). At higher concentrations, these oils lead to rancidity and reduced overall acceptance of the cheese. Moreover, color differences arise from the β-carotene loss in milk fat, with vegetable oil replacement resulting in paler cheese. Olive oil maintains some pigment at 2%, which is below the visual detection threshold, aligning with positive panellist scores [33].

The sensory characteristics of the braided cheese samples with vegetable oils differed from those of the control samples. The sensory panelists scored cheese samples fortified with 2% (OO) and (SO) more favorably than other treatments. Full-fat cheese got a much higher taste score than all of the low-fat cheese types. However, the evaluators deemed all cheese samples satisfactory. These findings indicate that substituting dairy fat with olive oil (OO) and sunflower oil (SO) is viable for creating a healthier and more functional cheese. These findings are consistent with [15], who indicated that low-fat cheeses received a lower overall score compared to the other cheese samples. This may be because of the markedly reduced fat content in the low-fat cheese. Moreover, full-fat cheese samples received far higher scores than low-fat cheese.

Conclusion

Fortifying skimmed milk with vegetable oils significantly influenced the composition, microbial quality, and sensory acceptability of Sudanese braided cheese. Among the tested formulations, 2% olive oil produced a cheese with lower calculated energy value (215 kcal 100 g^{-1}, 27% reduction vs. control), reduced fat content (9.0% vs. 24.0%), relatively high protein content (27.39 g 100 g^{-1}, equivalent to 2% corn oil), and favourable sensory acceptability (highest overall acceptance score: 4.24 ± 0.66 on a 5-point scale). However, claims that this product is definitively healthier, cost-effective, or commercially ready are not supported by the current data and require additional analyses including: (a) gas chromatographic fatty acid profiling to substantiate cardiovascular health benefits; (b) instrumental texture profile analysis to evaluate mechanical properties; (c) shelf-life microbial and sensory stability testing; (d) economic analysis of ingredient and production costs; and (e) large-scale consumer acceptability trials (n > 100) beyond the trained panel used herein.

Study limitation

Several limitations of the study are highlighted, including the statistical design, which had limited replication and lacked individual panellist scores necessary for full factorial analysis, leading to caution in interpreting the reported main effects. A recommendation for future studies is to ensure minimum replication of five per cell and retain individual observations for robust analysis. Additionally, fatty acid profiling was not conducted; thus, cardiovascular health claims regarding replacing saturated fats with unsaturated oils are based on indirect evidence rather than direct analysis. Future research should include complete profiling of saturated fatty acids (SFA), monounsaturated fatty acids (MUFA), and polyunsaturated fatty acids (PUFA). The microbiological analysis was also limited, focusing on total bacterial counts without pathogen-specific testing or shelf-life studies, particularly highlighting concerns with the bacterial load in the sunflower oil treatment, which needs further investigation. Moreover, the study tested a narrow range of oil concentrations (2%, 3%, and 4%), leaving the possibility that optimal concentrations may lie outside this range unaddressed.

It should be noted that the present study determined only total viable bacterial counts and yeast/mold counts. Pathogen-specific analyses — including screening for Escherichia coli, Salmonella spp., Listeria monocytogenes, and Staphylococcus aureus — were not conducted. Consequently, while the observed reduction in total bacterial loads in vegetable oil-treated samples is encouraging, no definitive conclusions regarding food safety or pathogen absence can be drawn from these data. This represents a significant limitation of the current study."

References

1. Briggs, M.A., Petersen, K.S. and Kris-Etherton, P.M. (2017), "Saturated fatty acids and cardiovascular disease: replacements for saturated fat to reduce cardiovascular risk", Healthcare (Healthcare), Vol. 5 No. 2, pp. 1-29. https://doi.org/10.3390/healthcare5020029

2. Siri-Tarino, P. W., Sun, Q., Hu, F. B., & Krauss, R. M. (2010). Saturated fatty acids and risk of coronary heart disease: modulation by replacement nutrients. Current atherosclerosis reports, 12(6), 384-390. https://doi.org/10.1007/s11883-010-0131-6

3. Lteif, L., Olabi, A., Kebbe-Baghdadi, O., and Toufeili, I. (2009). The characterization of the physicochemical

and sensory properties of full-fat, reduced-fat and low-fat ovine and bovine Halloumi. J. Dairy Sci., 92 4135–4145. https://doi.org/10.3168/jds.2009-2070

4. Chavan, R.S., Khedkar, C.D. and Bhatt, S. (2016), "Fat replacer", in Caballero, B., Finglas, P. and Toldrá, F. (Eds), The Encyclopedia of Food and Health, Academic Press, Oxford, Vol. 2, pp. 589-595.

5. Ali, R. F., El-Anany, A. M., & Mousa, H. M. (2021). The effect of partially or totally replacing milk fat by jojoba oil in Domiati cheese production on some nutritional and quality properties. Food Sci. Nutr. J., 51(1), 191-204.ژ https://doi.org/10.1108/NFS-03-2020-0077

6. Altahir, M. O., Elgasim, E. A., & Mohamed Ahmed, I. A. (2014). Ripening of Sudanese Braided (Muddaffara) Cheese Manufactured from Raw or Pasteurized Milk: Effect of Heat Treatment and Salt Concentration on the Physicochemical PropertiesInt. J. Food Sci., 2014(1), 698263.ژhttps://doi.org/10.1155/2014/698263

7. Abdalla, M., & Eldin, H. (2018). Effect of Milk Type and Salt Concentration on th e Physicochemical Characteristics of Mudaffara (Braided) Cheese. Adv. Res., 13(5), 1-9.ژ DOI: 10.9734/AIR/2018/33121

8. Abdel Razig, A. K. (2000). Quality attributes of braided cheese (Mudaffara) as affected by level of salt and storage temperature, Ph.D. Thesis, University of Khartoum, Sudan.

9. Association of Official Analytical Chemists (2003). Official Method of Analysis. 17th ed. Association of Official Analytical Chemists, Washington D.C. 7, 65–68.

10. Codex Alimentarius Commission. (2018). General standard for the labelling of prepackaged foods (CXS 1-1985). Food & Agriculture Organization of the United Nations.

11. Harrigan, W. F. (1998). Laboratory methods in food microbiology. Gulf professional publishing.

12. Tamime, A. Y. (2011). Processed Cheese and Analogues. First edition, Blackwell publishing ltd.

13. SAS Institute, Inc. (2011). SAS Companion for the Microsoft Windows Environment (Version 8.1). Car, NC: SAS Institute, Inc. Science, 77, 1783–1788.

14. El-Salam, B. A. A. (2015). Effect of milk fat replacement with vegetable oil and/or whey protein concentrate on microstructure, texture and sensory characteristics of fresh soft cheese.ژ Int. J. Dairy Sci. ,(10) 3, 117-125. DOI: 10.3923/ijds.2015.117.125

15. Hilliou, L. (2021). Structure–elastic properties relationships in gelling carrageenans. Polymers, 13(23), 4120. https://doi.org/10.3390/polym13234120

16. Kavas, G., Oysun, G., Kinik, O., & Uysal, H. (2004). Effect of some fat replacers on chemical, physical and sensory attributes of low-fat white pickled cheese. Food Chem., 88(3), 381-388. https://doi.org/10.1016/j.foodchem.2004.01.054

17. Sulejmani, E., Beqiri, L., & Popeski-Dimovski, R. (2021). Effect of vegetable fat on the texture, colour and sensory properties of Macedonian white brined cheese. Mljekarstvo.71(1), 25-34.ژ https://doi.org/10.15567/mljekarstvo.2021.0103.

18. Rogers, N. R., McMahon, D. J., Daubert, C. R., Berry, T. K., & Foegeding, E. A. (2010). Rheological properties and microstructure of Cheddar cheese made with different fat contents. J. Dairy Sci.., 93(10), 4565-4576.ژ https://doi.org/10.3168/jds.2010-3494

19. Hayaloglu, A. A., Guven, M. E. H. M. E. T., Fox, P. F., & McSweeney, P. L. H. (2005). Influence of starters on chemical, biochemical, and sensory changes in Turkish white-brined cheese during ripening. J. Dairy Sci., 88(10), 3460-3474.ژ https://doi.org/10.3168/jds.S0022-0302(05)73030-7

20. Romieh, E.; A. Michaelidou; C. G. Biliaderis, and G. K. Zerfiridis (2002). Low-fat white-brined cheese made from bovine milk and two commercial fat mimetics: chemical, Physical and Sensory Attributes. Int. Dairy J., 12: 525-540. https://doi.org/10.1016/S0958-6946(02)00043-2

21. Felfoul, I., Bornaz, S., Baccouche, A., Sahli, A., & Attia, H. (2015). Low-fat Gouda cheese made from bovine milk-olive oil emulsion: physicochemical and sensory attributes. J. Food Sci. Technol, 52, 6749-6755.ژ

22. Collins, Y. F., McSweeney, P. L., & Wilkinson, M. G. (2003). Lipolysis and free fatty acid catabolism in cheese: a review of current knowledge. Int. Dairy J., 13(11), 841-866. https://doi.org/10.1016/S0958-6946(03)00109-2

23. Dalgleish, D. G. (2011). On the structural models of bovine casein micelles—review and possible improvements. Soft matter, 7(6), 2265-2272. https://doi.org/10.1039/c0sm00806k

24. Guinee, T. P., Auty, M. A., & Mullins, C. (1999). Observations on the microstructure and heat-induced changes in the viscoelasticity of commercial cheeses. Aust. J. Dairy Technol.,, 54(2), 84.

25. Michalski, M. C., Camier, B., Briard, V., Leconte, N., Gassi, J. Y., Goudédranche, H., ... & Fauquant, J. (2004). The size of native milk fat globules affects physico-chemical and functional properties of Emmental

cheese. lait, 84(4), 343-358. https://doi.org/10.1051/lait:2004012

26. Romero, A., Beaumal, V., David-Briand, E., Cordobes, F., Guerrero, A., & Anton, M. (2011). Interfacial and oil/water emulsions characterization of potato protein isolates.. J. Agric. Food Chem., 59(17), 9466-9474. https://doi.org/10.1021/jf2019853

27. Bielecka, M., and Cichosz, G. (2020). The effect of milk fat replacement and the addition of Lactobacillus paracasei LPC-37 on the sensory properties of cheeses. Mljekarstvo, 70(1), 28-39. https://doi.org/10.15567/mljekarstvo.2020.0103

28. Abd El-Aziz, M., Salama, H. H., & Sayed, R. S. (2023). Plant extracts and essential oils in the dairy industry: A review. Foods Raw Mater, 11, 321-337. https://doi.org/10.21603/2308-4057-2023-1-547

29. Hamad, M. N. E. F., El-Bushuty, D. H., & Abdallah, A. M. (2021). Studies on fatty acids composition, antioxidants and antibacterial activity of some Egyptian vegetable oils. J. Food Dairy Sci., 12(1), 17-22. DOI: 10.21608/jfds.2021.59377.1013

30. Rudan, M. A., Barbano, D. M., Yun, J. J., & Kindstedt, P. S. (1999). Effect of fat reduction on composition, proteolysis, functionality and yield of Mozzarella cheese. J. Dairy Sci.,, 82, 661–662. https://doi.org/10.3168/jds.S0022-0302(99)75282-3

31. Merrill, R. K., Oberg, C. J, & McMahon, D. J. (1994). A method for manufacturing reduced fat Mozzarella cheese. J. Dairy Sci.,. 77:1783-1789. https://doi.org/10.3168/jds.S0022-0302(94)77119-8

32. Beauchamp, G. K., Keast, R. S., Morel, D., Lin, J., Pika, J., Han, Q., ... & Breslin, P. A. (2005). Ibuprofen-like activity in extra-virgin olive oil. Nature, 437(7055), 45-46. https://doi.org/10.1038/437045a

33. Noziere, P., Graulet, B., Lucas, A., Martin, B., Grolier, P., & Doreau, M. (2006). Carotenoids for ruminants: From forages to dairy products. Anim. Feed Sci. Technol., 131(3-4), 418-450. 10.1016/j.anifeedsci.2006.06.018

Integrated Health Research Journal (IHRJ)

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

RESEARCH ARTICLE

Climate Change and the Changing Landscape of Central Nervous System Infections and Neuropsychiatric Morbidities in Northwest Nigeria: A Large-Scale Epidemiological Study

Abdullahi Abdulwahab Yakubu[1]*, Summayyah Muhammad Bashar[2], Audu Ishaq Aveka[1], Abdullahi Mohammed Asara[3], Mivanyi Musa Murinyi[4], Sani Khalid[2], Fahad Abubakar Saulawa[5], Bashir Adam Yakasai[2]

[1] Department of Psychiatry, Ahmadu Bello University, Zaria, Nigeria | [2] Department of Psychiatry, Ahmadu Bello University Teaching Hospital, Zaria, Nigeria | [3] Department of Internal Medicine, Ahmadu Bello University Teaching Hospital, Zaria, Nigeria | [4] Department of Child and Adolescent Mental Health Services, Lincolnshire Partnership NHS Foundation Trust (LPFT), Galaxy Suite, Boston Archway Centre, United Kingdom | [5] Department of Community Medicine, Ahmadu Bello University Teaching Hospital, Zaria, Nigeria

*Correspondence should be addressed to Abdullahi Abdulwahab Yakubu (email: ayabdullahi@abu.edu.ng)

Abstract

Background: Climate change is postulated to alter the epidemiology of infectious diseases, particularly in vulnerable regions like sub-Saharan Africa. The potential impact on central nervous system (CNS) infections and subsequent neuropsychiatric sequelae remains inadequately characterised in Northwest Nigeria.

Objectives: This study aimed to investigate the associations between climate change indicators (including temperature, rainfall patterns, extreme heat days, and humidity) and the incidence of CNS infections, including atypical presentations, and associated neuropsychiatric morbidities.

Methods: A cross-sectional study was conducted involving 20,000 participants from Northwest Nigeria over 24 months (January 2023 to December 2024). Data were collected using pre-validated instruments, including a structured questionnaire, clinical proforma for CNS infection diagnosis, the Composite International Diagnostic Interview (CIDI) for neuropsychiatric assessment, and meteorological data from the Nigerian Meteorological Agency (NiMet). Statistical analyses involved multivariable logistic regression to determine associations, controlling for confounders (age, sex, education, HIV status). Spearman's correlation coefficients were also calculated.

Results: Among the 20,000 participants, a significant positive association was found between rising average temperatures and the incidence of CNS infections (aOR: 1.45, 95% CI: 1.32-1.59). Similarly, aberrant rainfall patterns were linked to an increased incidence of atypical CNS infections (aOR: 1.78, 95% CI: 1.60-1.98). Extreme heat days (>40°C) were also associated with CNS infections (aOR: 1.28, 95% CI: 1.15-1.42). Participants with a diagnosed CNS infection had a substantially higher prevalence of subsequent neuropsychiatric morbidities, including depression (18.5%), anxiety disorders (15.2%), and cognitive impairments (12.8%), compared to those without ($p<0.001$). In contrast, non-CNS infections were associated with lower neuropsychiatric prevalence (depression: 8.2%).

Conclusion: Climate change is significantly associated with an increasing burden of CNS infections and related neuropsychiatric morbidities in Northwest Nigeria. These findings underscore the urgent need for integrated public health strategies that incorporate climate adaptation measures into neurological and mental health frameworks. Healthcare professionals should routinely screen post-CNS infection patients for psychiatric sequelae, and policymakers must invest in climate-resilient surveillance systems.

Keywords: Central Nervous System Infections, Climate Change, Neuropsychiatric Disorders

Citation: Yakubu AA, Bashar SM, Aveka AI, Asara AM, Murinyi MM, Khalid S, Saalawa FA, Yakasa BA. Climate change and the changing landscape of central nervous system infections and neuropsychiatric morbidities in Northwest Nigeria: a large-scale epidemiological study. Integrated Health Research Journal. 2026;3(2):31-39. https://doi.org/10.47963/gkpndt95

Received 31st January 2026; **Accepted** 9th June 2026; **Published** 14th September 2026.

Introduction

The profound and accelerating impact of climate change on global health is one of the defining challenges of the 21st century [1]. Its effects are not uniformly distributed, with regions in the Global South, particularly sub-Saharan Africa, bearing a disproportionate burden due to pre-existing vulnerabilities, weak health systems, and socioeconomic pressures [2,3]. Among the myriad health consequences, the nexus between climate change and infectious disease dynamics is particularly alarming. Changes in temperature, precipitation, and humidity can expand the geographical range of vectors, alter pathogen life cycles, and disrupt human-environment interactions, thereby increasing the transmission of infectious agents [4,5].

Central nervous system (CNS) infections, including meningitis, encephalitis, and myelitis, represent a significant cause of mortality and long-term disability worldwide [6]. In the African "meningitis belt," to which Northern Nigeria belongs, climatic factors have long been recognised as key drivers of seasonal meningitis epidemics, primarily caused by *Neisseria meningitidis* [7]. However, the changing climate is hypothesised to be facilitating the emergence of "atypical" CNS infections, including those caused by fungi, arboviruses (e.g., dengue, West Nile virus), and water-borne pathogens, which were previously uncommon in the region [8,9]. The pathophysiological link between these infections and neurological damage often involves neuroinflammation; a complex immune response within the brain and spinal cord that, while aimed at clearing pathogens, can cause significant collateral damage to neural tissues [10].

This neuroinflammatory cascade is increasingly implicated in the aetiology of a spectrum of neuropsychiatric morbidities, including depression, anxiety, psychosis, and cognitive decline [11,12]. Following a CNS infection, the persistent activation of microglia and elevated levels of pro-inflammatory cytokines can disrupt neurotransmitter systems, neurogenesis, and synaptic plasticity, creating a vulnerable substrate for psychiatric illness [13]. While the association between CNS infections and subsequent mental health disorders has been established in other contexts [14], the potential amplification of this pathway by climate change remains a critical, yet under-researched, area, especially in Northwest Nigeria. This region is characterised by its semi-arid climate, experiencing some of the most extreme temperature fluctuations and variable rainfall patterns in the country [15].

This study, therefore, sought to bridge this knowledge gap by investigating, on an unprecedented scale, the associations between climate change variables, the incidence of CNS infections (including atypical forms), and the resulting burden of neuropsychiatric morbidities in a large cohort from Northwest Nigeria. The findings are critical for informing predictive models, public health preparedness, and clinical management strategies in a rapidly changing environment [8].

Methods

Study Design

This was a cross-sectional study.

Study Setting

The study was conducted in the seven states comprising Northwest Nigeria: Jigawa, Kaduna, Kano, Katsina, Kebbi, Sokoto, and Zamfara, over 24 months (January 2023 to December 2024). The region has an estimated population of over 40 million people and is predominantly semi-arid.

Sample Size Determination

The sample size of 20,000 was calculated using the Cochran formula for cross-sectional studies ($n=Z^2\times p(1-p)/d^2$), with an estimated prevalence of CNS infections of 5% from previous regional studies [16], a margin of error of 0.5%, a design effect of 1.5, and a 95% confidence level.

Sampling Method

A multi-stage stratified cluster sampling technique was employed. This method was chosen to ensure representativeness across the diverse agro-ecological zones and population densities of the seven states. First, two Local Government Areas (LGAs) were randomly selected from each state (total 14 LGAs) to capture intra-state variation. Second, within each LGA, clusters (households) were selected using probability proportional to size (PPS). PPS ensures that larger settlements contributed proportionally more participants, reflecting the true population distribution. The state-wise sample sizes were: Kano (n=4,500), Kaduna (n=3,200), Katsina (n=3,000), Sokoto (n=2,500), Zamfara (n=2,400), Kebbi (n=2,200), Jigawa (n=2,200). All consenting individuals aged 15 and above within selected households were enrolled until the state-specific quota was met. Table 1 shows the state-wide distribution of the participants.

Inclusion Criteria

The inclusion criteria were: (1) Permanent resident (≥6 months) in one of the selected Northwest states; (2) Aged 15 years and above; (3) Provided informed consent (or assent with parental consent for minors).

Exclusion Criteria

The exclusion criteria were: (1) History of significant head injury; (2) Pre-existing major neurodevelopmental disorder (e.g., autism spectrum disorder); (3) Active CNS infection at the time of enrolment that precluded interview; (4) Unwillingness to participate.

Study Instruments

The following instruments were used for data collection;

1. Sociodemographic and Clinical Proforma: A structured questionnaire adapted from the WHO STEPS instrument [17], previously validated and used in Nigeria [18], to capture age, sex, education, occupation, and past medical history.

2. CNS Infection Diagnostic Proforma: A detailed clinical proforma for physicians to record signs, symptoms, laboratory findings (cerebrospinal fluid analysis, PCR, serology), and neuroimaging results (where available) to diagnose CNS infections according to WHO guidelines [19]. Diagnoses were categorised as bacterial meningitis, viral encephalitis, fungal meningitis, tuberculous meningitis, and other atypical infections. This proforma was piloted and validated in a tertiary hospital in Kano, showing high inter-rater reliability (Cohen's $\kappa = 0.89$).

3. Composite International Diagnostic Interview (CIDI): A fully structured, lay-administered diagnostic instrument for the assessment of mental disorders according to ICD-11 and DSM-5 criteri [20]. The CIDI has been extensively validated in Nigeria and across Africa, demonstrating good sensitivity and specificity for common neuropsychiatric conditions [21,22]. It was used to assess for major depressive disorder, generalised anxiety disorder, cognitive impairment syndromes, and additionally eating disorders and somatic symptom disorder (the latter two showed no significant between-group differences).

4. Meteorological Data: Historical and contemporary climate data (mean annual temperature, rainfall patterns, humidity, annual number of extreme heat days >40°C, wind speed, and dust haze days) for each LGA for the preceding 10-year period (2015-2025) were obtained from the Nigerian Meteorological Agency (NiMet) [15]. The calculation of the 1°C temperature change was performed per LGA using the 10-year mean annual temperature deviation from the regional baseline (2015–2020 mean).

Study Procedure

Data were collected by trained research assistants fluent in both English and Hausa. The study purpose was explained, and written or thumb-printed informed consent was obtained from all participants. Interviews were conducted in private settings using a structured questionnaire. Confidentiality and anonymity was maintained throughout the research process.

Ethical Consideration

The study procedures were reviewed and approved by the Health Research Ethic Committee of Ahmadu Bello University Teaching Hospital, Shika-Zaria (Ref: ABUTHZ/HREC/C37/2024). Informed written consent was obtained from all participants prior to their inclusion in the study. Confidentiality and anonymity of participants was maintained throughout the research process. Participants were duly informed they could withdraw from the study at any time without any consequences.

Statistical Analysis

Data were analysed using Stata version 17.0. Descriptive statistics were presented as frequencies and percentages for categorical variables and means (± standard deviation) for continuous variables. The primary outcomes were (i) diagnosis of a CNS infection and (ii) presence of a neuropsychiatric morbidity. Multivariable logistic regression was chosen because both primary outcomes are binary (present/absent), allowing estimation of adjusted odds ratios (aOR) while controlling for multiple confounders simultaneously. Climate exposure variables were entered as follows: mean temperature as a continuous variable (per 1°C increase); rainfall patterns as a categorical variable (stable vs. aberrant, based on coefficient of variation >30%); extreme heat days as a continuous variable (per 10-day increase). Multivariable logistic regression models were used to assess the association between climate variables (exposure) and the primary outcomes, adjusting for potential confounders including age, sex, socioeconomic status, and HIV status because these factors are known from prior literature to independently influence infection risk (HIV, age) or healthcare access (sex, education), and adjusting for them isolates the specific effect of climate variables. Adjusted Odds Ratios (aOR) with 95% Confidence Intervals (CI) were reported. A p-value of <0.05 was considered statistically significant. Spearman's rank correlation coefficients (r) were calculated between climate variables and outcome prevalence at the LGA level.

Results

A total of 20,000 participants were successfully enrolled and included in the final analysis. The sociodemographic characteristics of the study population are summarised in Table 2. The sample was predominantly young (60% aged 15–34 years), with a slight female majority (51%), and 32.5% had no formal education.

Table 3 shows the frequency of infectious diseases among participants. Among the 20,000 participants, a total of 1,850 (9.3%) were diagnosed with a central nervous system (CNS) infection. Bacterial meningitis was the most common CNS infection, accounting for 840 cases (4.2% of all participants), followed by viral encephalitis in 560 participants (2.8%), fungal meningitis in 220 participants (1.1%), tuberculous meningitis in 180 participants (0.9%), and other atypical CNS infections in 50 participants (0.3%). In comparison, non-CNS infections were more frequent, affecting 6,500 participants (32.5%). Among these, respiratory infections were the predominant category, occurring in 3,700 participants (18.5%), followed

Table 1: State-wise distribution of participants (probability proportional to size)

State	Frequency (n)	Percentage (%)
Kano	4,500	22.5
Kaduna	3,200	16.0
Katsina	3,000	15.0
Sokoto	2,500	12.5
Zamfara	2,400	12.0
Kebbi	2,200	11.0
Jigawa	2,200	11.0

by gastrointestinal infections in 2,440 participants (12.2%), and urinary tract infections in 360 participants (1.8%).

Table 4 presents the age-stratified incidence of CNS infections (including bacterial meningitis, viral encephalitis, fungal meningitis, tuberculous meningitis, and other atypical infections) among the 20,000 study participants from Northwest Nigeria. The highest age-specific incidence was observed in the 35–44 age group (10.4%), followed closely by the 25–34 and 45–54 age groups (10.0% and 10.4%, respectively). The lowest incidence was recorded among the youngest age group (15–24 years: 7.2%) and the oldest age group (≥55 years: 8.3%). The overall incidence of CNS infections in the study population was 9.3% (95% CI: 8.9–9.7).

Table 5 presents the state-wise association between temperature increase and CNS infection. State-wise analysis revealed a clear geographical gradient in the association between temperature increase and CNS infections, as shown in Table 2C. The strongest associations were observed in Sokoto (aOR: 1.62, 95% CI: 1.45-1.81) and Kebbi (aOR: 1.58, 95% CI: 1.41-1.77), while Kano showed the lowest but still significant association (aOR: 1.38, 95% CI: 1.24-1.54). This pattern suggests that the more arid, borderline states may be most vulnerable to climate-driven infection emergence. Figure 1 shows a colour-coded map of Northwest Nigeria with LGA-level distribution of CNS infection prevalence, depression prevalence, and temperature anomaly. The north–south gradient is visually evident, with higher temperatures and higher disease burden concentrated in Sokoto and Kebbi.

Table 6 presents the associations between climate variables and both CNS and non-CNS infections using multivariable logistic regression, adjusting for age, sex, education, and HIV status. A 1°C increase in the 10-year average temperature was associated with a 45% increased odds of a CNS infection diagnosis (aOR: 1.45, 95% CI: 1.32-1.59), compared to a 21% increased odds of any non-CNS infection (aOR: 1.21, 95% CI: 1.12-1.31). Residence in an LGA classified as having "highly aberrant" rainfall patterns was strongly associated with a 78% increased odds of being diagnosed with an atypical CNS infection (e.g., fungal, arboviral) compared to LGAs with "stable" rainfall (aOR: 1.78, 95% CI: 1.60-1.98), while the same exposure was associated with a 35% increased odds of non-CNS infections (aOR: 1.35, 95% CI: 1.20-1.52). Extreme heat days (>40°C, per 10-day increase) were independently associated with CNS infections (aOR: 1.28, 95% CI: 1.15-1.42). Spearman's correlation between mean temperature and LGA-level CNS infection incidence was $r = 0.62$ ($p < 0.001$); for aberrant rainfall and atypical CNS infections, $r = 0.58$ ($p < 0.001$).

Table 7 presents the prevalence of neuropsychiatric morbidities stratified by infection history, comparing participants with CNS infection, those with non-CNS infection, and those without any infection. The highest prevalence of major depressive disorder (18.5%, n=342), generalised anxiety disorder (15.2%, n=281), and cognitive impairment (12.8%, n=237) was observed among participants with a history of CNS infection. Those with non-CNS infections had intermediate prevalence rates (depression: 8.2%, n=533; anxiety: 6.9%, n=449; cognitive impairment: 5.5%, n=358), while participants without any infection had the lowest rates (depression: 3.4%, n=393; anxiety: 2.8%, n=331; cognitive impairment: 2.4%, n=277). All overall comparisons across the three groups were statistically significant ($p<0.001$), and pairwise comparisons between each group also reached significance ($p<0.001$). This dose–response relationship suggests that while systemic inflammation from any infection confers some risk of neuropsychiatric morbidity, direct CNS invasion produces the greatest burden.

Table 2: Sociodemographic characteristics of the study population (N = 20,000)

Characteristic	Frequency (n)	Percentage (%)
Age group (years)		
15–24	5,800	29.0
25–34	6,200	31.0
35–44	4,500	22.5
45–54	2,300	11.5
≥55	1,200	6.0
Sex		
Male	9,800	49.0
Female	10,200	51.0
Educational level		
No formal education	6,500	32.5
Primary	5,200	26.0
Secondary	5,800	29.0
Tertiary	2,500	12.5

Table 3: Frequency of infectious diseases among participants (N = 20,000)

Infection type	Frequency (n)	Percentage (%)
CNS infections (total)	1,850	9.3
Bacterial meningitis	840	4.2
Viral encephalitis	560	2.8
Fungal meningitis	220	1.1
Tuberculous meningitis	180	0.9
Other atypical	50	0.3
Non-CNS infections (total)	6,500	32.5
Respiratory	3,700	18.5
Gastrointestinal	2,440	12.2
Urinary tract	360	1.8

Table 4: Age-stratified incidence of central nervous system (CNS) infections among study participants (N = 20,000)

Age group (years)	Total participants (n)	Participants with CNS infection (n)	Age-specific incidence of CNS infection (%)	95% Confidence Interval
15–24	5,800	420	7.2	6.6–7.9
25–34	6,200	620	10.0	9.3–10.8
35–44	4,500	470	10.4	9.6–11.3
45–54	2,300	240	10.4	9.2–11.8
≥55	1,200	100	8.3	6.9–10.0
Total	20,000	1,850	9.3	—

Table 5: State-wise association between temperature increase and CNS infection (aOR)

State	aOR (95% CI)	p-value
Sokoto	1.62 (1.45–1.81)	<0.001
Kebbi	1.58 (1.41–1.77)	<0.001
Zamfara	1.51 (1.35–1.69)	<0.001
Katsina	1.45 (1.30–1.62)	<0.001
Jigawa	1.43 (1.28–1.60)	<0.001
Kaduna	1.42 (1.27–1.59)	<0.001
Kano	1.38 (1.24–1.54)	<0.001

Table 6: Association between climate variables and infectious outcomes (multivariable logistic regression)

Exposure variable	Outcome	aOR (95% CI)	p-value
Per 1°C increase in mean temperature	Any CNS infection	1.45 (1.32–1.59)	<0.001
	Any non-CNS infection	1.21 (1.12–1.31)	<0.001
Aberrant rainfall (vs. stable)	Atypical CNS infection	1.78 (1.60–1.98)	<0.001
	Any non-CNS infection	1.35 (1.20–1.52)	<0.001
Extreme heat days (per 10-day increase)	Any CNS infection	1.28 (1.15–1.42)	<0.001

Model adjusted for age, sex, education, and HIV status.

Table 7: Prevalence of neuropsychiatric morbidities by infection history

Neuropsychiatric morbidity	With CNS infection (n = 1,850)	With non-CNS infection (n = 6,500)	Without any infection (n = 11,650)	p-value*
Major depressive disorder	342 (18.5%)	533 (8.2%)	393 (3.4%)	<0.001
Generalised anxiety disorder	281 (15.2%)	449 (6.9%)	331 (2.8%)	<0.001
Cognitive impairment	237 (12.8%)	358 (5.5%)	277 (2.4%)	<0.001

*p-value reflects overall comparison across the three groups (CNS infection, non-CNS infection, no infection). All pairwise comparisons were significant at $p < 0.001$.

Two neuropsychiatric conditions assessed (eating disorders and somatic symptom disorder) showed no significant difference between the CNS infection and non-infection groups ($p = 0.24$ and $p = 0.31$, respectively.

Discussion

This large-scale epidemiological study of 20,000 individuals in Northwest Nigeria provides compelling evidence linking climate change to an increased burden of CNS infections and subsequent neuropsychiatric morbidities. Our findings illuminate a critical and escalating public health crisis driven by environmental change.

The robust association between rising temperatures and the overall incidence of CNS infections aligns with established models of bacterial meningitis in the African meningitis belt [7,23]. Higher temperatures and low humidity facilitate nasopharyngeal mucosal damage and the transmission of respiratory pathogens like *Neisseria meningitidis*. However, our study extends this understanding by demonstrating a particularly strong link between aberrant rainfall patterns and the emergence of *atypical* CNS infections. The addition of extreme heat days as a significant predictor further supports the climate-infection nexus. This finding is consistent with research from other parts of West Africa, where unusual flooding has been linked to outbreaks of water-borne and vector-borne diseases [8,24]. For instance, expanded mosquito breeding sites from erratic rainfall can increase the transmission of arboviruses with neuroinvasive potential, such as West Nile virus, which is an emerging threat in the region [9]. Notably, the state-wise gradient (highest aOR in Sokoto/Kebbi, lowest in Kano) suggests that arid, borderline regions may be most vulnerable to climate-driven infection emergence.

The high prevalence of neuropsychiatric sequelae following CNS infections is a major finding of this study. The observation that 18.5% of individuals with a CNS infection developed depression and 12.8% developed

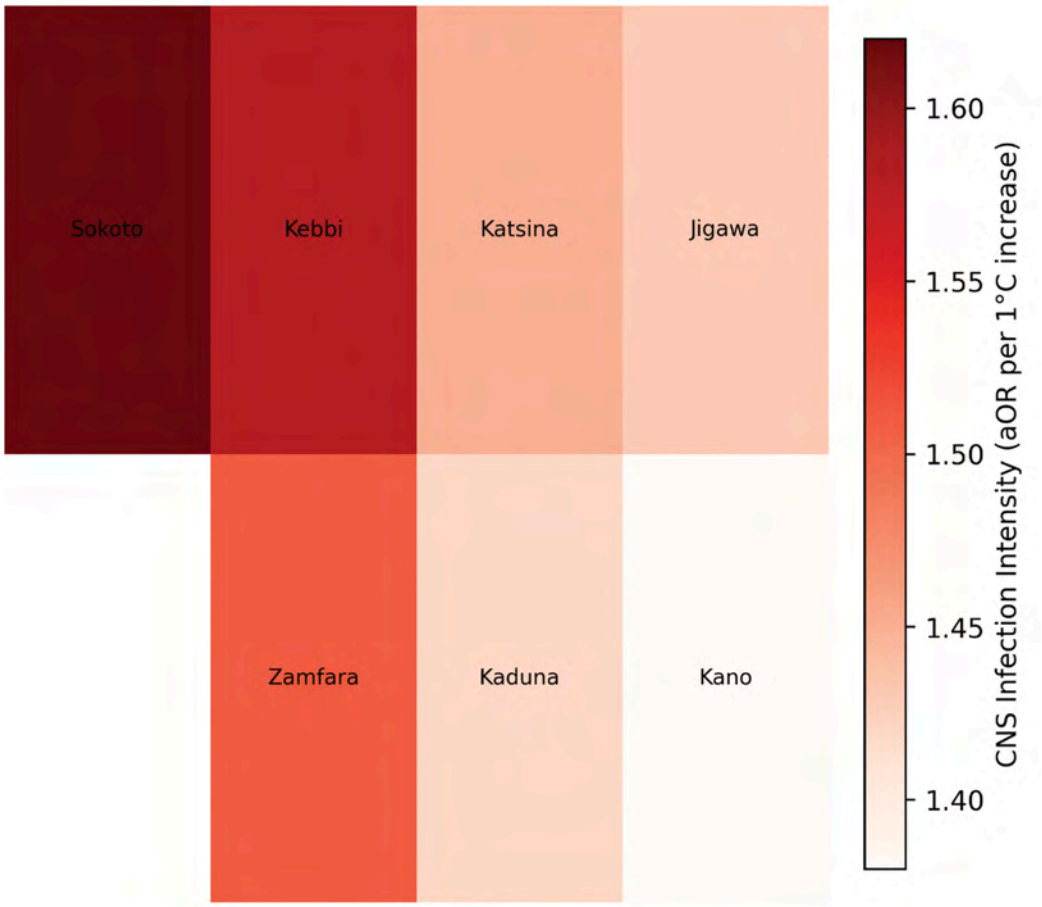

Figure 1: Spatial distribution of CNS infection prevalence, depression prevalence, and temperature anomaly across Local Government Areas (LGAs) in Northwest Nigeria

cognitive impairment underscores the long-term disability associated with these conditions. Importantly, the intermediate prevalence of these morbidities following non-CNS infections (depression 8.2%) supports a dose–response relationship: systemic inflammation from any infection confers some risk, but direct CNS invasion and neuroinflammation produce the greatest burden. This is supported by the growing body of literature on neuroinflammation, where CNS infections trigger a persistent inflammatory state that disrupts key neural circuits involved in mood regulation and cognition [10,12]. A study from Uganda similarly found high rates of cognitive impairment in survivors of cryptococcal meningitis [25], while research from high-income countries has long established the link between encephalitis and subsequent psychiatric illness [14]. Our study confirms that this burden is substantial in the Nigerian context and is likely being magnified by the increasing incidence of the underlying infections.

Implications for Public Health Policy and Climate Adaptation

The findings carry urgent practical implications. First, health policymakers should integrate meteorological early warning systems with infectious disease surveillance. Specifically, when NiMet predicts a 1°C above-average temperature or an aberrant rainfall season, targeted meningitis/arbovirus preparedness (e.g., vaccine stockpiles, vector control) should be triggered. Second, healthcare professionals in Northwest Nigeria must routinely screen patients with a history of CNS infection for depression, anxiety, and cognitive impairment using validated tools such as the CIDI or PHQ-9. Third, cross-sectoral adaptation measures are needed: flood-resistant housing to reduce water-borne pathogen exposure, improved drainage to limit mosquito breeding sites, and public awareness campaigns linking climate, infection, and mental health. Fourth, legislators should fund climate-resilient health infrastructure (e.g., cooling centres during heatwaves) and support research into neuroprotective interventions for infection survivors.

When viewed from a global perspective, our results contribute to the increasingly urgent discourse on climate change and neurological health [1,26]. The Intergovernmental Panel on Climate Change (IPCC) has consistently highlighted the health vulnerabilities of regions like Northwest Nigeria [3]. Our data provide granular, population-level evidence that these climatic threats are manifesting as severe neurological and mental health burdens. The syndemic nature of climate change, infectious disease, and neuropsychiatric illness creates a feedback loop that exacerbates health inequalities and challenges already fragile health systems [27].

Conclusion

This study establishes a clear and concerning link between climate change, CNS infections, and neuropsychiatric morbidities in Northwest Nigeria. The findings indicate that the region is facing a growing epidemic of brain health disorders, fuelled by environmental changes. This necessitates a paradigm shift in public health response. Therefore, healthcare professionals should systematically assess mental health in every patient recovering from meningitis, encephalitis, or other CNS infections. Early detection and treatment of depression and anxiety can prevent chronic disability. Researchers should conduct longitudinal studies to establish causality between specific climate variables and neuropsychiatric outcomes, and investigate whether anti-inflammatory or neuroprotective interventions can reduce post-infection morbidity. There is need to develop and test climate-adaptive vaccine delivery systems. Legislators and policymakers should immediately allocate resources to integrate climate monitoring with neurological surveillance, strengthen primary care mental health services in high-risk states (Sokoto, Kebbi), and invest in climate-resilient water, sanitation, and housing infrastructure. Failure to act will deepen health inequalities and undermine regional development.

Recommendations

Based on the findings of this study, it is strongly recommended that the public health authorities in Nigeria, particularly in the vulnerable Northwest region, urgently integrate climate adaptation and neurological health surveillance into their core policy frameworks. This should involve establishing an early warning system that links meteorological data with outbreaks of central nervous system infections and ensuring that neurology and mental health services are strengthened to manage the escalating burden of neuropsychiatric sequelae.

Ignoring this climate-neurohealth nexus will have profound consequences for population health, social stability, and economic development in Nigeria and similar regions worldwide.

Limitations

The cross-sectional design limits our ability to infer definitive causality. While we adjusted for key confounders, residual confounding from unmeasured factors (e.g., nutritional status, specific co-infections) is possible. Furthermore, the diagnosis of CNS infections in resource-limited settings can be challenging, and some cases may have been misclassified, though the use of a standardised clinical proforma mitigated this risk. We did not directly measure neuroinflammatory markers (e.g., CSF cytokines), so the mechanistic link via neuroinflammation remains inferential. The climate data were LGA-level, not individual-level, which may introduce ecological fallacy; however, this is standard in climate-health research.

Authors' Contributions

AAY, SMB, AIA, AMA, MMM, BAY, and FAS conceptualised and designed the study. AAY, SMB, AIA, AMA, BAY, and FAS were involved in data collection and analysis. AAY, SMB, AIA, AMA, MMM, BAY, and FAS drafted and revised the manuscript. All authors critically reviewed for intellectual content, approved the final version, and agreed to be accountable for all aspects of the work.

Availability of Research Data

Data are available upon reasonable request from the corresponding author.

Funding

No direct funding was received for this research. Logistical support for fieldwork was provided in-kind by participating state and local government authorities.

Conflict of Interests

The authors declare no conflict of interest.

Acknowledgements

We thank the study participants, research assistants, and the staff of the participating institutions for their support and cooperation throughout the study.

References

1. Watts N, Amann M, Arnell N, Ayeb-Karlsson S, Beagley J, Belesova K, et al. The 2020 report of The Lancet Countdown on health and climate change: responding to converging crises. Lancet. 2021;397(10269):129-70.

2. World Health Organization. Climate change and health [Internet]. 2021 [cited 2024 May 15]. Available from: https://www.who.int/news-room/fact-sheets/detail/climate-change-and-health

3. IPCC. Climate Change 2022: Impacts, Adaptation and Vulnerability. Contribution of Working Group II to the Sixth Assessment Report of the Intergovernmental Panel on Climate Change. Cambridge University Press; 2022.

4. Rocklöv J, Dubrow R. Climate change: an enduring challenge for vector-borne disease prevention and control. Nat Immunol. 2020 May;21(5):479-483. doi: 10.1038/s41590-020-0648-y. Erratum in: Nat Immunol. 2020 Jun;21(6):695. doi: 10.1038/s41590-020-0692-7. PMID: 32313242; PMCID: PMC7223823.

5. Mora C, McKenzie T, Gaw IM, Dean JM, von Hammerstein H, Knudson TA, Setter RO, Smith CZ, Webster KM, Patz JA, Franklin EC. Over half of known human pathogenic diseases can be aggravated by

climate change. Nat Clim Chang. 2022;12(9):869-875. doi: 10.1038/s41558-022-01426-1. Epub 2022 Aug 8. PMID: 35968032; PMCID: PMC9362357.

6. Steinmetz J, Seeher K, Schiess N et al. Global, regional, and national burden of disorders affecting the nervous system, 1990–2021: a systematic analysis for the Global Burden of Disease Study 2021. The Lancet Neurology, 2024; 23, 344-381

7. Sultan B, Labadi K, Guégan J-F, Janicot S (2005) Climate Drives the Meningitis Epidemics Onset in West Africa. PLoS Med 2(1): e6. https://doi.org/10.1371/journal.pmed.0020006

8. Okogun GR, Anosike JC, Okere AN, Nwoke BE. Ecology of mosquitoes of Midwestern Nigeria. J Vector Borne Dis. 2005 Mar;42(1):1-8. PMID: 15999454.

9. Fagbami AH, Onoja AB. Dengue haemorrhagic fever: An emerging disease in Nigeria, West Africa. J Infect Public Health. 2018 Nov-Dec;11(6):757-762. doi: 10.1016/j.jiph.2018.04.014. Epub 2018 Apr 26. PMID: 29706314.

10. DiSabato DJ, Quan N, Godbout JP. Neuroinflammation: the devil is in the details. J Neurochem. 2016 Oct;139 Suppl 2(Suppl 2):136-153. doi: 10.1111/jnc.13607. Epub 2016 May 4. PMID: 26990767; PMCID: PMC5025335.

11. Miller AH, Raison CL. The role of inflammation in depression: from evolutionary imperative to modern treatment target. Nat Rev Immunol. 2016 Jan;16(1):22-34. doi: 10.1038/nri.2015.5. PMID: 26711676; PMCID: PMC5542678.

12. Khandaker GM, Cousins L, Deakin J, Lennox BR, Yolken R, Jones PB. Inflammation and immunity in schizophrenia: implications for pathophysiology and treatment. Lancet Psychiatry. 2015 Mar;2(3):258-270. doi: 10.1016/S2215-0366(14)00122-9. Epub 2015 Feb 25. PMID: 26359903; PMCID: PMC4595998.

13. Yirmiya R, Rimmerman N, Reshef R. Depression as a microglial disease. Trends Neurosci. 2015 Oct;38(10):637-658. doi: 10.1016/j.tins.2015.08.001. PMID: 26442697.

14. Rocha ND, de Moura SK, da Silva GAB, Mattiello R, Sato DK. Neurological sequelae after encephalitis associated with herpes simplex virus in children: systematic review and meta-analysis. BMC Infect Dis. 2023 Jan 26;23(1):55. doi: 10.1186/s12879-023-08007-3. PMID: 36703115; PMCID: PMC9878875.

15. Nigerian Meteorological Agency (NiMet). Nigerian Climate Review [Internet]. Abuja: NiMet; 2023.

16. Akpede O, Abiodun PO, Sykes M, Salami CE. Childhood bacterial meningitis beyond the neonatal period in southern Nigeria: changes in organisms/antibiotic susceptibility. East Afr Med J. 1994 Jan;71(1):14-20. PMID: 8055756.

17. World Health Organization. WHO STEPS surveillance manual: the WHO STEPwise approach to chronic disease risk factor surveillance. Geneva: World Health Organization; 2005.

18. Ulasi II, Ijoma CK, Onodugo OD. A community-based study of hypertension and cardio-metabolic syndrome in semi-urban and rural communities in Nigeria. BMC Health Serv Res. 2010 Mar 19;10:71. doi: 10.1186/1472-6963-10-71. PMID: 20302648; PMCID: PMC2858142.

19. World Health Organization. Meningitis Laboratory Manual. 2nd ed. Geneva: WHO; 2011.

20. Kessler RC, Ustün TB. The World Mental Health (WMH) Survey Initiative Version of the World Health Organization (WHO) Composite International Diagnostic Interview (CIDI). Int J Methods Psychiatr Res. 2004;13(2):93-121. doi: 10.1002/mpr.168. PMID: 15297906; PMCID: PMC6878592.

21. Gureje O, Lasebikan VO, Kola L, Makanjuola VA. Lifetime and 12-month prevalence of mental disorders in the Nigerian Survey of Mental Health and Well-Being. Br J Psychiatry. 2006 May;188:465-71. doi: 10.1192/bjp.188.5.465. PMID: 16648534.

22. Jenkins R, Njenga F, Okonji M, Kigamwa P, Baraza M, Ayuyo J, Singleton N, McManus S, Kiima D. Prevalence of common mental disorders in a rural district of Kenya, and socio-demographic risk factors. Int J Environ Res Public Health. 2012 May;9(5):1810-9. doi: 10.3390/ijerph9051810. Epub 2012 May 9. PMID: 22754474; PMCID: PMC3386589.

23. Pérez García-Pando C, Stanton MC, Diggle PJ, Trzaska S, Miller RL, Perlwitz JP, Baldasano JM, Cuevas E, Ceccato P, Yaka P, Thomson MC. Soil dust aerosols and wind as predictors of seasonal meningitis incidence in Niger. Environ Health Perspect. 2014 Jul;122(7):679-86. doi: 10.1289/ehp.1306640. Epub 2014 Mar 17. PMID: 24633049; PMCID: PMC4080544.

24. Sanou AM, Nikiéma AS, Sausy A, Diendéré J, Ouattara MNG, Badiel ABS, Bonkoungou I, Ouédraogo HG, Hübschen JM. Serologic Evidence of Circulation of Six Arboviruses (Dengue Virus, Chikungunya Virus, Zika Virus, Rift Valley Virus, Yellow Fever Virus, Crimean-Congo Hemorrhagic Fever Virus) in Four Regions of Burkina Faso, West Africa. Trop Med Infect Dis. 2025 Dec 9;10(12):345. doi: 10.3390/tropicalmed10120345. PMID: 41441581; PMCID: PMC12737632.

25. Nsangi L, Hullsiek KH, Dai B, Namudde A, Menya G, Ssebambulidde K, Tugume L, Nuwagira E, Rhein J, Williams DA, Musubire AK, Boulware DR, Meya DB, Abassi M. Neurocognitive Impairment Among

Cryptococcal Meningitis Survivors in Uganda, a Prospective Cohort Study. Open Forum Infect Dis. 2025 Jan 29;12(2):ofaf054. doi: 10.1093/ofid/ofaf054. PMID: 40008306; PMCID: PMC11850114.

26. Bilbo SD, Schwarz JM. The immune system and developmental programming of brain and behavior. Front Neuroendocrinol. 2012 Aug;33(3):267-86. doi: 10.1016/j.yfrne.2012.08.006. Epub 2012 Sep 9. PMID: 22982535; PMCID: PMC3484177.

27. Horton R, Beaglehole R, Bonita R, Raeburn J, McKee M, Wall S. From public to planetary health: a manifesto. Lancet. 2014 Mar 8;383(9920):847. doi: 10.1016/S0140-

Integrated Health Research Journal (IHRJ)

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

RESEARCH ARTICLE

Socioeconomic Disparities in Self-Reported Breast and Cervical Cancer Diagnosis and Treatment Among Women of Reproductive Age: A National Survey

Gloria Anyimadu[1], Benjamin Akwasi Konja[1], Emmanuel Kweku Ocran [1], Livingstone Agyapong[1], Agyapong Nana Ama Frimpomaa[3], Kwame Kumi Asare[1, 2*]

[1] Biomedical and Clinical Research Centre, College of Allied Health Sciences, University of Cape Coast, Cape Coast, Ghana. | [2] Department of Immunology, Noguchi Memorial Institute for Medical Research, University of Ghana, Accra, Ghana. | [3] Department of Clinical Nutrition and Dietetics, School of Allied Health Sciences, University of Cape Coast, Cape Coast, Ghana, Ghana.

*Correspondence should be addressed to Kwame Kumi Asare (email: kwame.asare@ucc.edu.gh)

Abstract

Background: Breast and cervical cancers are leading causes of morbidity and mortality among women worldwide, with disproportionate burdens in low- and middle-income countries. Socioeconomic disparities influence awareness, diagnosis, and treatment, yet population-level evidence from sub-Saharan Africa remains limited. This study examined the prevalence, socio-demographic patterns, and treatment uptake of self-reported breast and cervical cancer among women of reproductive age using nationally representative survey data.

Methods: Secondary data from the Demographic and Health Survey (DHS) were analyzed, including 32,156 women aged 15–49 years. A weighted subsample of 16,716 women with complete cancer-related data was used to assess self-reported breast and cervical cancer diagnoses. Descriptive statistics summarized socio-demographic and health-related characteristics using frequencies and percentages. Bivariate associations between explanatory variables and outcomes were assessed using design-adjusted Pearson's chi-square tests.

Results: Self-reported prevalence of breast and cervical cancer was low, at 0.17% (n = 29) and 0.19% (n = 31), respectively. Among women with a reported diagnosis, 27.54% of breast cancer cases and 45.87% of cervical cancer cases reported receiving treatment. Among women who received breast cancer treatment, the majority resided in rural areas (84.2%), compared with 65.5% among those who did not receive treatment. The poorest wealth quintile accounted for over half of both treated (52.5%) and untreated women (54.2%); however, the richest wealth quintile was more represented among treated women (25.6%) than untreated women (6.9%). Cervical cancer treatment likewise varied according to selected socio-demographic and reproductive characteristics. A greater proportion of treated women resided in rural areas (59.5%) than in urban areas (40.5%). Treatment uptake was highest among women in the middle wealth quintile (34.3%) and richer quintile (41.9%).

Conclusion: Socioeconomic disparities influence self-reported breast cancer, while gaps in treatment uptake for both cancers highlight structural barriers in care. Strengthening early detection, equitable access to treatment, and public awareness programs is critical. It is important to note that the results are exploratory and descriptive. Further research including clinically verified diagnoses and broader age groups is needed to better understand patterns of cancer diagnosis and healthcare utilisation.

Keywords: Breast cancer, Cervical cancer, Socioeconomic disparities, Self-reported diagnosis, Treatment uptake, DHS, Sub-Saharan Africa

Citation: Anyimadu G, Konja BA, Ocran EK, Agyapong L, Frimpomaa ANA, Asare KK. Socioeconomic disparities in self-reported breast and cervical cancer diagnosis and treatment amongst women of reproductive age: a national survey. Integrated Health Research Journal. 2026;3(2):40-51. https://doi.org/10.47963/ngxt4592

Received 26th February 2026; **Accepted** 27th July 2026; **Published** 14th September 2026.

Introduction

Breast and cervical cancers remain major public health concerns globally and are the leading causes of cancer-related morbidity and mortality among women, with the highest burden of deaths occurring in low- and middle-income countries (LMICs)[1-4] . Despite advances in early detection and treatment, substantial disparities persist in cancer burden and access to care across socioeconomic and geographic contexts [5].

In sub-Saharan Africa, this continues to rise due to demographic transitions, urbanization, and changing reproductive and lifestyle patterns [6, 7].Cervical cancer is largely preventable through human papillomavirus (HPV) vaccination and regular screening, yet limited access to screening services and treatment contributes to high incidence and mortality rates in the region [8, 9]. Similarly, breast cancer outcomes in LMICs remain poor, largely due to late presentation, low awareness, inadequate diagnostic infrastructure, and financial barriers to treatment [10].

Socio-demographic and reproductive factors including residence, wealth status, parity, pregnancy status, and nutritional status have been associated with cancer risk and healthcare utilisation in various settings [11, 12]. Socioeconomic inequalities, in particular, play a critical role in influencing awareness, screening uptake, timely diagnosis, and access to treatment services [13, 14]. However, evidence from nationally representative population-based datasets in many African countries remains limited, especially regarding self-reported diagnosis and treatment patterns [15, 16].

The Demographic and Health Surveys (DHS) provide an opportunity to examine population-level patterns of disease and healthcare access using standardized and nationally representative data[17,18]. While DHS surveys traditionally focus on maternal and child health, fertility, and nutrition, recent surveys have incorporated modules capturing non-communicable disease indicators, including self-reported cancer diagnoses and treatment.

Understanding the prevalence of self-reported breast and cervical cancer, as well as the socio-demographic factors associated with diagnosis and treatment uptake, is essential for informing national cancer control strategies and addressing inequities in care. Therefore, this study aimed to (1) describe the socio-demographic characteristics of women aged 15–49 years, (2) determine the prevalence of self-reported breast and cervical cancer, (3) examine factors associated with cancer diagnosis, and (4) assess patterns of treatment uptake among diagnosed cases using nationally representative DHS data.

By identifying key disparities in cancer diagnosis and treatment, the findings of this study may contribute to evidence-based policy development and targeted interventions to improve early detection and equitable access to cancer care.

Methodology

Study Design, Data Source and Setting

This study used secondary data from the 2022 Kenya Demographic and Health Survey (KDHS), part of the DHS-8 phase, a nationally representative cross-sectional survey conducted under the Demographic and Health Surveys (DHS) Program. The KDHS provides standardized data on population health, fertility, maternal and child health, nutrition, and selected non-communicable diseases, ensuring comparability across countries through uniform protocols. The 2022 KDHS was implemented by the Kenya National Bureau of Statistics in collaboration with ICF International. The data are publicly available through the DHS Program and provide estimates at national and subnational levels. The sample was drawn from the Kenya Household Master Sample Frame using a two-stage stratified sampling design. In the first stage, 1,692 clusters (enumeration areas) were selected from urban and rural strata using equal probability selection. In the second stage, households were selected systematically within each cluster. This analysis used the Individual Record (IR) dataset. The source population comprised women aged 15–49 years, and the final weighted sample included 32,156 women. Sampling weights adjusted for unequal selection probabilities, non-response, and other sampling biases. Although cervical cancer screening targets women aged 25–49 years, this study included women aged 15–24 years to capture early screening patterns across the full reproductive age range.

Sampling Procedure

The DHS employs a stratified two-stage cluster sampling design based on the most recent national population and housing census. In the first stage, enumeration areas (EAs) are selected using probability proportional to size within defined strata (typically region and urban–rural residence). In the second stage, households are systematically selected from each sampled EA. All eligible women within selected households are invited to participate. The survey design ensures national representativeness, as well as representativeness by region and place of residence. Sampling weights are provided in the DHS dataset to adjust for unequal probabilities of selection and non-response.

Study Population

The analysis included 32,156 women aged 15–49 years who had complete data on key socio-demographic, reproductive, and nutritional variables; this constituted the analytic sample for describing socio-demographic characteristics (Table 1). Of these 32,156 women, 15,440 (48.0%) were excluded from the cancer-related analyses

Table 1. Socio-demographic Characteristics

Variables	Weighted Frequency N (%)
Age	
15-24	12,026(37.40)
25-34	10,217(31.77)
35-49	9,912(30.83)
Highest Educational Level	
No education	1,769(5.50)
Primary	11,686(36.34)
Secondary	12,549(39.03)
Higher	6,149(19.12)
Type of place of residence	
Urban	13,143(40.87)
Rural	19,013(51.13)
Current marital status	
Never in union	10,437(32.46)
Married	15,482(48.15)
Living with partner	2,339(5.78)
Widowed	907(2.82)
Divorced	454(1.41)
No longer living together	2,534(7.88)
Wealth quantile	
Poorest	8,440(16.53)
Poorer	6,311(19.63)
Middle	6,528(20.30)
Richer	6,750(20.99)
Richest	7,249(22.54)
Nutritional status	
Currently pregnant	
No or unsure	30,394(94.52)
Yes	1,762(5.48)

Table 1. Socio-demographic Characteristics (cont'd)

Variables	Weighted Frequency N (%)
Births in last five years	
No births	18,544(57.67)
1 birth	10,179(31.65)
2 births	3,035(9.44)
3 births	368(1.14)
4 births	29(0.09)
5 births	1(0.00)
Body Mass Index	
Underweight	1,513(9.17)
Normal weight	8,656(52.50)
Overweight	3,995(24.23)
Obesity	1,680(10.19)
Morbid obesity	645(3.91)
Diagnosis	
Told they had breast cancer	
No	16,687(99.83)
Yes	29(0.17)
Told they had cervical cancer	
No	16,685(99.81)
Yes	31(0.19)
Treatment	
Receiving treatment for breast cancer (n=29)	
No	21(72.46)
Yes	8(27.54)
Receiving treatment for cervical cancer (n=31)	
No	17(54.13)
Yes	14(45.87)

because they had incomplete information on breast and/or cervical cancer diagnosis, leaving a weighted subsample of 16,716 respondents (52.0%) with complete cancer diagnosis data; this subsample was used for all breast and cervical cancer diagnosis analyses (Table 2). The exclusion was therefore entirely attributable to missing cancer-diagnosis data rather than any other eligibility criterion. Analyses of treatment uptake were further restricted to women who self-reported a diagnosis of breast cancer (n = 29) or cervical cancer (n = 31). The flow of participants through these successive analytic samples is summarised in Figure 3.

Study Variables

Outcome Variables

The primary outcomes were:

1. Self-reported diagnosis of breast cancer (coded "1" as Yes and "0" No).
2. Self-reported diagnosis of cervical cancer (coded "1" as Yes and "0" No).
3. Receipt of treatment among women who reported a diagnosis of breast or cervical cancer (coded "1" as Yes and "0" No).

Table 2. Factors Associated with Self-Reported Breast and Self-Reported Cervical Cancer

Variables	Self-Reported Breast Cancer		X^2	p-value	Self-Reported Breast Cancer		X^2	p-value
	Weighted No (%)	Weighted Yes (%)			Weighted No (%)	Weighted Yes (%)		
Residence			0.694	0.405			0.219	0.640
Urban	6,842(41.0)	9(29.3)			6,836(41.0)	14(46.2)		
Rural	9,845(59.0)	20(70.7)			9,849(59.0)	17(53.8)		
Wealth quantile			13.247	0.010			6.600	0 .159
Poorest	2,725(16.3)	16(53.7)			2,738(16.4)	2(8.8)		
Poorer	3,215(19.3)	2(6.6)			3,216(19.3)	2(5.1)		
Middle	3,494(20.9)	3(12.4)			3,491(20.9)	6(19.9)		
Richer	3,427(20.5)	5(15.3)			3,416(20.5)	16(50.9)		
Richest	3,824(22.9)	3(12.0)			3,823(22.91)	5(15.4)		
Nutritional status								
Currently pregnant			0.927	0.336			0.056	0.813
No or unsure (Ref)	15,758 (94.4)	929 (5.6)			15,754(94.4)	29 (92.2)		
Yes	25(85.8)	4(14.2)			931(5.6)	2 (7.8)		
Births in last five years			9.487	0.091			2.431	0.787
No births (Ref)	9,675(58.0)	9(30.5)			9,661(57.9)	22(74.0)		
1 birth	5,222(31.3)	13(45.0)			5,229(31.3)	6(20.2)		
2 births	1,580(9.5)	7(24.5)			1,586(9.5)	1(2.2)		
3 births	190(1.1)	0			189(1.1)	2(3.7)		
4 births	18(0.1)	0			18(0.1)	0		
5 births	1(0.0)	0			1(0.0)	0		
Body Mass Index			4.051	0.399			0.821	0.936
Underweight (Ref)	1,511 (9.2)	1 (4.13)			1,510(9.2)	2(5.8)		
Normal weight	8,637(52.5)	19(66.7)			8,639(52.5)	17(56.9)		
Over weight	3,987(24.2)	8(26.3)			3,985(24.2)	9(31.5)		
Obesity	1,679(10.2)	1(2.9)			1,679 (10.2)	2(4.8)		
Morbid obesity	644(3.9)	0			644(3.9)	1(1.1)		

Independent Variables

Explanatory variables were selected based on prior literature and data availability and included:

a. Place of residence (urban/rural)
b. Wealth quintile (poorest, poorer, middle, richer, richest)
c. Current pregnancy status (yes/no or unsure)
d. Number of births in the last five years (0, 1, 2, 3, 4, 5)
e. Body Mass Index (BMI) categorized as underweight, normal weight, overweight, obese, and morbidly obese

Socio-demographic characteristics such as age, education level, marital status, and wealth index were also described.

Data Management and Statistical Analysis

Data were analyzed using Stata version 17. Sampling weights were applied to account for unequal selection probabilities, non-response, and the complex survey design, including clustering and stratification, to obtain nationally representative estimates. Descriptive statistics summarized socio-demographic and health-related characteristics using frequencies and percentages. Bivariate associations between explanatory variables and outcomes were assessed using design-adjusted Pearson's chi-square tests (svy: tab). All analyses focused on women aged 15–49 years, consistent with DHS survey coverage. This restriction limits generalisability to older women, who may have a higher burden of cancer. Finally, the self-reported nature of cancer diagnosis and treatment introduces potential misclassification and reporting bias, likely leading to underestimation of true prevalence due to limited screening access and diagnostic confirmation in the surveyed population.

Results

Socio-demographic Characteristics

A total of 32,156 women were included in the analysis. Most were aged 15–24 years (37.40%), followed by 25–34 years (31.77%) and 35–49 years (30.83%). Secondary education was the most common attainment (39.03%), followed by primary (36.34%), higher (19.12%), and no formal education (5.50%). Slightly over half resided in rural areas (51.13%), while 40.87% were urban residents. Regarding marital status, 48.15% were married, 32.46% had never been in a union, and the remainder were cohabiting (5.78%), widowed (2.82%), divorced (1.41%), or separated (7.88%). Wealth status was relatively evenly distributed across quintiles, ranging from 16.53% in the poorest to 22.54% in the richest group. Most respondents were not pregnant at the time of the survey (94.52%), and 57.67% reported no births in the preceding five years. In terms of nutritional status, 52.50% had a normal BMI, 24.23% were overweight, 10.19% obese, 9.17% underweight, and 3.91% morbidly obese.

Among women with complete cancer data (n = 16,716), self-reported prevalence was 0.17% for breast cancer (n = 29) and 0.19% for cervical cancer (n = 31). Of those diagnosed, 27.54% of breast cancer cases and 45.87% of cervical cancer cases reported receiving treatment.

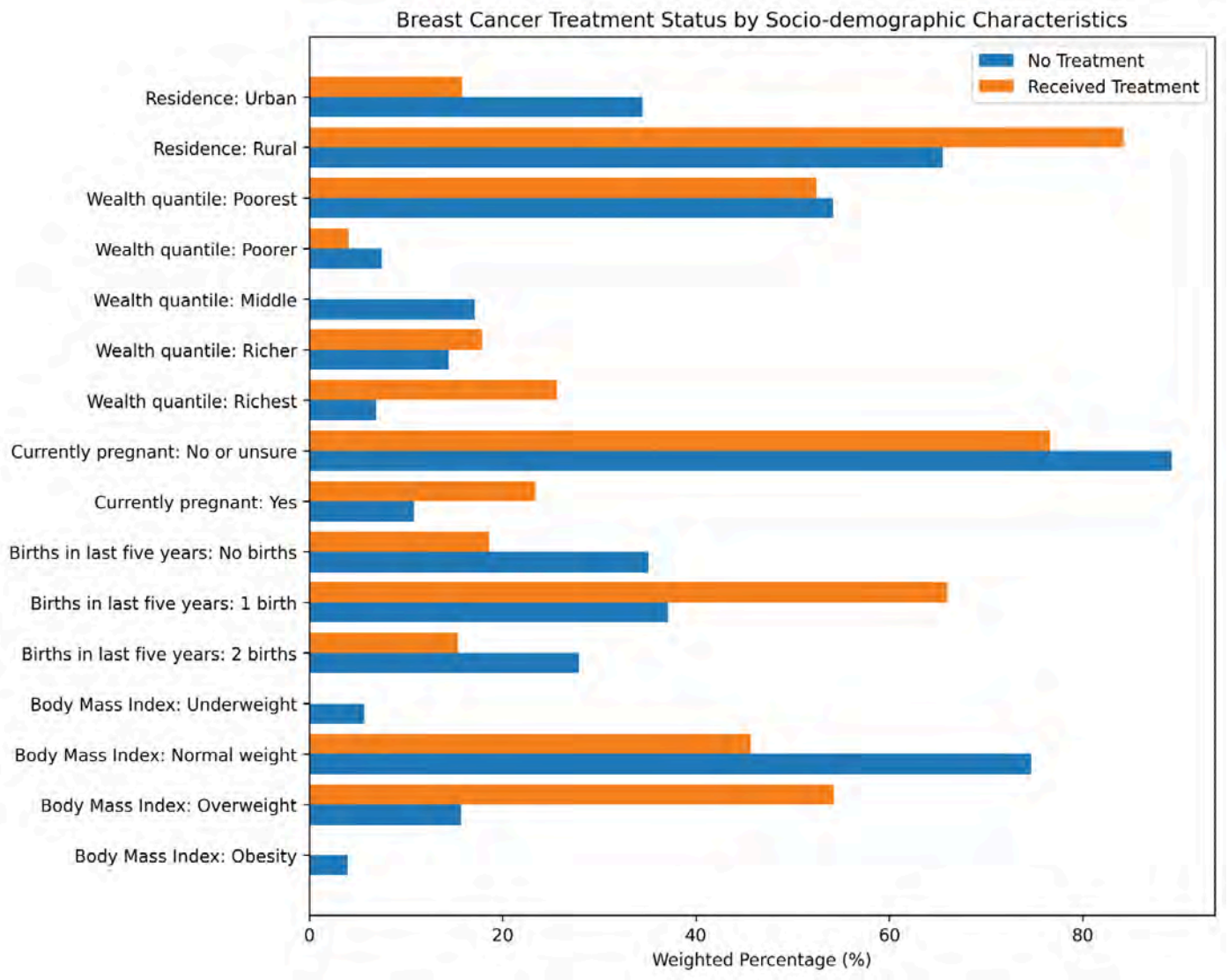

Figure 1: Weighted percentage distribution of selected socio-demographic and reproductive characteristics among women self-reporting a breast cancer diagnosis (n = 29), comparing those who received treatment with those who did not. Percentages are DHS-sampling-weight-adjusted column percentages calculated within each treatment group (Yes/No). .

Overall, self-reported cancer prevalence was low, while treatment coverage among diagnosed cases remained suboptimal (Table 1).

Prevalence of Self-Reported Breast Diagnosis

Among women who self-reported breast cancer, 70.7% resided in rural areas, while 29.3% lived in urban areas. More than half of the breast cancer cases (53.7%) were observed among women in the poorest wealth quintile, followed by the richer (15.3%), middle (12.4%), richest (12.0%), and poorer (6.6%) wealth quintiles. Regarding reproductive characteristics, 45.0% of women with breast cancer had one birth in the preceding five years, 30.5% had no births, and 24.5% had two births. With respect to nutritional status, most breast cancer cases occurred among women with normal body mass index (66.7%), followed by overweight (26.3%), underweight (4.1%), and obese women (2.9%) (Table 2).

Prevalence of Self-Reported Cervical Cancer Diagnosis

Among women who self-reported cervical cancer, 53.8% resided in rural areas and 46.2% in urban areas. The highest proportion of cervical cancer cases was observed among women in the richer wealth quintile (50.9%), followed by the middle (19.9%), richest (15.4%), poorest (8.8%), and poorer (5.1%) wealth quintiles. Regarding reproductive history, cervical cancer cases were distributed across women with varying numbers of births in the preceding five years, with no marked differences between categories. Most cervical cancer cases occurred among women with normal body mass index (56.9%), followed by overweight (31.5%), underweight (5.8%), obese (4.8%), and morbidly obese women (1.1%) (Table 2).

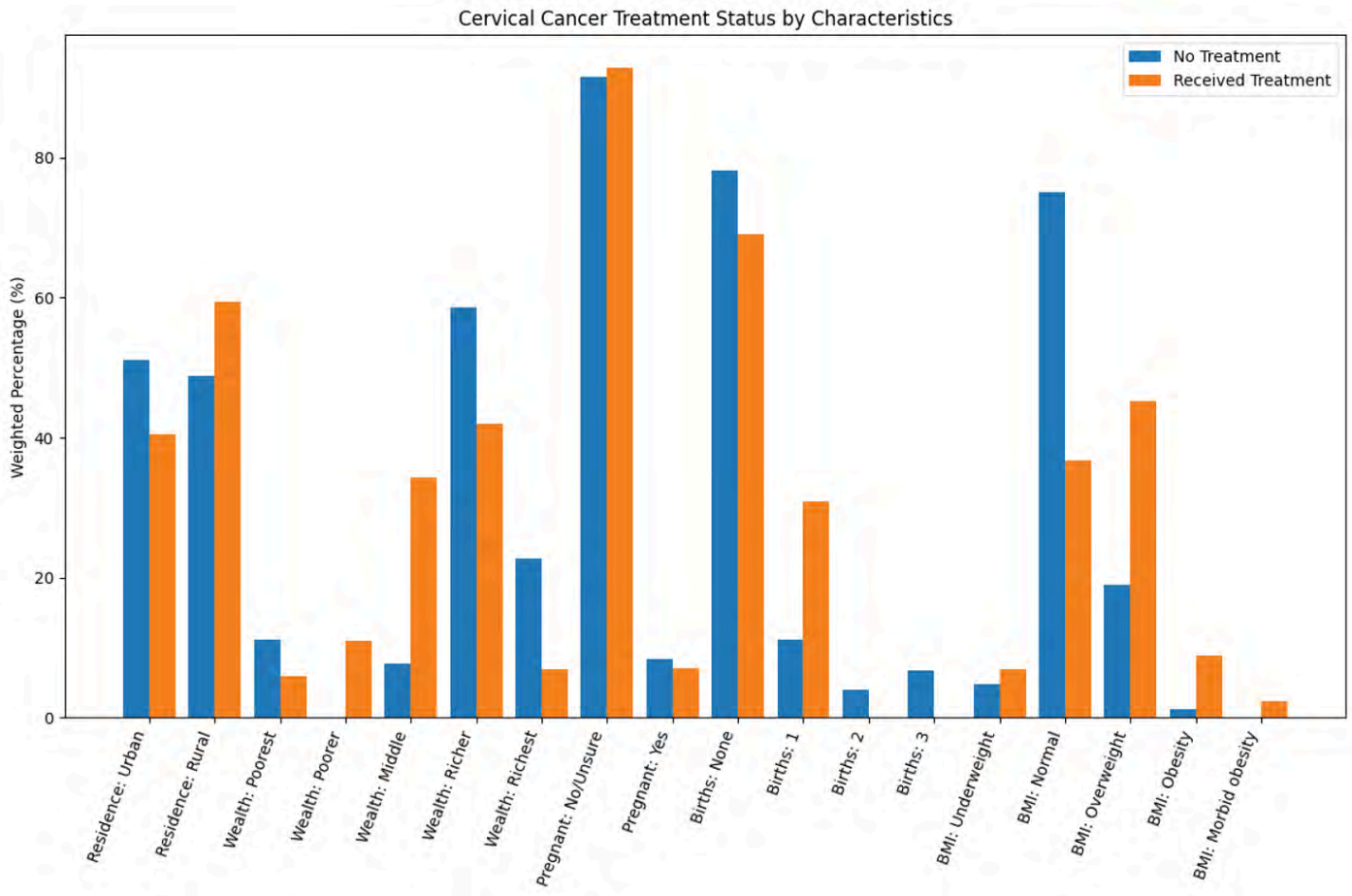

Figure 2: Weighted percentage distribution of selected socio-demographic and reproductive characteristics among women self-reporting a cervical cancer diagnosis (n = 31), comparing those who received treatment with those who did not. Percentages are DHS-sampling-weight-adjusted column percentages calculated within each treatment group (Yes/No). BMI = Body Mass Index.

Factors Association with Self-Reported Breast Cancer diagnosis

There was no statistically significant association between place of residence and self-reported breast cancer (χ^2 = 0.694, p = 0.405). Wealth quintile was significantly associated with breast cancer (χ^2 = 13.247, p = 0.010). Current pregnancy status was not significantly associated with breast cancer (χ^2 = 0.927, p = 0.336). Likewise, the number of births in the past five years showed no statistically significant association (χ^2 = 9.487, p = 0.091). Body mass index was also not significantly associated with breast cancer (χ^2 = 4.051, p = 0.399) (Table 2).

Factors Association with Self-Reported Cervical Cancer diagnosis

There was no statistically significant association between place of residence and cervical cancer (χ^2 = 0.219, p = 0.640). Wealth quintile was not significantly associated with cervical cancer (χ^2 = 6.600, p = 0.159). Similarly, current pregnancy status (χ^2 = 0.056, p = 0.813) and the number of births in the past five years (χ^2 = 2.431, p = 0.787) showed no statistically significant associations with cervical cancer. Body mass index was also not significantly associated with cervical cancer (χ^2 = 0.821, p = 0.936) (Table 2).

Characteristics of Women Receiving and Not Receiving Breast Cancer Treatment

Among women who received breast cancer treatment, the majority resided in rural areas (84.2%), compared with 65.5% among those who did not receive treatment. The poorest wealth quintile accounted for over half of both treated (52.5%) and untreated women (54.2%); however, the richest wealth quintile was more represented among treated women (25.6%) than untreated women (6.9%). Current pregnancy was reported by 23.4% of treated women compared with 10.8% of untreated women. Most treated women had one birth in the previous five years (66.0%), whereas untreated women were more evenly distributed across no births (35.1%), one birth (37.1%), and two births (27.9%). Regarding BMI, overweight women constituted the largest proportion of the treated group (54.3%), while normal-weight women predominated among untreated women (74.7%). Overall, treated women were more likely than untreated women to reside in rural areas, belong to the richest wealth quintile, be currently pregnant, have had one recent birth, and be overweight (Figure 1).

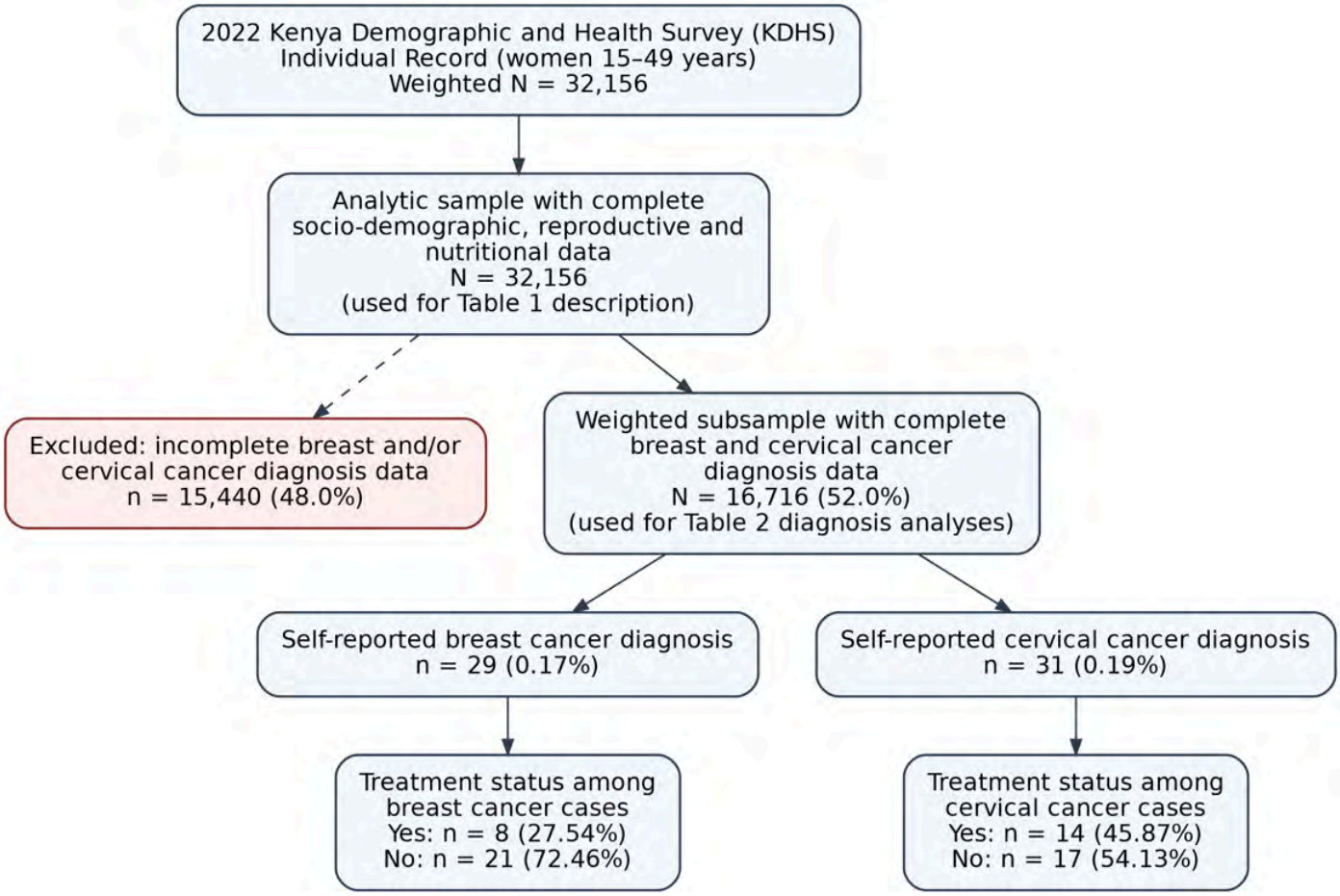

Figure 3: Flow diagram of the analytic sample. Women aged 15–49 years with complete socio-demographic, reproductive and nutritional data (N = 32,156) formed the sample described in Table 1. Of these, 15,440 (48.0%) were excluded from the cancer-related analyses because they had incomplete breast and/or cervical cancer diagnosis data, leaving a weighted subsample of 16,716 (52.0%) women with complete diagnosis data, used for the diagnosis analyses in Table 2. Treatment-uptake analyses were further restricted to women who self-reported a diagnosis of breast cancer (n = 29) or cervical cancer (n = 31).

Distribution of Cervical Cancer Treatment Status by Selected Characteristics

Cervical cancer treatment likewise varied according to selected socio-demographic and reproductive characteristics. A greater proportion of treated women resided in rural areas (59.5%) than in urban areas (40.5%). Treatment uptake was highest among women in the middle wealth quintile (34.3%) and richer quintile (41.9%). Most women receiving treatment were not pregnant at the time of the survey (92.9%) and had no births within the previous five years (69.1%). Overweight women constituted the largest proportion of treated participants (45.2%). Overall, a greater proportion of treated women were rural residents, of middle-to-higher wealth status, had one recent birth, and were overweight, compared with untreated women (Figure 2).

Discussion

This study examined the prevalence of self-reported breast and cervical cancer, factors associated with these cancers, and patterns of treatment uptake among women of reproductive age using nationally representative survey data. Overall, the prevalence of both cancers was low, with only 0.17% of women reporting a breast cancer diagnosis and 0.19% reporting a cervical cancer diagnosis. Furthermore, treatment coverage among diagnosed women remained poor, with only 27.54% of women with breast cancer and 45.87% of those with cervical cancer reporting that they were receiving treatment. These findings should be interpreted as reflecting awareness of diagnosis and access to diagnostic services rather than the true population prevalence of cancer among women aged 15–49 years. Because diagnoses were self-reported and restricted to women of reproductive age, the observed prevalence likely underestimates the actual prevalence, particularly among older women who are at substantially greater risk of both cancers. Underdiagnosis, low screening coverage, and limited awareness may have further contributed to the low prevalence observed in this study [19,20].

The bivariate analysis further demonstrated that wealth status was the only characteristic significantly associated with self-reported breast cancer, whereas residence,

pregnancy status, recent parity, and body mass index were not associated with self-reported breast cancer diagnosis. More than half of women with breast cancer belonged to the poorest wealth quintile, suggesting that socioeconomic disadvantage may influence breast cancer diagnosis or the distribution of disease within this population. Previous studies have shown that socioeconomic position influences breast cancer awareness, participation in screening, timely diagnosis, and access to healthcare services through differences in education, financial resources, and health-seeking behaviour [21–23]. Nevertheless, because the present study relied on self-reported diagnoses and identified only a small number of breast cancer cases, these findings should be interpreted cautiously. The significant association with wealth may partly reflect disparities in healthcare utilisation or diagnostic opportunities rather than true differences in disease diagnosis.

In contrast, none of the selected characteristics, including residence, wealth status, pregnancy status, parity, and body mass index, showed statistically significant associations with self-reported cervical cancer. Although descriptive results indicated that cervical cancer cases were proportionally more common among women in the richer wealth quintile and among rural residents, these differences did not reach statistical significance. This finding suggests that, within this nationally representative sample, self-reported cervical cancer diagnosis was relatively similar across socioeconomic and reproductive groups. However, the small number of diagnosed cases substantially reduced statistical power and may have limited the ability to detect meaningful associations. Similar observations have been reported in low- and middle-income countries where low screening coverage and delayed diagnosis obscure underlying socioeconomic differences in cervical cancer prevalence [24–28].

Despite the low prevalence of self-reported diagnosis of both cancers, treatment coverage remained suboptimal, particularly among women with breast cancer, where fewer than one-third reported receiving treatment. Likewise, more than half of women diagnosed with cervical cancer were not receiving treatment. These findings highlight persistent gaps across the cancer care continuum, including delayed diagnosis, inadequate referral systems, limited availability of oncology services, financial barriers, transportation challenges, and sociocultural factors influencing healthcare utilisation [21–23]. Similar barriers have been documented across many low-resource settings where specialised cancer services remain concentrated in major urban centres and are often inaccessible to large segments of the population.

With respect to breast cancer treatment, descriptive findings suggested variation across socioeconomic and reproductive characteristics. A greater proportion of treated women resided in rural areas compared with untreated women, while women in the richest wealth quintile represented a larger proportion of treated cases than untreated cases despite most diagnosed women belonging to the poorest wealth quintile. In addition, treated women were more likely to be currently pregnant, have had one birth within the previous five years, and be overweight. These patterns may indicate that contact with maternal health services and greater financial resources facilitate earlier referral and treatment initiation. Pregnancy and recent reproductive healthcare encounters may increase opportunities for clinical examination, counselling, and referral, while higher socioeconomic status may improve the ability to afford diagnostic investigations and treatment costs [29–32]. However, because these observations are descriptive and based on a very small number of treated women, they should not be interpreted as evidence of causal relationships.

Similarly, cervical cancer treatment varied across selected characteristics. Treated women were more likely to reside in rural areas and belonged predominantly to the middle and richer wealth quintiles. Most treated women were not pregnant, had no births within the previous five years, and were overweight. Although rural populations are frequently reported to experience substantial barriers to specialised healthcare, including long travel distances and shortages of oncology services, the greater proportion of treated rural women observed in this study may reflect successful referral pathways, targeted health interventions, or differences in healthcare-seeking behaviour among women who had already received a diagnosis [24–28]. Likewise, the higher representation of women from middle and richer wealth households among treated cases supports previous evidence that economic resources influence access to diagnostic services, treatment initiation, and continuity of care by reducing both direct and indirect healthcare costs [29–32]. Nevertheless, because wealth status was not significantly associated with self-reported cervical cancer diagnosis and the number of diagnosed women was limited, these descriptive differences may simply reflect random variation rather than true socioeconomic inequalities in treatment uptake [33–37].

Furthermore, reproductive characteristics appeared to show little influence on cervical cancer treatment. Most treated women were not pregnant and had no recent births, although descriptive differences were observed between treated and untreated groups. These findings suggest that reproductive factors may play a limited role in determining treatment uptake once cervical cancer has been diagnosed. Likewise, overweight women constituted the largest proportion of treated cervical cancer cases, whereas women with normal body weight represented the largest proportion of untreated cases. Although overweight and obesity have been associated with differences in healthcare utilisation and cancer outcomes in some settings, body mass index was not significantly associated with self-reported cervical cancer diagnosis in this study [38–43]. Consequently, these descriptive differences should be interpreted cautiously given the limited sample size.

Taken together, the findings indicate that although socioeconomic characteristics particularly wealth status may influence the prevalence of self-reported breast cancer and patterns of treatment uptake for both cancers, statistically significant associations were largely absent, especially for cervical cancer. The consistently low treatment coverage observed for both breast and cervical cancer underscores important deficiencies in access to timely diagnosis and effective treatment among women of reproductive age. Strengthening screening programmes, improving referral systems, expanding equitable access to oncology services, and reducing financial barriers remain critical priorities for improving cancer outcomes in low-resource settings. Future studies incorporating clinically verified diagnoses, larger numbers of confirmed cancer cases, and longitudinal follow-up are needed to better understand determinants of self-reported cervical cancer diagnosis and treatment uptake and to identify effective strategies for improving access to comprehensive cancer care [44, 45].

Strengths and Limitations

A major strength of this study is the use of nationally representative survey data, which enhances the generalisability of the findings to women of reproductive age. The large sample size, standardized data collection procedures, and rigorous sampling design provide reliable population-level estimates of prevalence of self-reported diagnosis of breast and cervical cancer and treatment uptake. Additionally, the study simultaneously examined disease diagnosis, associated characteristics, and treatment patterns, providing a broader understanding of the cancer care continuum among women of reproductive age.

However, several limitations should be acknowledged. First, both breast and cervical cancer diagnoses were self-reported rather than clinically verified, making the findings susceptible to recall bias, reporting bias, and potential misclassification. Second, the analysis was restricted to women aged 15–49 years, excluding older women who bear the greatest prevalence of both cancers. Third, the cross-sectional design precludes causal inference between the selected characteristics and self-reported cervical cancer diagnosis or treatment uptake. Finally, the very small number of women reporting breast or cervical cancer substantially limited statistical power, reducing the precision of the estimates and the ability to detect significant associations. Consequently, the findings relating to treatment patterns and associated characteristics should be interpreted cautiously and confirmed using larger studies with clinically confirmed diagnoses.

Implications for Policy and Practice

The findings suggest potential gaps in cancer awareness, diagnosis, and treatment among reproductive-age women. Strengthening prevention efforts should prioritise improved public awareness, expanded screening coverage, and integration of basic cancer services into primary healthcare systems. Given observed socioeconomic differences in reported outcomes, policies that reduce financial and geographic barriers to care may improve access to diagnosis and treatment. Expanding HPV vaccination and early detection services is also important for reducing future disease prevalence in this population.

Conclusion

This study highlights important socioeconomic patterns in self-reported breast cancer and reveals gaps in treatment uptake for both breast and cervical cancers among women of reproductive age. Although few identified cases of self-reported cancers, the findings emphasize the importance of strengthening early detection systems and addressing structural barriers to cancer care. Further research with clinically verified diagnoses and broader age groups is needed to better understand the patterns of cancer prevalence and treatment access.

Acknowledgements

We express our profound gratitude to DHS program for permitting us to use DHS data for the studies. We also thank the staff of the Biomedical and Clinical Research Centre for supporting the study.

Author contribution

Conceptualization, K.K.A; Data curation, G. A, B. A. K, E.K.O, L.A; Formal analysis, K.K.A, G. A, B. A. K, E.K.O, L.A; Methodology, G. A, B. A. K, E.K.O, L.A; Writing– original draft, K.K.A; Writing – review & editing. G. A, B. A. K, E.K.O, L.A.

Funding: No funding was received for this research.

Declaration:

Conflicts of Interest: No, there is no conflict of interest.

Ethical Considerations: The DHS protocol received ethical approval from the relevant national ethics review committees and the Institutional Review Board (IRB) of ICF. Written informed consent was obtained from all participants prior to data collection. Permission to use the dataset was obtained from the DHS Program. The current analysis was based on anonymized, publicly available secondary data and therefore did not require additional ethical approval.

Data Availability: The datasets analyzed in this study are not included in the manuscript. They are publicly available from the DHS Program (https://dhsprogram.com) upon reasonable request and approval.

References

1. Li Y, Song W, Gao P, Guan X, Wang B, Zhang L, Yao Y, Guo Y, Wang Y, Jiang S, Sun S. Global, regional, and national burden of breast, cervical, uterine, and ovarian cancer and their risk factors among women from 1990 to 2021, and projections to 2050: findings from the global burden of disease study 2021. BMC cancer. 2025 Feb 24;25(1):330.

2. Arbyn M, Weiderpass E, Bruni L, de Sanjosé S, Saraiya M, Ferlay J, Bray F. Estimates of incidence and mortality of cervical cancer in 2018: a worldwide analysis. The Lancet Global Health. 2020 Feb 1;8(2):e191-203.

3. Denny L, de Sanjose S, Mutebi M, Anderson BO, Kim J, Jeronimo J, Herrero R, Yeates K, Ginsburg O, Sankaranarayanan R. Interventions to close the divide for women with breast and cervical cancer between low-income and middle-income countries and high-income countries. The Lancet. 2017 Feb 25;389(10071):861-70.

4. Torre LA, Islami F, Siegel RL, Ward EM, Jemal A. Global cancer in women: burden and trends. Cancer epidemiology, biomarkers & prevention. 2017 Apr 1;26(4):444-57.

5. Rajabpour MV, Nemati S, Seyyedsalehi MS, Nahvijou A, Abdi S, Garousi M, Omranipour R, Abdollahi A, Aghili M, Motlagh A, Javanmad SH. Socioeconomic disparities impacting breast cancer care and survival in Iran. Scientific Reports. 2025 Oct 21;15(1):36776.

6. Adisu MA, Habtie TE, Kitaw TA, Gessesse AD, Woreta BM, Derso YA, Zemariam AB. The rising burden of female cancer in Ethiopia (2000–2021) and projections to 2040: Insights from the global burden of disease study. Plos one. 2025 Oct 7;20(10): e0333787.

7. McCormack VA, Boffetta P. Today's lifestyles, tomorrow's cancers: trends in lifestyle risk factors for cancer in low-and middle-income countries. Annals of Oncology. 2011 Nov 1;22(11):2349-57.

8. Wirtz C, Mohamed Y, Engel D, Sidibe A, Holloway M, Bloem P, Kumar S, Brotherton J, Reis V, Morgan C. Integrating HPV vaccination programs with enhanced cervical cancer screening and treatment, a systematic review. Vaccine. 2022 Mar 31;40:A116-23.

9. Okunade KS, Adejimi AA, John-Olabode SO, Oshodi YA, Oluwole AA. An overview of HPV screening tests to improve access to cervical cancer screening amongst underserved populations: from development to implementation. Risk management and healthcare policy. 2022 Jan 1:1823-30.

10. Afaya A, Ramazanu S, Bolarinwa OA, Yakong VN, Afaya RA, Aboagye RG, Daniels-Donkor SS, Yahaya AR, Shin J, Dzomeku VM, Ayanore MA. Health system barriers influencing timely breast cancer diagnosis and treatment among women in low and middle-income Asian countries: evidence from a mixed-methods systematic review. BMC Health Services Research. 2022 Dec 31;22(1):1601.

11. Gadiraju P, Vanlalhruaii C, Dehury RK, Singh P, Ahmad I, Dehury P. Role of social determinants of health in reproductive cancer care among women: A cross-sectional survey from diverse demographic and regional settings in India. Asia Pacific Journal of Health Management. 2024 Oct;19(2):65-73.

12. Islam MR, Islam H, Siddiqua SM, Al Ayub SB, Saha B, Akter N, Islam R, Khatun N, Craver A, Ahsan H. Understanding Cancer Risk Among Bangladeshi Women: An Explainable Machine Learning Approach to Socio-Reproductive Factors Using Tertiary Hospital Data. InHealthcare 2025 Jun 15 (Vol. 13, No. 12, p. 1432). MDPI.

13. Scott EC, Hoskin PJ. Health inequalities in cancer care: a literature review of pathways to diagnosis in the United Kingdom. EClinicalMedicine. 2024 Oct 1;76.

14. Zapata-Moya ÁR, Willems B, Bracke P. The (re) production of health inequalities through the process of disseminating preventive innovations: the dynamic influence of socioeconomic status. Health Sociology Review. 2019 May 4;28(2):177-93.

15. Temane MD, Mbele SK, Tsawe M. Determinants of self-reported chronic disease diagnoses among older persons in South Africa. African Journal of Primary Health Care & Family Medicine. 2024 Apr 30;16(1):4425.

16. Mwanga DM, Kipchirchir IC, Muhua GO, Newton CR, Kadengye DT. Accounting for clustering for self-reported outcomes in the design and analysis of population-based surveys: A case study of estimation of prevalence of epilepsy in Nairobi, Kenya. Frontiers in Research Metrics and Analytics. 2025 Sep 1;10:1583476.

17. Asare KK, Aboagye YO, Mohammed MD, Darko M, Adjei C, Emmanuels HF, Boakye AN, Asiedu E. False-positive and false-negative malaria rapid diagnostic test results: evidence from a nationally representative survey of children in Ghana. Malaria Journal. 2026 Jan 3.

18. Iqbal A, Ahsan KZ, Jamil K, Haider MM, Khan SH, Chakraborty N, Streatfield PK. Demographic, socioeconomic, and biological correlates of hypertension in an adult population: evidence from the Bangladesh demographic and health survey 2017–18. BMC Public Health. 2021 Jun 26;21(1):1229.

19. Clair PS, Gaudette É, Zhao H, Tysinger B, Seyedin R, Goldman DP. Using self-reports or claims to assess

disease prevalence: it's complicated. Medical Care. 2017 Aug 1;55(8):782-8.

20. Stavrou E, Vajdic CM, Loxton D, Pearson SA. The validity of self-reported cancer diagnoses and factors associated with accurate reporting in a cohort of older Australian women. Cancer epidemiology. 2011 Dec 1;35(6):e75-80.

21. Ahmad IA. A scoping review of barriers within the cancer care continuum: Addressing screening, diagnosis, and treatment disparities for an equitable future. Advances in Medicine, Psychology, and Public Health. 2025 Mar 3;2(2):96-106.

22. Mansour R, Abdel-Razeq H, Al-Hussaini M, Shamieh O, Al-Ibraheem A, Al-Omari A, Mansour AH. Systemic barriers to optimal cancer care in resource-limited countries: Jordanian healthcare as an example. Cancers. 2024 Mar 11;16(6):1117.

23. Patel B, Kircher SM, Rodriguez GM. Disparities Along the Cancer Care Continuum: The Role of Social Drivers of Health on Gastrointestinal Malignancies. Advances in Oncology. 2025 May 1;5(1):267-81.

24. Moss JL, Liu B, Feuer EJ. Urban/rural differences in breast and cervical cancer incidence: the mediating roles of socioeconomic status and provider density. Women's Health Issues. 2017 Nov 1;27(6):683-91.

25. Yeşilfidan D, Özkan M, Adana F. Comparison of cervical Cancer-Related knowledge, attitudes, and behaviors among women in urban and rural regions. Bmc Public Health. 2025 Jul 28;25(1):2561.

26. Zahnd WE, James AS, Jenkins WD, Izadi SR, Fogleman AJ, Steward DE, Colditz GA, Brard L. Rural–urban differences in cancer incidence and trends in the United States. Cancer Epidemiology, Biomarkers & Prevention. 2018 Nov 1;27(11):1265-74.

27. Goodwin BC, Rowe AK, Crawford-Williams F, Baade P, Chambers SK, Ralph N, Aitken JF. Geographical disparities in screening and cancer-related health behaviour. International journal of environmental research and public health. 2020 Feb;17(4):1246.

28. Keruakous AR, Soror N, Jiménez S, Ashley R, Keruakous M, Sadek BT. Barriers driving health care disparities in utilization of age-appropriate screening. Frontiers in Public Health. 2023 Mar 3;11:1100466.

29. Lin C, Mella-Velazquez A, Braund WE, Tu P. Disparities in Healthcare-Seeking Behavior and Decision Preference Among Hispanics: A Comparative Study Across Races/Ethnicities, SES, and Provider Types. Journal of Multidisciplinary Healthcare. 2024 Dec 31:3849-62.

30. Li L, Fu L, Li H, Liu T, Sun J. Emerging trends and patterns in healthcare-seeking behavior: A systematic review. Medicine. 2024 Feb 23;103(8):e37272.

31. Lyra-González I, Cuello M, Anderson D, Echeverri M. Socioeconomic disparities and health literacy: Unraveling the impact on diagnostic and cancer care in Uruguay. Journal of cancer policy. 2024 Jun 1;40:100472.

32. Castro S, Sosa E, Lozano V, Akhtar A, Love K, Duffels J, Raz DJ, Kim JY, Sun V, Erhunmwunsee L. The impact of income and education on lung cancer screening utilization, eligibility, and outcomes: a narrative review of socioeconomic disparities in lung cancer screening. Journal of thoracic disease. 2021 Jun;13(6):3745.

33. Galindo JF, Formigari GM, Zeferino LC, Carvalho CF, Ursini EL, Vale DB. Social determinants influencing cervical cancer diagnosis: an ecological study. International journal for equity in health. 2023 May 25;22(1):102.

34. Mahumud RA, Keramat SA, Ormsby GM, Sultana M, Rawal LB, Alam K, Gow J, Renzaho AM. Wealth-related inequalities of women's knowledge of cervical cancer screening and service utilisation in 18 resource-constrained countries: evidence from a pooled decomposition analysis. International journal for equity in health. 2020 Mar 26;19(1):42.

35. Cetina-Pérez L, Luvián-Morales J, Delgadillo-González M, Castro-Eguiluz D, Galicia-Carmona T, Rely K, Vaca González R, Lugo-Martínez G, García-Barrientos N, Nateras A. Sociodemographic characteristics and their association with survival in women with cervical cancer. BMC cancer. 2024 Feb 1;24(1):161.

36. Srilalitha V, Kumar BH, Chakorkar S, Srudeepthi M. Addressing Health Disparities: Strategies for Achieving Health Equity in Low-Resource Setting. Journal of Neonatal Surgery. 2025;14(4):368-77.

37. Van Zyl C, Badenhorst M, Hanekom S, Heine M. Unravelling 'low-resource settings': a systematic scoping review with qualitative content analysis. BMJ global health. 2021 Jun 3;6(6).

38. Nafissi N, Faraji M, Hosseini M, Shojaee L, Ziaei F, Akbari ME, Mousavie SH. Relationships between reproductive risk factors for breast cancer and tumor molecular subtypes. Asian Pacific journal of cancer prevention: APJCP. 2018;19(7):1767.

39. Troisi R, Bjørge T, Gissler M, Grotmol T, Kitahara CM, Myrtveit Saether SM, Ording AG, Sköld C, Sørensen HT, Trabert B, Glimelius I. The role of pregnancy, perinatal factors and hormones in maternal cancer risk: a review of the evidence. Journal of internal medicine. 2018 May;283(5):430-45.

40. García-Sancha N, Corchado-Cobos R, Pérez-Losada J. Understanding susceptibility to breast cancer: from risk factors to prevention strategies. International Journal of Molecular Sciences. 2025 Mar 25;26(7):2993.

41. Sung H, Siegel RL, Torre LA, Pearson-Stuttard J, Islami F, Fedewa SA, Goding Sauer A, Shuval K, Gapstur SM, Jacobs EJ, Giovannucci EL. Global patterns in excess body weight and the associated cancer burden. CA: a cancer journal for clinicians. 2019 Mar;69(2):88-112.

42. Hidayat K, Du X, Shi BM. Body fatness at a young age and risks of eight types of cancer: systematic review and meta-analysis of observational studies. Obesity Reviews. 2018 Oct;19(10):1385-94.

43. Islami F, Goding Sauer A, Gapstur SM, Jemal A. Proportion of cancer cases attributable to excess body weight by US state, 2011-2015. JAMA oncology. 2019 Mar;5(3):384-92.

44. Hendriksen JM, Geersing GJ, Moons KG, de Groot JA. Diagnostic and prognostic prediction models. Journal of Thrombosis and Haemostasis. 2013 Jun;11:129-41.

45. Moons KG, Altman DG, Reitsma JB, Ioannidis JP, Macaskill P, Steyerberg EW, Vickers AJ, Ransohoff DF, Collins GS. Transparent Reporting of a multivariable prediction model for Individual Prognosis or Diagnosis (TRIPOD): explanation and elaboration. Annals of internal medicine. 2015 Jan 6;162(1):W1-73.

Integrated Health Research Journal (IHRJ)

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

RESEARCH ARTICLE

Utilization and Diagnostic Yield of Chest X-Rays in a Tertiary Hospital in Nigeria: A Retrospective Observational Study

Godwin Enosakhare Okungbowa[1], Oghogho J. Usuanlele[1]

[1] Department of Radiography and Radiation Science, School of Basic Medical Sciences, College of Medical Sciences, University of Benin, Edo State, Nigeria

*Correspondence should be addressed to Godwin Enosakhare Okungbowa (email: enosakhare.okungbowa@uniben.edu)

Abstract

Background: Chest X-ray (CXR) is an important radiological tool for the diagnosis and management of cardiopulmonary disease. The aim of this study is to assess the patterns of chest X-ray utilization and radiographic findings at the University of Benin Teaching Hospital (UBTH), Nigeria.

Methods: A retrospective observational study of 1,624 patients who underwent chest X-ray examination at UBTH between January and December 2024.

Results: More females (58.1%, n = 943) were referred for CXR than males (41.9%, n = 681). The most common clinical indication was respiratory symptoms (29.5%, n = 480). Patients aged 36–50 years had the highest referral rate. The majority of referrals originated from the General Practice Clinic (GPC) (33.4%, n = 542). A high proportion of CXR results (65.1%, n = 1,058) were normal, while 34.9% (n = 566) showed abnormal findings. Cardiovascular changes were the most frequent abnormality (25.8%, n = 419). The majority of CXRs obtained for medical fitness/screening were normal (98.8%, n = 256).

Conclusion: This retrospective observational study found that CXRs are frequently ordered for diverse indications, with a high proportion yielding normal results (65.1%), particularly among referrals from the GPC. Cardiovascular changes were the most common abnormal finding. These findings highlight the need for more targeted clinical criteria to guide CXR utilization and reduce unnecessary radiation exposure.

Keywords: chest X-ray findings; chest X-ray referrals; chest X-ray request; clinical indication; patterns of findings.

Citation: Okungbowa GEO, Usuanlele OJ. Utilization and diagnostic yield of chest X-rays in a tertiary hospital in Nigeria: a retrospective observational study. Integrated Health Research Journal. 2026;3(2):52-58. https://doi.org/10.47963/f39caw57

Received 10th March 2026; **Accepted** 24th April 2026; **Published** 14th September 2026.

Introduction

A chest X-ray (CXR) is a type of projection radiograph used to diagnose conditions affecting the chest, its contents, and nearby structures. It remains the most common radiographic examination performed globally, with 8,789,840 undertaken in 2017/18 in the United Kingdom [1]. In the United States, approximately 129 million CXRs are performed annually [2]. CXRs are indicated for a range of clinical conditions, including pulmonary infection, cardiomegaly, congestive heart failure, lung masses, rib fractures, pleural effusion, and pneumothorax. They are also used for pre-operative assessment, pre-admission screening, and occupational medical examinations.

Chest X-rays have proven to be an important tool for diagnosing numerous cardiopulmonary conditions. Patients are referred for CXRs from diverse medical and surgical units, including the Intensive Care Unit (ICU), Accident and Emergency (A&E), Medical Emergency Response (MER), Oncology, Paediatric Emergency, and Neurology.

Routine admission CXRs rarely yield significant clinical value (<4%), such as altering patient management or identifying previously undetected disease [3]. Adverse consequences of unwarranted CXRs include unnecessary radiation exposure, financial cost, and the possibility of generating false-positive results that trigger further diagnostic investigations [4]. Diagnostic radiation has been implicated as a contributor to malignancy; one study estimated that approximately 1,861 cases, or 0.6% of all cancers in the United Kingdom, were attributable to diagnostic radiation [5].

Despite the widespread use of CXRs in Nigerian tertiary hospitals, there is limited published evidence on utilization patterns, referral sources, and diagnostic yield in this setting. This knowledge gap is particularly relevant in a resource-constrained health system such as Nigeria's, where radiology capacity is limited and unnecessary investigations carry both direct and indirect costs. The present study addresses this gap by examining CXR request patterns and radiographic findings at the University of Benin Teaching Hospital (UBTH), a major tertiary referral centre in southern Nigeria, in order to provide baseline data to inform more targeted referral practices.

Methods

Study Design

This was a retrospective observational study. Data were extracted from radiology request forms and radiologist reports submitted to the Radiology Department of UBTH during the period January to December 2024.

Study Setting and Participants

The study was conducted at UBTH, a tertiary referral hospital in Benin City, Edo State, southern Nigeria. All 1,624 consecutive conventional CXR requests registered during the study period were included using a census sampling technique. No records met the exclusion criteria.

Data Collection

Pro forma and checklist instruments were used to extract data from referral forms and radiologists' reports. Content validity was ensured through supervisor review. All CXR reports were formal departmental reports generated by qualified radiologists at UBTH. A single radiologist report per examination was used, and discordant or uncertain reports were not re-adjudicated in this study (see Limitations).

Operational Definitions

The following definitions were applied for classification of radiographic findings:

Normal findings: chest X-ray with no identifiable cardiopulmonary or musculoskeletal abnormality as reported by the reviewing radiologist.

Cardiovascular changes: radiographic findings including cardiomegaly, pulmonary vascular congestion, or other cardiac contour abnormalities.

Infectious findings: radiographic features consistent with pulmonary infection, including consolidation, air bronchograms, or interstitial infiltrates. Pneumonia, as a common infectious pulmonary condition, is classified and reported as a subcategory of infectious findings in this study.

Other abnormal findings: any remaining radiographic finding not classified above, including pleural effusion, pneumothorax, bony lesions, and pulmonary masses.

PEPFAR/DOT Referral Category

In UBTH, PEPFAR and DOT refer to a co-located HIV/AIDS and tuberculosis clinic that functions as an integrated referral unit for patients enrolled in the President's Emergency Plan for AIDS Relief (PEPFAR)

Table 1: Demographic Characteristics of Participants (N = 1,624). Percentages are column-based.

Characteristic	Frequency	Percentage
Gender		
Female	943	58.1%
Male	681	41.9%
Age Group (years)		
0–18	144	8.9%
19–35	432	26.6%
36–50	498	30.7%
51–65	316	19.5%
65+	234	14.4%
Total	1,624	100.0%

programme and the Directly Observed Therapy (DOT) programme for tuberculosis. For the purposes of this analysis, referrals from this integrated unit were grouped together and are consistently labelled "PEPFAR/DOT" throughout the manuscript and tables.

Statistical Analysis

Data were analysed using IBM SPSS version 28.0. Descriptive statistics are reported as frequencies and percentages. Inferential analysis used the Fisher's exact test which is an alternative to Chi-square test where expected frequency is less than 5. No outliers were identified in the dataset. Level of statistical significance was set at $p < 0.05$. All percentages in Tables 1, 2, 3, and 6 are column-based; percentages in Tables 4 and 5 are presented within each column of findings (column-based).

Ethics

Ethical approval was obtained from the Health Research and Ethics Committee of UBTH. Patient identifiers, including names and hospital numbers, were removed from the dataset prior to analysis to ensure anonymity. Data were stored securely on a password-protected institutional device and accessed only by the research team.

Results

Table 1 shows the demographic characteristics of participants. The study included 1,624 participants, of whom 58.1% (n = 943) were female and 41.9% (n = 681) were male. The majority of participants were aged 36–50 years (30.7%), followed by those aged 19–35 years (26.6%). The least represented age group was 0–18 years (8.9%), while older adults aged 65 years and above accounted for 14.4%.

Table 2 shows the clinical indications and referral units for CXR. The most common clinical indication was respiratory symptoms (29.5%, n = 480), followed by cardiovascular indications (24.6%, n = 400) and pre-operative workup (21.4%, n = 348). Medical fitness/screening accounted for 15.9% (n = 259), while infectious disease (3.7%), other medical conditions (3.4%), trauma (0.9%), and oncology (0.4%) comprised the remainder. The predominant referral source was the GPC (33.4%, n = 542), followed by the National Health Insurance Scheme (NHIS) clinic (16.4%, n = 266) and the Surgical Out-Patient Department (SOP) (12.0%, n = 195). The Consultant Out

Table 2: Clinical Indications and Referral Ward/Unit for CXR (N = 1,624). Percentages are column-based.

Category	Frequency	Percentage
Clinical Indication		
Respiratory Symptoms	480	29.5%
Cardiovascular	400	24.6%
Pre-operative	348	21.4%
Medical Fitness/Screening	259	15.9%
Infectious Disease	60	3.7%
Other Medical Conditions	56	3.4%
Trauma	15	0.9%
Oncology	6	0.4%
Referral Ward/Unit		
GPC	542	33.4%
NHIS	266	16.4%
SOP	195	12.0%
Other Specialties	130	8.0%
COPD*	117	7.2%
Gynaecology	102	6.3%
Emergency/Medical Wards	99	6.1%
Cardiology	65	4.0%
PEPFAR/DOT	63	3.9%
Paediatrics	24	1.5%
Family Medicine	21	1.3%
Total	1,624	100.0%

GPC = General Practice Clinic; NHIS = National Health Insurance Scheme; SOP = Surgical Out-Patient Department; COPD* = Consultant Out Patient Department; PEPFAR/DOT = integrated HIV/AIDS and tuberculosis clinic (President's Emergency Plan for AIDS Relief / Directly Observed Therapy).

Table 3: Radiographic Findings from Chest X-rays (N = 1,624). Percentages are column-based.

Finding	Total, n (%)
Normal	1,058 (65.1%)
Cardiovascular Changes	419 (25.8%)
Infectious Findings (Pneumonia)	51 (3.1%)
Other Abnormal Findings	96 (5.9%)
Total	1,624 (100.0%)

Pneumonia is classified as a subcategory of infectious findings.

Table 4: Association Between Demographic Characteristics, clinical indications and Radiographic Findings. Values are n (column %).

Characteristic	Cardiovascular Changes N = 419	Normal N = 1,058	Other Findings N = 96	Infectious Findings (Pneumonia) N = 51
Demographic characteristics				
Gender				
Female	317 (75.7%)	572 (54.1%)	39 (40.6%)	15 (29.4%)
Male	102 (24.3%)	486 (45.9%)	57 (59.4%)	36 (70.6%)
Age Group (years)				
0–18	6 (1.4%)	93 (8.8%)	15 (15.6%)	27 (52.9%)
19–35	39 (9.3%)	360 (34.0%)	21 (21.9%)	12 (23.5%)
36–50	147 (35.1%)	330 (31.2%)	15 (15.6%)	3 (5.9%)
51–65	113 (27.0%)	170 (16.1%)	24 (25.0%)	6 (11.8%)
65+	108 (25.8%)	102 (9.6%)	21 (21.9%)	3 (5.9%)
Clinical indications†				
Cardiovascular	158 (37.7%)	230 (21.7%)	9 (9.4%)	3 (5.9%)
Medical Fitness/Screening	3 (0.7%)	256 (24.2%)	0 (0.0%)	0 (0.0%)
Otherb	33 (7.9%)	83 (7.8%)	18 (18.8%)	3 (5.9%)
Pre-operative	105 (25.1%)	210 (19.8%)	30 (31.3%)	3 (5.9%)
Respiratory Symptoms	120 (28.6%)	279 (26.4%)	39 (40.6%)	42 (82.4%)

Patient Department (COPD*) accounted for 7.2% (n = 117), Gynaecology 6.3% (n = 102), Emergency/Medical Wards 6.1% (n = 99), Other Specialties 8.0% (n = 130), Cardiology 4.0% (n = 65), PEPFAR/DOT 3.9% (n = 63), Paediatrics 1.5% (n = 24), and Family Medicine 1.3% (n = 21).

Table 3 shows the radiographic findings. The majority of CXR results (65.1%, n = 1,058) were normal. Among abnormal findings (34.9%, n = 566), cardiovascular changes were most common (25.8%, n = 419), followed by other abnormal findings (5.9%, n = 96). Infectious findings, including pneumonia as a subcategory, accounted for 3.1% (n = 51). The majority of CXRs therefore yielded no clinically significant pathology.

Table 4 shows the association between demographic characteristics, clinical indications and radiographic findings. A gender-based analysis showed that females had a higher prevalence of cardiovascular changes (75.7%, n = 317) compared to males (24.3%, n = 102). Infectious findings (pneumonia) were more common in males (71%, n = 36) than females (29%, n = 15). Among age groups, infectious findings were predominantly observed in children aged 0–18 years (53% of infectious cases), while cardiovascular changes were most frequent in the 36–50 age group (35%). These distributions are consistent with established epidemiological patterns. The table also shows that cardiovascular indications were most frequently associated with cardiovascular changes (37.7%, n = 158), with a small proportion of infectious findings also recorded in this group (5.9%, n = 3). Medical fitness/screening referrals yielded normal CXRs in 98.8% of cases (n = 256). Respiratory symptom referrals had the highest proportion of infectious findings (82.4%, n = 42) and other abnormal findings (40.6%, n = 39). Pre-operative referrals

Table 5: Distribution of Radiographic Findings by Referral Unit (N = 1,624). Values are n (column %). Percentages are column-based.

Referral Unit	Total N = 1,624	Normal N = 1,058	Cardiovascular Changes N = 419	Infectious Findings (Pneumonia) N = 51	Other Findings N = 96
Cardiology	65 (4.0%)	47 (4.4%)	18 (4.3%)	0 (0.0%)	0 (0.0%)
COPD*	117 (7.2%)	48 (4.5%)	45 (10.7%)	3 (5.9%)	21 (21.9%)
Emergency/Medical Wards	99 (6.1%)	24 (2.3%)	51 (12.2%)	6 (11.8%)	18 (18.8%)
Family Medicine	21 (1.3%)	18 (1.7%)	3 (0.7%)	0 (0.0%)	0 (0.0%)
GPC	542 (33.4%)	368 (34.8%)	147 (35.1%)	9 (17.6%)	18 (18.8%)
Gynaecology	102 (6.3%)	66 (6.2%)	36 (8.6%)	0 (0.0%)	0 (0.0%)
NHIS	266 (16.4%)	236 (22.3%)	24 (5.7%)	0 (0.0%)	6 (6.3%)
Other Specialties	130 (8.0%)	98 (9.3%)	32 (7.6%)	0 (0.0%)	0 (0.0%)
Paediatrics	24 (1.5%)	0 (0.0%)	3 (0.7%)	21 (41.2%)	0 (0.0%)
PEPFAR/DOT	63 (3.9%)	30 (2.8%)	15 (3.6%)	9 (17.6%)	9 (9.4%)
SOP	195 (12.0%)	123 (11.6%)	45 (10.7%)	3 (5.9%)	24 (25.0%)
Total	1,624 (100%)	1,058 (65.1%)	419 (25.8%)	51 (3.1%)	96 (5.9%)

GPC = General Practice Clinic; NHIS = National Health Insurance Scheme; PEPFAR/DOT = integrated HIV/AIDS and tuberculosis clinic; SOP = Surgical Out-Patient Department; COPD* = Consultant Out-Patient Department. Data are presented as n (column %).

showed cardiovascular changes in 25.1% (n = 105) and other abnormal findings in 31.3% (n = 30). A statistically significant association was observed between clinical indication and radiographic finding (Fisher's exact $p < 0.001$), indicating that clinical indication is strongly associated with the likelihood and type of pathology detected.

Table 5 shows the distribution of radiographic findings by referral unit. Cardiovascular changes were most common among GPC referrals (35.1%, n = 147) and Emergency/Medical Ward referrals (12.2%, n = 51). Infectious findings were most frequent among referrals from Paediatrics (41.2%, n = 21) and PEPFAR/DOT (17.6%, n = 9), consistent with the high prevalence of respiratory infections in these patient groups. Referrals from NHIS and Gynaecology were associated with the lowest proportions of abnormal findings.

Discussion

This study examined CXR utilization and radiographic findings at a tertiary hospital in southern Nigeria. The predominant finding was a high proportion of normal radiographs (65.1%), particularly among referrals from the GPC. These results raise important questions about referral appropriateness in resource-limited settings.

Al Shahrani and Al-Surimi [6] found that 96.8% of ICU patients underwent daily routine CXRs, with 73% of clinicians expressing preference for an on-demand approach. The present study differs in context: rather than ICU-dominated utilization, we observed a broad distribution of referral indications, with respiratory symptoms (29.5%) and cardiovascular indications (24.6%) accounting for the largest shares. This broader distribution suggests that CXR use in this Nigerian tertiary setting extends well beyond intensive care, consistent with its role as a general diagnostic workhorse in a resource-constrained environment.

Gupta et al. [7] reported that 85.7% of CXRs in a paediatric ICU were linked to ventilated patients. The present study encompasses a wider indication spectrum, including respiratory, cardiovascular, pre-operative, and screening referrals. This reflects the breadth of CXR application in a general tertiary hospital, as opposed to a specialist ICU setting.

The finding that 31% of recipients were aged 36–50 years is broadly consistent with Gaget et al. [8]'s observation of increased plain radiograph use among older Australians. In the Nigerian context, this age group likely represents working-age adults with a higher burden of cardiovascular and respiratory disease, contributing to the observed predominance of cardiovascular changes (25.8%) as the most frequent abnormality.

The 65.1% normal CXR rate observed in this study is consistent with Porter et al. [9]'s finding that routine post-operative CXRs rarely lead to a change in clinical management (0.4%). The high proportion of normal results in the present study was particularly marked in medical fitness/screening referrals (98.8% normal), supporting the recommendation to restrict routine pre-employment or pre-admission CXRs. Comparable findings have been reported from another tertiary institution in Nigeria which reported that only 10% of routine CXRs had abnormal findings in their centre, with cardiomegaly as the leading abnormality, underscoring a regionally consistent pattern of broad CXR utilization with limited incremental diagnostic yield [10].

Infectious findings (pneumonia) were observed in 3.1% of the overall sample but were disproportionately concentrated in paediatric referrals (52.9% of infectious cases were in the 0–18 year age group) and in PEPFAR/DOT referrals (17.6%), consistent with the high prevalence of respiratory infections in immunocompromised and paediatric populations. Saraya et al.[11] described consolidation as the dominant finding in paediatric Mycoplasma pneumoniae pneumonia. The low overall prevalence of infectious findings in the present study suggests that pneumonia is not the primary driver of CXR demand at this institution; rather, cardiovascular and respiratory symptom indications dominate.

A notable gender disparity was observed: females accounted for 75.7% of cardiovascular changes, a pattern that may reflect sex-specific differences in the presentation of hypertensive heart disease and cardiomegaly in this population, which warrants further investigation.

The CXR referral landscape at UBTH is dominated by the GPC, which generated one-third of all requests. The GPC's high normal-CXR rate (34.8%) suggests that clinical decision support tools or pre-referral checklists could help optimise referral practice.

Limitations

This study has several limitations that should be considered when interpreting the findings. First, the retrospective design relied on existing records, which precluded verification of clinical details or independent review of radiological reports. Although no records were excluded due to incomplete documentation in the present study, the reliance on routine clinical records rather than prospectively collected standardised data introduces the possibility of information bias, particularly with respect to variability in how clinical indications were documented across different referral units. Second, as a single-centre study at one tertiary hospital in Edo State, the findings may not be generalisable to primary or secondary care settings, or to other regions of Nigeria. Selection bias inherent to this setting should be noted, as the patient population and referral patterns of a tertiary institution may differ substantially from those of lower-level facilities. Third, potential classification and reporting bias may have arisen from reliance on a single radiologist report per examination without inter-rater reliability assessment. Fourth, this study did not apply a validated appropriateness framework (such as the American College of Radiology Appropriateness Criteria) against which referrals could be formally benchmarked; therefore, conclusions regarding referral appropriateness should be interpreted with caution. Finally, recall bias is not applicable given the record-based retrospective design; however, future prospective studies incorporating standardised data collection instruments would allow for more robust assessment of referral patterns and diagnostic yield across diverse Nigerian healthcare settings.

Conclusion

This retrospective observational study found that CXRs at UBTH are frequently ordered for diverse indications, with a high proportion yielding normal results (65.1%). Cardiovascular changes were the most common abnormal finding, particularly in females and in middle-aged and older adults. Infectious findings were concentrated in paediatric and PEPFAR/DOT referrals. The high proportion of normal radiographs, especially among medical fitness/screening and GPC referrals, indicates that targeted referral criteria and clinical decision support may help optimize CXR utilization and reduce unnecessary radiation exposure in this setting.

Declarations

Conflict of Interest

The authors declare no conflicts of interest.

Data Availability

The data that support the findings of this study are available from the corresponding author upon reasonable request, subject to applicable institutional data-sharing policies.

Ethical Approval

Ethical approval was obtained from the Health Research and Ethics Committee of the University of Benin Teaching Hospital. Patient identifiers were removed prior to analysis to ensure anonymity, and data were stored securely on a password-protected institutional device.

References

1. Small L. The role of clinical history in the interpretation of chest radiographs. Radiography. 2021;27:698–703.

2. Mettler FA Jr, Bhargavan M, Faulkner K, et al. Radiologic and nuclear medicine studies in the United States and worldwide: frequency, radiation dose, and comparison with other radiation sources - 1950–2007. Radiology. 2009;253(2):520–531.

3. Malnick S, Duek G, Beilinson N. Routine chest X-ray on hospital admission: does it contribute to diagnosis or treatment? Isr Med Assoc J. 2010;12:357–61.

4. Hubbell F, Greenfield S, Tyler J. The impact of routine admission chest X-ray films on patient care. Invest Radiol. 1985;20:644–6.

5. Parkin DM, Darby SC. Cancers in 2010 attributable to ionising radiation exposure in the UK. Br J Cancer. 2011;105:S57–S65.

6. Al Shahrani A, Al-Surimi K. Daily routine versus on-demand chest radiograph policy and practice in adult ICU patients — clinician's perspective. BMC Med Imaging. 2018;18:4.

7. Gupta R, Nallasamy K, Williams V. Prescription practice and clinical utility of chest radiographs in a paediatric intensive care unit: a prospective observational study. BMC Med Imaging. 2021;21:44.

8. Gaget V, Inacio MC, Tivey DR. Trends in utilisation of plain x-rays by older Australians (2010–2019). BMC Geriatr. 2022;22:100.

9. Porter ED, Fay KA, Hasson RM. Routine chest X-rays after thoracic surgery are unnecessary. J Surg Res. 2020;250:188–92.

10. Akinola RA, Akhigbe AO, Mohammed AS, Jaiyesimi MO, Osinaike OO, Jinadu FO, et al. Evaluation of routine chest X-rays performed in a tertiary institution in Nigeria. Int J Cardiovasc Res. 2014;3(4).

11. Saraya T, Watanabe T, Tsukahara Y. The correlation between chest X-ray scores and the clinical findings in children and adults with Mycoplasma pneumoniae pneumonia. Intern Med. 2017;56:2845–9.

Integrated Health Research Journal (IHRJ)

The Official Journal of the College of Health and Allied Sciences

RESEARCH ARTICLE

Computational-Aided Drug Discovery Approaches Exploring Therapeutic Potential of Global Health Priority Box Compounds Against *Schistosoma haematobium* Infection

Jonathan Cobbinah[1], William Owusu[1], Abdul-Samad Alhassan[1], Emmanuel Adu Sarpong[1], Nicholas Donkor[1], Pius K. Sam[1], Alberta Serwah Anning[1], George Ghartey-Kwansah[1*]

[1] Department of Biomedical Sciences, School of Allied Health Sciences, University of Cape Coast, Ghana

Correspondence should be addressed to George Ghartey-Kwansah (email: george.ghartey-kwansah@ucc.edu.gh)

Abstract

Background: Urinary schistosomiasis caused by *Schistosoma haematobium* remains a major global health burden, with nearly 800 million people at risk worldwide. The growing concern over reduced praziquantel efficacy underscores the urgent need for alternative therapeutic agents. Advances in computational drug discovery provide an efficient framework for identifying novel antischistosomal candidates targeting parasite-specific proteins.

Objective: This study employed integrative computational drug discovery approaches to evaluate Global Health Priority (GHP) Box compounds for therapeutic potential against *S. haematobium,* focusing on the 23-kDa integral membrane protein (Sh23) as a putative drug target.

Methodology: The Sh23 protein was identified and structurally characterized as a potential therapeutic target. A curated library of 80 GHP Box compounds was subjected to virtual screening with PyRx, yielding 33 top-scoring candidates based on binding affinity. These candidates were further evaluated with ADMET-AI for *in silico* pharmacokinetic and toxicity profiling, with MolSoft for drug-likeness assessment, and with the PASS platform (Way2Drug) for biological activity prediction.

Results: MMV1262756 emerged as the lead compound, demonstrating strong binding affinity to Sh23 protein, low predicted clinical toxicity (0.14), high drug-likeness (0.87), and favorable predicted activity related to urological disorders.

Conclusion: This study identifies MMV1262756 as a promising antischistosomal candidate and highlights the utility of computationally driven drug discovery in accelerating the identification of therapeutic candidate for S. haematobium. The findings support the potential of bioinformatics-guided strategies to address emerging challenges in praziquantel efficacy and advance schistosomiasis control.

Keywords: Schistosomiasis; *Schistosoma haematobium*; Global Health Priority Box Compounds; Molecular Docking; ADMET Profiling; PASS Prediction.

Citation: Cobbinah J, Owusu W, Alhassan A-S, Sarpong EA, Donkor N, Sam PI, Anning AS, Ghartey-Kwansah G. Computational-aided drug discovery approaches exploring therapeutic potential of Global Health Priority Box compounds against *Schistosoma haematobium* infection. Integrated Health Research Journal. 2026;3(2):59-66. https://doi.org/10.47963/ghbf5j40

Received 26th March 2026; **Accepted** 24th July 2026; **Published** 8th September 2026.

Introduction

Schistosomiasis, also known as bilharzia, remains one of the most devastating neglected tropical diseases globally and ranks second only to malaria in parasitic disease burden. More than 250 million people are infected across 78 countries, with an estimated 500,000 deaths annually [1,2]. The disease is caused by trematode parasites of the genus *Schistosoma*, with *Schistosoma haematobium* responsible for approximately two-thirds of cases in Africa, where over

90% of individuals requiring treatment reside [3,4]. Chronic infection with *S. haematobium* is associated with severe urogenital morbidity, including hematuria, bladder fibrosis, hydronephrosis, and increased risk of squamous cell carcinoma of the bladder, underscoring its substantial clinical and socioeconomic impact.

A key determinant of *S. haematobium* survival and pathogenicity is the 23 kDa integral membrane protein (Sh23), a member of the tetraspanin family that is abundantly expressed during the schistosomula stage and localized on the parasite tegument [5]. Sh23 is implicated in host–parasite interactions through its role in maintaining tegumental integrity, parasite adhesion, and modulating host immune responses [6]. Mechanistically, Sh23 participates in membrane organization and signal transduction, facilitating parasite adaptation within the host environment and contributing to immune evasion by masking antigenic epitopes and modulating host inflammatory pathways [7]. Its surface accessibility, stage-specific expression, and functional relevance make Sh23 an attractive yet underexplored molecular target for therapeutic intervention.

Despite decades of control efforts, praziquantel remains the sole widely used antischistosomal drug [8]. However, growing evidence of reduced drug sensitivity, absence of prophylactic activity, limited efficacy against immature parasite stages, and the risk of resistance development highlight critical gaps in current treatment strategies. Furthermore, most existing drug discovery efforts have focused on a narrow range of parasite targets, leaving key tegumental proteins such as Sh23 insufficiently characterized and poorly exploited in therapeutic development. This represents a major unmet need in schistosomiasis research [9].

Recent advances in computational drug discovery offer powerful tools for accelerating the identification of novel antischistosomal agents [10]. Structure-based virtual screening, pharmacokinetic prediction, and machine learning–driven prioritization of compounds have significantly reduced the cost and time associated with early-stage drug development [11]. When combined with curated compound libraries such as the Global Health Priority Box developed by the Medicines for Malaria Venture (MMV), these approaches provide a unique opportunity to systematically explore previously untapped molecular targets in *S. haematobium*.

To date, no comprehensive computational study has systematically evaluated Global Health Priority Box compounds against Sh23 or integrated molecular docking, pharmacokinetic profiling, and biological activity prediction to identify targeted inhibitors of this protein. Moreover, the mechanistic and therapeutic potential of Sh23 as a drug target remains largely unexplored compared with other schistosome proteins. This study addresses these critical gaps by implementing an integrative computational framework that combines structure-based virtual screening and advanced in silico drug discovery approaches to identify and prioritize novel candidate compounds targeting Sh23. By focusing on a biologically relevant yet underutilized tegumental protein, this work provides new mechanistic insights and establishes a rational pipeline for the development of next-generation antischistosomal therapeutics.

Materials and Methods.

Target Protein Retrieval and Validation

The 23 kDa integral membrane protein of *Schistosoma haematobium* (Sh23) was selected as the therapeutic target due to its crucial role in parasite adhesion and survival. The protein sequence (UniProt accession: AF-Q26499-F1) was retrieved from the AlphaFold Protein Structure Database(https://alphafold.ebi.ac.uk/) in PDB format. To further validate the accuracy of the predicted structure of the Sh23 protein, the model was uploaded to the SWISS-MODEL platform for structural validation. SWISS-MODEL is widely used for homology modeling and performs automated alignment of a query protein structure with known experimental templates. After alignment, the analysis showed a 100% sequence identity between the AlphaFold-predicted structure and the closest homologous protein in the SWISS-MODEL database. This perfect match confirmed that the predicted amino acid sequence and folding pattern of Sh23 are consistent with experimentally validated data, thereby reinforcing the reliability of the model.

In addition, the integrity and confidence of the predicted structure were evaluated using the pLDDT score, which was 90.56 for this 23 kDa integral membrane protein from *Schistosoma haematobium* (Sh23). A pLDDT value this high indicates very high confidence, supporting the accuracy and stability of the predicted structure [12].

Protein Preparation

The retrieved Sh23 structure was processed using BIOVIA Discovery Studio. Water molecules were removed, hydrogen atoms were added, bond orders were corrected, and geometry optimization was carried out to ensure structural fidelity [13,14]. The finalized protein model was saved as a PDB file for subsequent molecular docking simulations.

Ligand Preparation

A total of 80 compounds from the Medicines for Malaria Venture (MMV) Global Health Priority (GHP) box were retrieved in SMILES format [15]. The SMILES notations were converted into three-dimensional PDB structures using the NovoPro SMILES-to-PDB converter. The generated structures were imported into BIOVIA Discovery Studio, where conformations were inspected and validated against their two-dimensional representations. Finalized

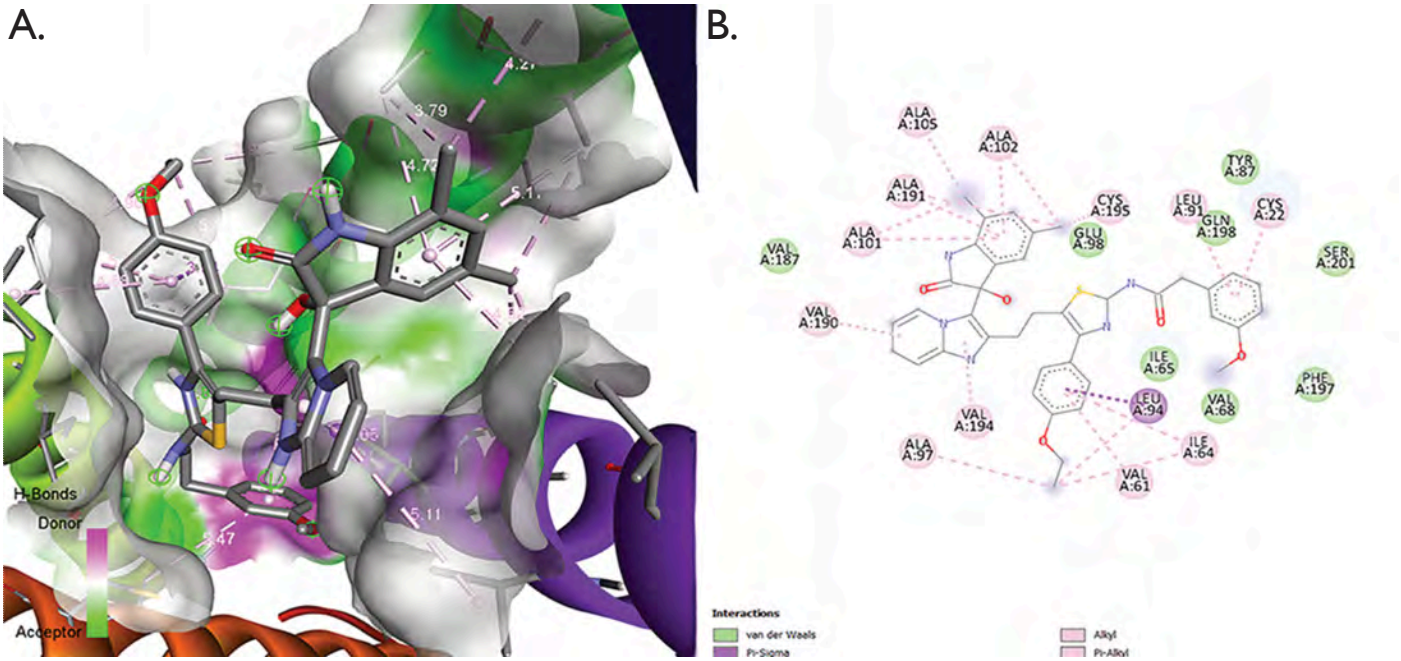

Figure 1: (A) 3D representation of MMV014853 docked to the 23 kDa integral membrane protein, illustrating hydrophobic contacts, π-alkyl interactions, and van der Waals stabilization within the binding pocket. (B) 2D interaction map highlighting key residues involved in ligand binding, including alkyl and π-alkyl interactions and van der Waals contacts.

ligands were stored in a dedicated library for downstream docking experiments.

Binding Pocket Prediction

The putative ligand-binding site of Sh23 was identified before docking simulations to ensure accurate targeting. Residue-level binding pocket analysis predicted an active site spanning residues 107-184, forming a well-defined cavity suitable for small-molecule interactions. No co-crystallized ligand or reference ligand was available for Sh23; therefore, we validated docking using alternative controls ("self-docking" of a template ligand), and the corresponding RMSD < 2.0 Å performed using PyRx (version 0.8, Scripps Research Institute, USA). This site served as the reference for docking grid box construction, ensuring that simulations explored biologically relevant binding regions [13].

Protein-Ligand Docking and Virtual Screening

Docking simulations were performed using PyRx (version 0.8, Scripps Research Institute, USA), which integrates AutoDock Vina for ligand-protein interaction analysis [16]. The docking grid box was centered at X = 11.25 Å, Y = 1.39 Å, and Z = –4.33 Å, with grid dimensions of 49.22 Å × 343.12 Å × 38.3 Å to fully encompass the predicted binding pocket. Exhaustiveness was set to 20 to maximize sampling accuracy. In this study, the docking validation metric is therefore limited to binding scores and interaction profiles.Binding affinity scores (kcal/mol) and RMSD values were used to rank the compounds. Ligands with binding energies ≤ -8.0 kcal/mol were considered high-affinity hits. Protein-ligand interactions were analyzed in detail, with hydrogen bonds, hydrophobic contacts, and electrostatic interactions visualized using BIOVIA Discovery Studio to confirm the stability and orientation of ligand binding.

Compound Characterization

ADMET and Drug-Likeness Profiling

The pharmacokinetic and toxicological profiles of the top 33 compounds were predicted using ADMET-AI (https://admet.ai.greenstonebio.com/) and MolSoft(https://www.molsoft.com/) servers. Submitted SMILES notations were analyzed for molecular descriptors, absorption, distribution, metabolism, excretion, and toxicity (ADMET) properties [17]. Predictions included hERG channel inhibition, mutagenicity, drug-induced liver injury, carcinogenicity, LD50, mitochondrial membrane potential disruption, and skin sensitization. Drug-likeness scores were calculated independently using MolSoft.

Biological Activity Prediction (PASS Analysis)

Biological activity spectra of the shortlisted compounds were predicted using the PASS (https://www.way2drug.com/passonline/predict.php)server. SMILES strings were evaluated for probability scores corresponding to potential pharmacological effects. Only activities relevant to *S. haematobium* infection and associated pathologies were considered for downstream analysis.

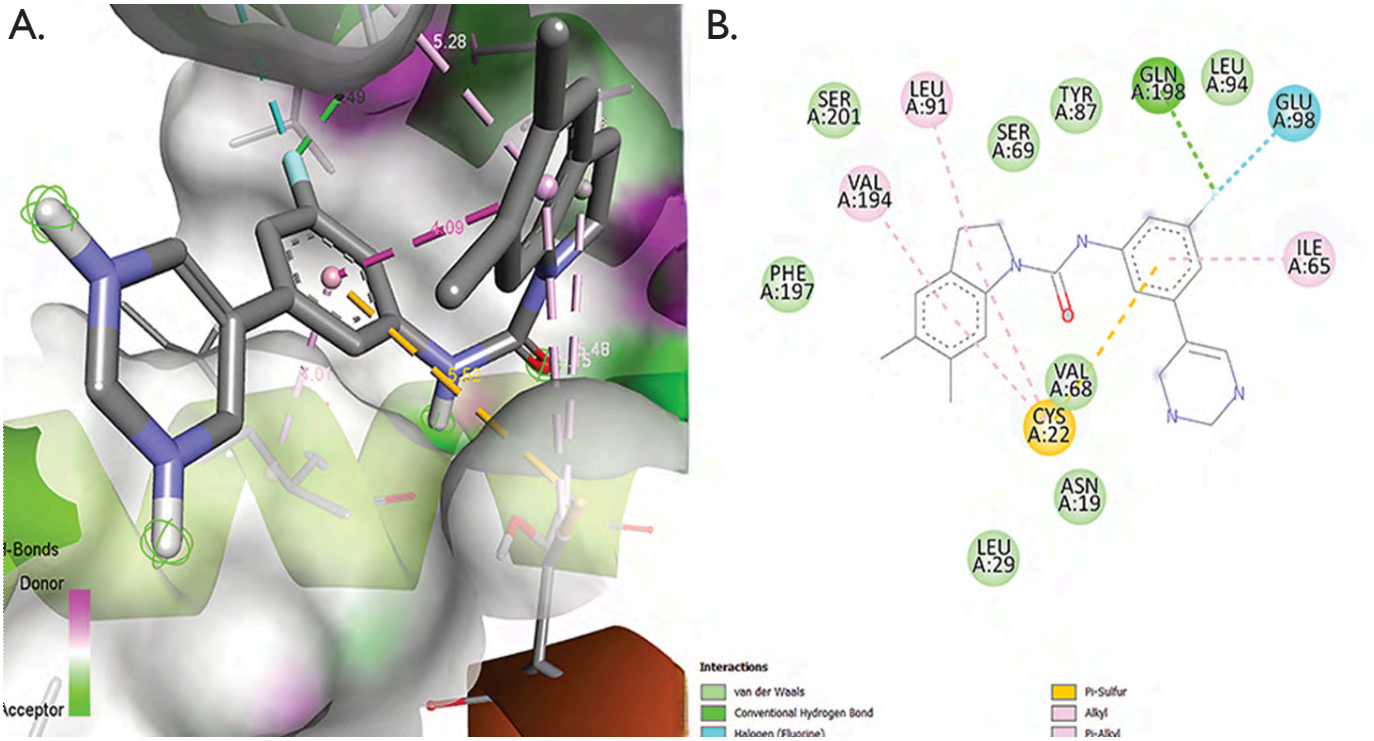

Figure 2: (A) 3D representations of MMV028822 docked to the 23 kDa integral membrane protein (AF-Q26499-F1), showing hydrogen bonding, π–sulfur interaction, and key hydrophobic/van der Waals contacts within the binding pocket. (B) 2D interaction map highlighting key residues involved in ligand binding, including alkyl and π-alkyl interactions and van der Waals contacts.

Similarly, molecular docking revealed that MMV028822 adopted a stable binding conformation within the active site of the 23 kDa integral membrane protein (AF-Q26499-F1), with a binding energy of -8.2 kcal/mol. The compound formed a key hydrogen bond with GLU A:98 and a π–sulfur interaction with CYS A:22, in addition to multiple hydrophobic and van der Waals contacts involving LEU A:29, ASN A:19, VAL A:68, VAL A:194, LEU A:94, PHE A:197, SER A:201, GLN A:198, and TYR A:87. These interactions collectively indicate a well-stabilized binding pose and strong affinity for the target site (Figure 2A–B).

Molecular docking revealed that MMV1262756 adopted a stable binding pose within the active site of the 23 kDa integral membrane protein (AF-Q26499-F1), with a binding energy of –8.2 kcal/mol (Figure 3A–B). The compound engaged in a π-anion interaction with GLU A:133, a π-sigma interaction with VAL A:36, and π–π stacking/T-shaped contacts with PHE A:134 and TRP A:51. Additional hydrophobic interactions with PHE A:40, TYR A:35, ALA A:32, and ILE A:58 contributed to overall complex stabilization and strong target affinity.

Physicochemical and ADMET Profiling

Physicochemical and ADMET profiling provide comprehensive insights into the properties of the studied compounds. Physicochemical profiling evaluates the compounds' physical and chemical characteristics, while ADMET analysis assesses their pharmacokinetic behavior, including absorption, distribution, metabolism, and excretion, as well as their toxicity profiles.

ADMET profiling of the 33 compounds revealed molecular weights (345.38-769.97 g/mol), logP (1.17-6.07), TPSA (37.19-154.73 Å²), and QED scores (0.13-0.74) (Table S2). Oral bioavailability scores ranged from 0.62–0.98, while plasma protein binding spanned 71.37%-100% (Table S3). Toxicity markers varied, with hERG inhibition (0.35-0.99) and clinical toxicity probabilities (0.07-0.82) (Table S4). Among all, MMV028822 and MMV1262756 showed superior drug-likeness alongside favourable pharmacokinetic properties compared with the reference, praziquantel (Table 1 & 2); MMV014853 showed favourable pharmacokinetics but a drug-likeness score below praziquantel.

Praziquantel, used as the reference control, demonstrated an overall favorable safety profile with low probabilities of cardiotoxicity (0.18), clinical toxicity (0.05), mutagenicity (0.06), and carcinogenicity (0.03). However, a relatively high likelihood of skin reactions (0.64) was observed, aligning with its known side effect profile. The compound showed moderate acute safety (LD50 = 2.75) and negligible mitochondrial toxicity (0.01). Despite its established efficacy, praziquantel recorded only a modest drug-likeness score (0.29), underscoring the need for more optimized alternatives (Table 2).

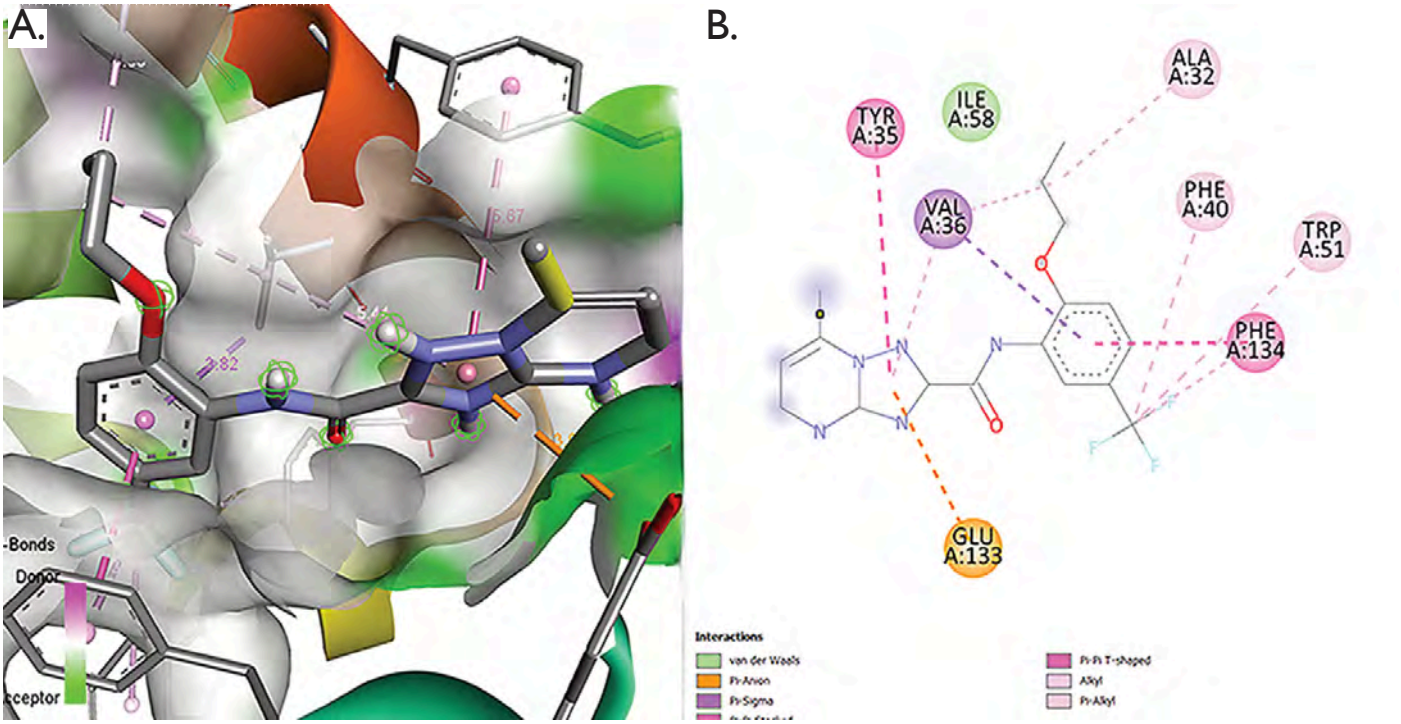

Figure 3: Illustration of the binding interactions of MMV1262756 (−8.2 kcal/mol) within the active site of the 23 kDa membrane protein (AF-Q26499-F1). **(A)** 3D visualization of the docking complex showing the ligand anchored in the binding cavity. **(B)** 2D interaction map depicting hydrogen bonds, π-alkyl contacts, and van der Waals interactions with key residues.

PASS Biological Activity Prediction

PASS provides an activity-spectrum view that helps distinguish which compounds are most likely to modulate biologically relevant functions which is going beyond docking or structural compatibility alone. It also enables fast triage under limited resources, since testing every compound experimentally is costly and time-intensive; PASS helps identify the most promising candidates early for downstream validation. The PASS analysis revealed distinct activity profiles across the evaluated compounds. MMV014853 was predicted as a membrane integrity agonist (Pa = 0.23; Pi = 0.26), suggesting limited therapeutic potential. MMV028822 demonstrated a broader activity spectrum, with predicted roles in urinary incontinence (Pa = 0.16), urologic disorders (Pa = 0.17), and antineurogenic pain (Pa = 0.21). Among the compounds, MMV1262756 emerged as the most promising, showing predicted activities in urologic disorders (Pa = 0.14), urinary incontinence (Pa = 0.13), and interleukin-2 antagonism (Pa = 0.10), with consistently low inactivity scores, highlighting its potential as a viable therapeutic candidate (Table S6).

Discussion

This study explored the potential of targeting the Sh23 tetraspanin protein in *Schistosoma haematobium* using an integrative computational drug discovery approach. These findings contribute significantly to the growing body of research by identifying potential anti-schistosomal

Table1: Predicted Pharmacokinetic Properties (ADME) of lead compounds and Praziquantel.

Compound ID	OR	CEP	Blood-Brain Barrier Penetration	Plasma Protein Binding Rate	CYP3A4 Inhibition	Half Life	Drug Clearance (Hepatocyte)
Praziquantel (control)	0.54	-4.45	0.99	62.60	0.77	0.00	34.40
MMV014853	0.96	-4.67	0.86	84.45	0.37	41.37	35.41
MMV028822	0.96	-4.63	0.93	97.28	0.99	68.79	35.69
MMV1262756	0.98	-4.73	0.89	100.00	0.33	0.00	43.07

Table 2: Predicted Toxicity and drug-likeness profiles of lead compounds and Praziquantel.

Compound ID	hERG Blocking	Clinical Toxicity	Mutagenicity	Carcinogenicity	Acute Toxicity LD50	SR	MMP	DLMS
Praziquantel (control)	0.18	0.05	0.06	0.03	2.75	0.64	0.01	0.29
MMV014853	0.44	0.21	0.45	0.23	2.85	0.26	0.47	0.24
MMV028822	0.73	0.24	0.12	0.12	2.68	0.16	0.46	0.66
MMV1262756	0.60	0.14	0.58	0.38	2.65	0.18	0.31	0.87

Abbreviations: DLMS = Drug-Likeness Model Score; MMP = Mitochondrial Membrane Potential; SR = Skin Reaction.

compounds from the Global Health Priority Box and demonstrating the utility of computational approaches in accelerating drug discovery. The study provides valuable insights into compound efficacy, safety, and pharmacokinetic properties, thereby supporting the development of new therapeutic options for *Schistosoma haematobium* infection. These chronic and often debilitating outcomes underscore the urgent need for improved and diversified therapeutic strategies beyond the current standard of care, which relies primarily on the anthelmintic drug Praziquantel. This study pioneers a computational pipeline for targeting the Sh23 tetraspanin protein in *Schistosoma haematobium,* revealing MMV1262756 as a standout lead from the Global Health Priority (GHP) Box library. The identification of these compounds therefore reflects not only their computational affinity for the Sh23 target but also their origin from a chemically validated library with prior relevance to infectious disease research. By identifying 33 high-affinity ligands through virtual screening and prioritizing three top candidates via docking and ADMET analysis, our findings illuminate Sh23's druggability and underscore the untapped potential of tegumental proteins in antischistosomal drug discovery.

The superior binding profiles of MMV014853, MMV028822, and especially MMV1262756 stem from multifaceted interactions within the Sh23 binding pocket among the leads. MMV1262756 distinguished itself with the most favorable overall profile. It combined strong binding affinity with the highest drug-likeness score (0.87), the lowest predicted clinical toxicity (0.14), and superior PASS-predicted activities in urologic disorders (Pa = 0.14), urinary incontinence (Pa = 0.13), and interleukin-2 antagonism (Pa = 0.10). These predicted pharmacological effects align closely with the immune-mediated pathology of schistosomiasis, in which chronic inflammation, bladder fibrosis, and increased risk of squamous cell carcinoma are driven by dysregulated host immune responses and urogenital tissue damage[19, 20]. In contrast, MMV014853 showed moderate toxicity concerns (higher mutagenicity and carcinogenicity, with a lower drug-likeness score), while MMV028822 offered a balanced but less optimal safety-efficacy ratio. These results directly address praziquantel's shortcomings, which include reduced sensitivity, immature-stage inefficacy, and adverse effects like hepatotoxicity, by proposing Sh23 inhibitors with complementary mechanisms. The PASS-predicted activities (Pa ≈ 0.10–0.21) fall within a low-confidence range, where values below 0.30 generally indicate weak or uncertain biological relevance. As such, these results should be interpreted cautiously as hypothesis-generating rather than definitive evidence of pharmacological activity. Predicted functions, including associations with urologic disorders, likely reflect indirect or symptom-modulating effects related to the pathophysiology of urogenital schistosomiasis rather than direct antiparasitic mechanisms. Similarly, the predicted antagonistic activity of MMV1262756 against interleukin-2 (IL-2) suggests that the compound may possess immunomodulatory properties. However, this prediction is based on computational analysis and remains speculative until confirmed through experimental validation.

Overall, PASS analysis provides limited but complementary insight within the computational framework. While MMV1262756 remains a promising candidate based on its binding affinity and pharmacokinetic profile, PASS predictions should be treated as secondary indicators, with compound prioritization primarily guided by structural and ADMET evidence and validated through further experimental studies.

Unlike praziquantel's tegumental disruption via calcium influx, Sh23 targeting exploits stage-specific vulnerability in schistosomula, potentially enabling prophylaxis against early infections. The GHP Box's proven utility in neglected tropical diseases (NTDs) validates this library as a cost-effective source, consistent with Hernandez, Veale et al.,[21, 22], while Kondapuram et al.,[23] affirm docking's reliability in parasitology. The identification of candidate compounds from an open-access library aligns with global efforts to expand affordable and scalable treatment strategies. Furthermore, while the compounds investigated here are synthetic or semi-synthetic molecules, this partially parallels the rationale underlying certain ethnobotanical practices, where plant-derived therapies are traditionally used to alleviate urinary symptoms and inflammation. Although no direct ethnopharmacological linkage can be

established for these specific compounds, the conceptual overlap underscores the importance of integrating computational findings with traditional knowledge systems in future research.

Currently, praziquantel remains the gold-standard treatment for schistosomiasis, yet its limitations, such as hepatotoxicity, skin reactions, and moderate drug-likeness, underscore the need for alternative therapies [23]. The predicted pharmacological and safety profile of MMV1262756 highlights its potential as a complementary or replacement therapy and supports the call for diversification of the anti-schistosomal drug arsenal. From a mechanistic perspective, targeting the Sh23 protein offers a novel therapeutic approach distinct from the action of praziquantel, which primarily disrupts parasite tegument integrity via calcium influx. In contrast, Sh23 inhibition may interfere with tegumental organization and host–parasite interactions during the schistosomula stage, suggesting potential utility in early infection control and possibly prophylaxis. This is particularly relevant given the limitations of praziquantel, including reduced sensitivity in some settings, lack of efficacy against immature parasite stages, and adverse effects such as hepatotoxicity and skin reactions [24, 25].

In summary, this work presents a streamlined computational pipeline that combines target prioritization, molecular docking, and multi-parameter evaluation to accelerate anti-schistosomal drug discovery. Among the screened ligands, MMV1262756 emerged as the most promising hit, warranting further in vitro and in vivo validation. Beyond *S. haematobium,* this integrative approach can be readily applied to other neglected tropical diseases, leveraging open-access libraries such as the GHP Box to expand therapeutic options [26, 27].

Conclusion

This study highlights the effectiveness of the effectiveness of integrating computational drug discovery approaches in identifying novel therapeutics against *Schistosoma haematobium*. Virtual screening of Global Health Priority (GHP) Box compounds against the Sh23 protein yielded MMV1262756 as the lead candidate, with a strong binding affinity of -8.2 kcal/mol, high drug-likeness score (0.87), and low predicted clinical toxicity (0.14). These attributes position MMV1262756 as a potential candidate to address the limitations of praziquantel. Future in vitro and in vivo studies are warranted to validate its therapeutic potential and advance it toward clinical development.

Acknowledgements

The authors would like to thank all individuals and institutions that contributed to the successful completion of this work. Their support, guidance, and valuable feedback are gratefully acknowledged.

Authors' contributions

GGK and ASA conceptualized and designed the study. JC, WO, ND and EAS collected the data. JC, EAS, WO, A-SA, and PKS analyzed the data. JC, EAS, ND, ASA, and GGK wrote and edited the manuscript. All authors read and approved the final version of the manuscript.

Funding

This research received no specific grant from any funding agency in the public, commercial, or not-for-profit sectors.

Conflict of Interest

The authors declare that there are no conflicts of interest regarding the publication of this paper.

References

1. Anderson RM, Turner HC, Farrell SH, Truscott JE,et al. Studies of the Transmission Dynamics, Mathematical Model Development and the Control of Schistosome Parasites by Mass Drug Administration in Human Communities. Advanced Parasitology. Doi:2016;94:199-246.10.1016/bs.apar.2016.06.003

2. LoVerde PT. Schistosomiasis. Adv Exp Med Biol. 2024;1454:75-105. Doi:10.1016/j.ijpddr.2021.05.002

3. Yamey G, McDade KK, Anderson RM, Bartsch SM, Bottazzi ME, Diemert D, et al. Vaccine value profile for schistosomiasis. Vaccine. 2024:126020. doi:10.1016/j.vaccine.2024.05.068

4. Au MFF, Williams GA, Hui JHL. Status Quo and Future Perspectives of Molecular and Genomic Studies on the Genus Biomphalaria-The Intermediate Snail Host of Schistosoma mansoni. Int J Mol Sci. 2023;24(5). doi:10.3390/ijms24054895.

5. Jafaru S. Antigens of Three Medically Important Schistosoma spp. doi:10.9734/ajriz/2022/v5i330139

6. Mekonnen GG, Tedla BA, Pearson MS, Becker L, Field M, Amoah AS, et al. Characterisation of tetraspanins from *Schistosoma haematobium* and evaluation of their potential as novel diagnostic markers. PLoS neglected tropical diseases. 2022;16(1):e0010151. doi: 10.1371/journal.pntd.0010151.

7. Oettle RC, Dickinson HA, Fitzsimmons CM, Sacko M, Tukahebwa EM, Chalmers IW, et al. Protective human IgE responses are promoted by comparable life-cycle dependent Tegument Allergen-Like expression in *Schistosoma haematobium* and Schistosoma mansoni infection. PLoS Pathog. 2023;19(5):e1011037. doi:10.1371/journal.ppat.1011037.

8. Bergquist R, Utzinger J, Keiser J. Controlling schistosomiasis with praziquantel: How much longer without a viable alternative? Infectious diseases of poverty. 2017;6(1):74. doi:10.1186/s40249-017-0286-2.

9. Soleymani N, Sadr S, Santucciu C, Dianaty S, Lotfalizadeh N, Hajjafari A, et al. Unveiling novel insights in helminth proteomics: Advancements, applications, and implications for parasitology and beyond. Biologics. 2024;4(3):314-44.doi:10.3390/biologics4030020.

10. Neves BJ, Muratov E, Machado RB, Andrade CH, Cravo PVL. Modern approaches to accelerate discovery of new antischistosomal drugs. Expert opinion on drug discovery. 2016;11(6):557-67. doi:10.1080/17460441.2016.1178230.

11. Ruiz DGT, Guevara-Pulido J. Recent advances in drug discovery and development through machine learning: A rational drug design (2000-2024). Revista Facultad de Ciencias Básicas. 2023;19(2):107-23. doi:10.18359/rfcb.7873.

12. Binbay FA, Rathod DC, George AAP, Imhof D. Quality Assessment of Selected Protein Structures Derived from Homology Modeling and AlphaFold. Pharmaceuticals. 2023;16(12):1662.doi:10.3390/ph16121662.

13. Mathur N, Chandra M, Sai S, Santoki KM, Vadhavana NN, Shah S, et al. *in silico* Docking: Protocols for Computational Exploration of Molecular Interactions. In: Podlipnik Č, editor. Unravelling Molecular Docking - From Theory to Practice. Rijeka: IntechOpen; 2024. doi: 10.5772/intechopen.1005527.

14. Ferreira LG, Dos Santos RN, Oliva G, Andricopulo AD. Molecular docking and structure-based drug design strategies. Molecules. 2015;20(7):13384-421. doi:10.3390/molecules200713384.

15. Gentile F, Yaacoub JC, Gleave J, Fernandez M, Ton A-T, Ban F, et al. Artificial intelligence–enabled virtual screening of ultra-large chemical libraries with deep docking. Nature Protocols. 2022;17(3):672-97. doi:10.1038/s41596-021-00659-2.

16. Dallakyan S, Olson AJ. Small-molecule library screening by docking with PyRx. Methods Mol Biol. 2015;1263:243-50. doi:10.1007/978-1-4939-2269-7_19.

17. De Carlo A, Ronchi D, Piastra M, Tosca EM, Magni P. Predicting ADMET Properties from Molecule SMILE: A Bottom-Up Approach Using Attention-Based Graph Neural Networks. Pharmaceutics. 2024;16(6). doi:10.3390/pharmaceutics16060776.

18. Batirel A, Regmi SK, Singh P, Mert A, Konety BR, Kumar R. Urological infections in the developing world: an increasing problem in developed countries. World Journal of Urology. 2020;38(11):2681-91. doi:10.1007/s00345-020-03120-3.

19. Yan-Rong L, Han-Guo X, Zhu-Yun C, Li-Zhen X, Rong-Yan Z. [Diagnosis and treatment of an imported case of schistosomiasis haematobium]. Zhongguo Xue Xi Chong Bing Fang Zhi Za Zhi. 2017;29(1):108-10. doi:10.1371/journal.pntd.0006171.

20. Lo NC, Addiss DG, Hotez PJ, King CH, Stothard JR, Evans DS, et al. A call to strengthen the global strategy against schistosomiasis and soil-transmitted helminthiasis: the time is now. The Lancet Infectious Diseases. 2017;17(2):e64-e9. doi: 10.1016/s1473-3099(16)30535-7

21. Hernandez HW, Soeung M, Zorn KM, Ashoura N, Mottin M, Andrade CH, et al. High Throughput and Computational Repurposing for Neglected Diseases. Pharm Res. 2018;36(2):27.doi:10.1007/s11095-018-2558-3

22. Veale CGL. Unpacking the Pathogen Box-An Open Source Tool for Fighting Neglected Tropical Disease. ChemMedChem. 2019;14(4):386-453. doi:10.1002/cmdc.201800755.

23. Kondapuram SK, Sarvagalla S, Coumar MS. Chapter 22 - Docking-Based Virtual Screening Using PyRx Tool: Autophagy Target Vps34 as a Case Study. In: Coumar MS, editor. Molecular Docking for Computer-Aided Drug Design: Academic Press; 2021. p. 463-77. doi:10.1016/b978-0-12-822312-3.00019-9

24. Balahbib A, El Omari N, Lghazi H, Hatoufi K, El Atki Y, Bouyahya A, et al. Therapeutic challenges of schistosomiasis: mechanisms of action and current limitations. Journal of Parasitic Diseases. 2025;49(3):498-512. doi:10.1007/s12639-025-01785-4.

25. Villamizar-Monsalve MA, López-Abán J, Vicente B, Peláez R, Muro A. Current drug strategies for the treatment and control of schistosomiasis. Expert Opin Pharmacother. 2024;25(4):409-20. doi: 10.1080/14656566.2024.2333372.

26. Midzi N, Bärenbold O, Manangazira P, Phiri I, Mutsaka-Makuvaza MJ, Mhlanga G, et al. Accuracy of different diagnostic techniques for *Schistosoma haematobium* to estimate treatment needs in Zimbabwe: Application of a hierarchical Bayesian egg count model. PLoS Negl Trop Dis. 2020;14(8):e0008451. doi: 10.1080/14656566.2024.2333372.

27. Ogwu MC, Izah SC. Potential Future Trends in Managing Tropical Diseases. In: Ogwu MC, Izah SC, editors. Technological Innovations for Managing Tropical Diseases. Cham: Springer Nature Switzerland; 2025. p. 329-56. doi:10.1007/978-3-031-82622-1_14.

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

Oksana Ryabinina[1,2]*, Richard HarryAsmah[3], Gabriella Amoakoma Ama Essuman [4], Emmanuel TimmyDonkoh[5], Nicholas Ekow Thomford[2,6,7], Gifty Boateng[8], Daniel Asamani[9]

[1] Department of Chemical Pathology, School of Medical Sciences, College of Allied Health Sciences, University of Cape Coast, Cape Coast, Ghana | [2] Pharmacogenomics and Genomic Medicine Group, School of Medical Sciences, College of Health and Allied Sciences, University of Cape Coast, Cape Coast, Ghana | [3] University of Health and Allied Sciences, Ho, Ghana | [4] Department of Medical Laboratory Sciences, School of Basic and Biomedical Sciences, University of Ghana, Accra, Ghana | [5] University of Energy and Natural Resources, Sunyani, Ghana | [6] Department of Pathology, Faculty of Health Sciences, University of Cape Town, Anzio Road, Observatory, Cape Town 7925, South Africa | [7] Department of Medical Biochemistry, School of Medical Sciences, College of Health and Allied Sciences, University of Cape Coast, Cape Coast, Ghana | [8] National Public Health and Reference Laboratory, Ghana Health Service, Accra, Ghana | [9] Greater Accra Regional Hospital, Ghana Health Service, Accra, Ghana

Correspondence should be addressed to Oksana Ryabinina (email: oksana.ryabinina@ucc.edu.gh)

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.

References

1. Bernstein DI, Bellamy AR, Hook EW, Levin MJ, Wald A, Ewell MG, et al. Epidemiology, clinical presentation, and antibody response to primary infection with herpes simplex virus type 1 and type 2 in young women. *Clin Infect Dis*. 2013;56(3):344-351. doi:10.1093/cid/cis891.

2. Harfouche M, Al-Mukdad S, Alareeki A, Osman AMM, Gottlieb S, Rowley J, et al. Estimated global and regional incidence and prevalence of herpes simplex virus infections and genital ulcer disease in 2020: mathematical modelling analyses. *Sex Transm Infect*. 2025;101(4):214-223. doi:10.1136/sextrans-2024-056307.

3. Chang JY, Balch C, Oh HS. Toward the eradication of herpes simplex virus: vaccination and beyond. *Viruses*. 2024;16(9):1476. doi:10.3390/v16091476.

4. Casto AM, Huang MLW, Xie H, Jerome KR, Wald A, Johnston CM, et al. Herpes simplex virus mistyping due to HSV-1 × HSV-2 interspecies recombination in viral gene encoding glycoprotein B. *Viruses*. 2020;12(8):860. doi:10.3390/v12080860.

5. Looker KJ, Garnett GP. A systematic review of the epidemiology and interaction of herpes simplex virus types 1 and 2. *Sex Transm Infect*. 2005;81(2):103-107. doi:10.1136/sti.2004.012039.

6. Looker KJ, Magaret AS, May MT, Turner KME, Vickerman P, Gottlieb SL, et al. Global and regional estimates of prevalent and incident herpes simplex virus type 1 infections in 2012. *PLoS One*. 2015;10(10): e0140765. doi:10.1371/journal.pone.0140765.

7. Looker KJ, Magaret AS, Turner KME, Vickerman P, Gottlieb SL, Newman LM. Global estimates of prevalent and incident herpes simplex virus type 2 infections in 2012. *PLoS One*. 2015;10(1):e0114989. doi:10.1371/journal.pone.0114989.

8. Johnston C, Corey L. Current concepts for genital herpes simplex virus infection: diagnostics and pathogenesis of genital tract shedding. *Clin Microbiol Rev*. 2015;29(1):149-161. doi:10.1128/cmr.00043-15.

9. Jaishankar D, Shukla D. Genital herpes: insights into sexually transmitted infectious disease. *Microb Cell*. 2016;3(9):438-450. doi:10.15698/mic2016.09.528.

10. Looker KJ, Elmes JAR, Gottlieb SL, Schiffer LM, Vickerman P, Turner KME, et al. Effect of HSV-2 infection on subsequent HIV acquisition: an updated systematic review and meta-analysis. *Lancet Infect Dis*. 2017;17(12):1303-1316. doi:10.1016/S1473-3099(17)30405-X.

11. Szpara ML, Gatherer D, Ochoa A, Greenbaum B, Dolan A, Bowden RJ, et al. Evolution and diversity in human herpes simplex virus genomes. *J Virol*. 2014;88(2):1209-1227. doi:10.1128/jvi.01987-13.

12. Kwofie TB, Ayensu F, Mutocheluh M, Narkwa P, Nguah SB, Turpin CA, et al. Seroprevalence of rubella virus, cytomegalovirus and herpes simplex virus-2 among pregnant women at the Komfo Anokye Teaching Hospital, Ghana. *J Public Health Dev Ctries*. 2015;1(2):56-63.

13. LeGoff J, Mayaud P, Gresenguet G, Weiss HA, Nzambi K, Frost E, et al. Performance of HerpeSelect and Kalon assays in detection of antibodies to herpes simplex virus type 2. *J Clin Microbiol*. 2008;46(6):1914-1918. doi:10.1128/jcm.02332-07.

14. Debrah O, Agyemang-Yeboah F, Asmah RH, Timmy-Donko E, Seini MM, Fondjo LA, et al. SERO-prevalence of herpes simplex virus type 1 and type 2 among women attending routine Cervicare clinics in Ghana. *BMC Infect Dis*. 2018;18:378. doi:10.1186/s12879-018-3288-1.

15. Ribes JA, Steele AD, Seabolt JP, Baker DJ. Six-year study of the incidence of herpes in genital and nongenital cultures in a Central Kentucky Medical Center patient population. *J Clin Microbiol*. 2001;39(9):3321-3325. doi:10.1128/jcm.39.9.3321-3325.2001.

16. Blankson PK, Blankson HNA, Obeng-Nkrumah N, Turkson AA, Tormeti D, Adamafio M, et al. Detection of herpes viruses in Ghanaian patients with periodontitis. *J Investig Clin Dent*. 2019;10(2):e12386. doi:10.1111/jicd.12386.

17. Xu F, Lee FK, Morrow RA, Steernberg MR, Luther KE, Dubin G, et al. Seroprevalence of herpes simplex virus type 1 in children in the United States. *J Pediatr*. 2007;151(4):374-377. doi:10.1016/j.jpeds.2007.04.065.

18. Hellenbrand W, Thierfelder W, Müller-Pebody B, Hamouda O, Breuer T. Seroprevalence of herpes simplex virus type 1 (HSV-1) and type 2 (HSV-2) in former East and West Germany, 1997–1998. *Eur J Clin Microbiol Infect Dis*. 2005;24(2):131-135. doi:10.1007/s10096-005-1286-x.

19. Khadr L, Harfouche M, Omori R, Schwarzer G, Chemaitelly H, Abu-Raddad LJ, et al. The epidemiology of herpes simplex virus type 1 in Asia: systematic review, meta-analyses, and meta-regressions. *Clin Infect Dis*. 2019;68(5):757-772. doi:10.1093/cid/ciy562.

20. Sukik L, Alyafei M, Harfouche M, Abu-Raddad LJ. Herpes simplex virus type 1 epidemiology in Latin America and the Caribbean: systematic review and meta-analytics. *PLoS One*. 2019;14(4):e0215487. doi:10.1371/journal.pone.0215487.

21. Ayoub HH, Chemaitelly H, Abu-Raddad LJ. Characterizing the transitioning epidemiology of herpes simplex virus type 1 in the USA: model-based predictions. *BMC Med*. 2019;17:57. doi:10.1186/s12916-019-1285-x.

22. Mouliom FHN, Nguwoh PS, Fokam J. Prévalence des infections à herpes simplex virus 1 et 2 chez les personnes vivant avec le VIH à Yaoundé : une Étude Sérologique. *Health Sci Dis*. 2016;17(3). doi:10.5281/hsd.v17i3.706.

23. Diawara S, Kane CT, Legoff J, Gaye AG, Mboup S, BÉLec L. Low seroprevalence of herpes simplex virus type 2 among pregnant women in Senegal. *Int J STD AIDS*. 2008;19(3):159-160. doi:10.1258/ijsa.2007.007139.

24. Reward EE, Muo SO, Orabueze INA, Ike AC. Seroprevalence of herpes simplex virus types 1 and 2 in Nigeria: a systematic review and meta-analyses. *Pathog Glob Health*. 2019;113(5):229-237. doi:10.1080/20477724.2019.1678938.

25. Kane CT, Diawara S, Ndiaye HD, Diallo PAN, Wade AS, Diallo AG, et al. Concentrated and linked epidemics of both HSV-2 and HIV-1/HIV-2 infections in Senegal: public health impacts of the spread of HIV. *Int J STD AIDS*. 2009;20(11):793-796. doi:10.1258/ijsa.2008.008414.

26. Sanders SA, Reinisch JM. Would You Say You "Had Sex" If ? *JAMA*. 1999;281(3):275-277. doi:10.1001/jama.281.3.275.

27. Harfouche M, Chemaitelly H, Abu-Raddad LJ. Herpes simplex virus type 1 epidemiology in Africa: systematic review, meta-analyses, and meta-regressions. *J Infect*. 2019;79(4):289-299. doi:10.1016/j.jinf.2019.07.012.

28. Chaabane S, Harfouche M, Chemaitelly H, Schwarzer G, Abu-Raddad LJ. Herpes simplex virus type 1 epidemiology in the Middle East and North Africa: systematic review, meta-analyses, and meta-regressions. *Sci Rep*. 2019;9:1136. doi:10.1038/s41598-018-37833-8.

29. Solomon L, Cannon M, Reyes M, Graber J, Wetherall N, Reeves W. Epidemiology of recurrent genital herpes simplex virus types 1 and 2. *Sex Transm Infect*. 2003;79(6):456-459. doi:10.1136/sti.79.6.456.

30. Lafferty WE, Downey L, Celum C, Wald A. Herpes simplex virus type 1 as a cause of genital herpes: impact on surveillance and prevention. *J Infect Dis*. 2000;181(4):1454-1457. doi:10.1086/315395.

31. Gupta R, Warren T, Wald A. Genital herpes. *Lancet*. 2007;370(9605):2127-2137. doi:10.1016/S0140-6736(07)61908-4.

32. Ashley-Morrow R, Krantz E, Wald A. Time course of seroconversion by HerpeSelect ELISA after acquisition of genital herpes simplex virus type 1 (HSV-1) or HSV-2. *Sex Transm Dis*. 2003;30(4):310-314. doi:10.1097/00007435-200304000-00007.

33. Wald A, Ashley-Morrow R. Serological testing for herpes simplex virus (HSV)–1 and HSV-2 infection. *Clin Infect Dis*. 2002;35(Suppl 2):S173-S182. doi:10.1086/342104.

34. Woolley PD, Lacey HB, Helsen K. Screening pregnant women for genital herpes. *Int J STD AIDS*. 1991;2(4):287-288. doi:10.1177/095646249100200413.

35. Baker DA, Pressley A, Meek L, Figueroa R, Yates B, Dix L. HSV serologic testing for pregnant women: willingness to be tested and factors affecting testing. *Infect Dis Obstet Gynecol*. 2011;2011:874820. doi:10.1155/2011/874820.

36. Peña KC, Adelson ME, Mordechai E, Blaho JA. Genital herpes simplex virus type 1 in women: detection in cervicovaginal specimens from gynecological practices in the United States. *J Clin Microbiol*. 2010;48(1):150-153. doi:10.1128/JCM.01336-09.