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Copyright AJCEM 2026: <https://dx.doi.org/10.4314/ajcem.v27i4.2>**Mini-Review****Open Access****The evidence gap: Vulvovaginal candidiasis research in African populations***^{1,2}Okeke, P. C. U., ^{1,2}Nwafia, I. N., and ^{1,2}Emeribe, S. C.¹Department of Medical Microbiology, University of Nigeria Teaching Hospital (UNTH), Ituku-Ozalla, Enugu, Nigeria²Department of Medical Microbiology, College of Medicine, Faculty of Basic Clinical Sciences, University of Nigeria, Ituku-Ozalla, Enugu, Nigeria*Correspondence to: princess.okeke@unn.edu.ng; Tel: +2348037117982; ORCID: <https://orcid.org/0009-0004-2522-2416>**Abstract:**

Vulvovaginal candidiasis (VVC) affects an estimated 70-75% of women at least once before menopause, and recurrent disease is estimated to affect approximately 138 million women annually worldwide. Within this global picture, sub-Saharan Africa carries a disproportionate share of non-*albicans* *Candida* infection and reported antifungal resistance, yet remains one of the least-studied regions for the mechanistic, immunological and therapeutic research now reshaping the field elsewhere. This mini-review summarizes the available African-specific evidence, identifies where that evidence stops short of matching the region's disease burden, and proposes concrete regional research priorities. The central challenge is not simply a shortage of prevalence surveys, of which a reasonable number now exist, but the near-total absence of African data from every mechanistic and translational thread currently advancing VVC science elsewhere: host immunogenetics, vaginal and gut microbiome characterization, novel antifungal evaluation, and vagina-specific diagnostic standards.

Keywords: Vulvovaginal candidiasis; Antifungal resistance; Non-*albicans* *Candida*; Research priorities; Host genetics; Africa

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Lacunes dans les données probantes: Recherche sur la candidose vulvo-vaginale dans les populations africaines*^{1,2}Okeke, P. C. U., ^{1,2}Nwafia, I. N., et ^{1,2}Emeribe, S. C.¹Département de Microbiologie Médicale, Centre Hospitalier Universitaire du Nigéria (UNTH), Ituku-Ozalla, Enugu, Nigéria²Département de Microbiologie Médicale, Collège de médecine, Faculté des Sciences Cliniques Fondamentales, Université du Nigéria, Ituku-Ozalla, Enugu, Nigéria*Correspondance à princess.okeke@unn.edu.ng; Tél: +2348037117982 ORCID: <https://orcid.org/0009-0004-2522-2416>**Résumé:**

La candidose vulvo-vaginale (CVV) touche environ 70 à 75 % des femmes au moins une fois avant la ménopause, et les récives affecteraient près de 138 millions de femmes chaque année dans le monde. Dans ce contexte mondial, l'Afrique subsaharienne concentre une part disproportionnée des infections à *Candida* non-*albicans* et des résistances aux antifongiques, tout en demeurant l'une des régions les moins étudiées en matière de recherche mécanistique, immunologique et thérapeutique, une recherche qui redéfinit actuellement le domaine ailleurs. Cette mini-synthèse résume les données probantes disponibles spécifiques à l'Afrique, identifie les lacunes de ces données par rapport à la prévalence de la maladie dans la région et propose des priorités de recherche régionales concrètes. Le principal défi ne réside pas seulement dans la pénurie d'enquêtes de prévalence, bien qu'il en existe désormais un nombre raisonnable, mais dans l'absence quasi totale de données africaines concernant tous les axes de recherche mécanistiques et translationnels qui font progresser la science de la candidose vulvo-vaginale ailleurs dans le monde :

immunogénétique de l'hôte, caractérisation du microbiome vaginal et intestinal, évaluation de nouveaux antifongiques et normes diagnostiques spécifiques au vagin.

Mots-clés: Candidose vulvo-vaginale; Résistance aux antifongiques; *Candida non-albicans*; Priorités de recherche; Génétique de l'hôte; Afrique

Introduction:

Vulvovaginal candidiasis remains one of the most common mucosal infections affecting women of reproductive age worldwide (1). Global surveillance and meta-analytic work over the past several years have substantially refined understanding of its pathogen spectrum, host determinants and treatment landscape (2,3,4). A recurring finding in this literature, however, is that the populations carrying the heaviest burden of non-*albicans* *Candida* (NAC) infection and antifungal resistance are also the populations from which the least primary research originates (5).

This is not a minor gap. If host genetics, vaginal microbiome composition, and the distribution of infecting *Candida* species differ meaningfully between the settings where mechanistic research is generated and the settings that carry a disproportionate share of the global disease burden, therapeutic strategies developed elsewhere cannot be assumed to translate without direct testing.

What African data currently show:

Hospital-based studies from several African countries have documented both the scale of the problem and its species-level texture. A Nigerian tertiary-hospital cohort identified douching as a common modifiable risk factor alongside a high overall prevalence of symptomatic disease (6). An Ethiopian cohort found that non-*albicans* species accounted for more than 40% of culture-confirmed isolates, a substantially higher proportion than is typically reported in North American or European series (7).

A systematic review and meta-analysis of 41 studies from sub-Saharan Africa, comprising over 15,000 participants, estimated a pooled VVC prevalence approaching one-third of screened women and confirmed that susceptibility testing was available for only a minority of the underlying studies (5). Most recently, a Ghanaian tertiary-care case series documented antifungal-resistant *Candida albicans* directly implicated in recurrent disease, underscoring that resistance, not only species distribution, is now a live clinical concern in the region (8). These studies establish the scale of the challenge; they do not, on their own, explain it.

Where the evidence stops

Four gaps stand out as particularly consequential. First, host-genetic susceptibility research in VVC has been conducted almost entirely in populations of European ancestry. We are aware of a single genome-wide association study extending this work to an African population, conducted in Nairobi, Kenya, which identified candidate susceptibility loci for recurrent disease (9). This is a valuable precedent, but it stands alone, and its candidate loci have not yet been mechanistically connected to any of the immune pathways implicated in the broader pathogenesis literature.

Second, host-immune correlates of colonization versus symptomatic disease, an active area of investigation elsewhere, remain minimally characterized in African cohorts. One study of cervical immune activation in colonized South African adolescents found a distinct pattern of T-helper-17-like cell activation associated with asymptomatic carriage (10), and a 2025 scoping review synthesizing immunological data from Uganda, Zambia, South Africa and Kenya found a coordinated inflammatory cytokine signature but noted that the underlying primary literature remains sparse and heterogeneous in methodology (11). Whether the immune determinants of symptomatic disease identified in non-African cohorts operate similarly here is simply unknown.

Third, the microbiome data underpinning newer probiotic and microbiome-directed strategies derive almost exclusively from non-African human cohorts and animal models, and evidence for commercially available *Lactobacillus* preparations in preventing VVC remains inconsistent even in the populations where it has been tested (12). Traditional fermented foods common across West African diets, such as 'ogi' and 'ugba', contain lactobacilli with plausible but uncharacterized anti-*Candida* potential (13). To our knowledge, none of these specific strains has been assayed for antifungal activity or tested within a microbiome-directed therapeutic framework, despite their obvious appeal as a low-cost, locally accessible intervention.

Fourth, the newer systemic antifungals now changing first-line practice elsewhere were evaluated primarily in North American and European trial populations, and their cost places

them outside routine reach in most African health systems (14). Meanwhile, standardized susceptibility testing itself has a validity problem specific to VVC: reference broth microdilution protocols are performed at neutral pH, while the vaginal environment is acidic, and susceptibility results can differ substantially under vaginally-relevant pH conditions (15,16). No antifungal agent used in VVC has a validated, vagina-specific susceptibility breakpoint anywhere, African data included.

Proposed priorities:

We propose four concrete, achievable priorities for African clinical microbiology research in this area. First, multicentre surveillance that pairs species identification with antifungal susceptibility testing as standard practice, rather than as an occasional add-on, building on the Ghanaian and Ethiopian precedents already established (7,8).

Second, extension of host-genetic and immune-correlate research beyond the single existing Kenyan cohort, ideally through multi-site African consortia that can achieve adequate sample sizes for genome-wide approaches (9).

Third, laboratory characterization of traditional fermented-food-derived lactobacilli for anti-*Candida* activity, as a direct, low-cost translational step building on existing food-microbiology literature (13).

Fourth, inclusion of African clinical sites in future trials of susceptibility breakpoint validation and novel antifungal evaluation, rather than post-hoc extrapolation from data generated elsewhere, alongside expanded molecular diagnostic capacity already emerging in some regional laboratories (17).

Conclusion:

The African evidence base for VVC is not empty, but it is structurally incomplete: strong on prevalence, thin on mechanism, and almost absent from the trials and cohort studies that will determine whether new diagnostic and therapeutic advances actually work in the populations that need them most. Closing this gap will require African-led, African-sited research at every level, from genomics to trial design, rather than continued reliance on evidence generated elsewhere and extrapolated after the fact.

Contributions of authors:

PCUO conceived the review concept and designed the study framework. SCE conducted the literature search and data extraction. PCUO

synthesized the evidence and drafted the initial manuscript. INN critically revised the manuscript for intellectual content. All authors reviewed and approved the final version of the manuscript.

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Conflicts of interest:

Authors declare no conflicts of interest.

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