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Bacterial and Fungal Coinfections among Patients with Tuberculosis in Africa: A Systematic Review

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A B S T R A C T

Tuberculosis (TB) remains a major public health challenge in Africa, where HIV prevalence varies considerably across countries but remains, overall, higher than the global average. Limited diagnostic capacity and the growing emergence of antimicrobial resistance further contribute to unfavorable treatment outcomes. Bacterial and fungal coinfections may complicate TB diagnosis and treatment, yet evidence from Africa remains fragmented. This systematic review aimed to synthesize available data on the prevalence, microbiological profiles, antimicrobial resistance patterns, and clinical implications of bacterial and fungal coinfections among TB patients in Africa. A systematic review was conducted according to PRISMA 2020 guidelines. PubMed/MEDLINE, ProQuest Central, and African Journals Online were searched for studies reporting bacterial and/or fungal coinfections among TB patients in Africa. Data extraction and quality assessment were performed independently by two reviewers using validated tools (NOS, AXIS, and JBI). Due to substantial methodological heterogeneity, a narrative synthesis was performed. Thirteen studies from nine African countries were included. Bacterial coinfections included non-tuberculous mycobacteria (13.9% to 36.6%), *Staphylococcus spp., Streptococcus spp., Haemophilus influenzae, Klebsiella pneumoniae,* and *Nocardia spp*. Fungal coinfections included chronic pulmonary aspergillosis (3.5%), *Candida albicans* (35.0%), dimorphic fungi (9.2%), and cryptococcosis. High levels of antimicrobial resistance were reported, including extended beta-lactam resistance among *K. pneumoniae* isolates and fluconazole resistance in 92.5% of fungal isolates. HIV coinfection frequently exacerbated disease severity and opportunistic infections. Bacterial and fungal coinfections among TB patients in Africa appear common and likely underdiagnosed. Strengthening microbiological and mycological diagnostic capacity, integrating antimicrobial resistance surveillance into TB programs, and conducting standardized multicenter studies are urgently needed to improve patient outcomes.

Introduction

Tuberculosis (TB) remains one of the leading causes of infectious mortality worldwide, affecting more than 10 million people each year and causing more than one million deaths, according to the World Health Organization's latest report on tuberculosis (1). The African region accounts for a significant proportion of these cases, a situation exacerbated by high HIV prevalence, poverty, malnutrition, and the growing emergence of antimicrobial resistance (1). Despite progress in molecular screening and access to antituberculosis treatments, treatment outcomes remain concerning in several African countries, particularly among patients with concomitant bacterial and/or fungal infections (2). Coinfection in tuberculosis patients poses a major clinical and public health challenge due to its diagnostic, therapeutic, and prognostic implications (3). As such, bacterial and fungal infections associated with tuberculosis can alter the clinical presentation, delay correct diagnosis, and complicate therapeutic management (3). Furthermore, in resource-limited African countries, coinfections associated with pulmonary tuberculosis often go unrecognized due to limited access to clinical microbiology and medical mycology services (4,5). This diagnostic shortfall encourages the use of empirical treatments that are sometimes inappropriate, resulting in increased mortality and heightened selective pressure favoring antimicrobial resistance (6).

Several studies have reported a high prevalence of secondary bacterial infections in patients with pulmonary tuberculosis, particularly involving *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa,* and *Streptococcus pneumoniae* (6,7). The high prevalence of HIV in sub-Saharan Africa exacerbates the risk of bacterial and fungal coinfections in tuberculosis patients, contributing to greater clinical severity as well as increased rates of treatment failure and mortality, particularly in cases of multidrug-resistant tuberculosis (2). Despite the growing importance of bacterial and fungal coinfections in tuberculosis patients, existing data in Africa remain scattered and poorly synthesized, with a predominance of isolated studies conducted in specific countries or among specific populations (3). To date, few systematic reviews have specifically and comprehensively assessed the prevalence of bacterial and fungal coinfections among tuberculosis patients in Africa, their antimicrobial resistance profiles, and their therapeutic and prognostic implications (8). Yet, a better understanding of these infectious interactions is essential for improving diagnostic strategies, optimizing antimicrobial treatments, and reducing tuberculosis-related mortality in African settings with a high disease burden (6).

In the light of the preceding context, this systematic review aims to compile and analyze available data from Africa on bacterial and fungal coinfections in patients with tuberculosis. Its objectives are to estimate the prevalence of these coinfections, characterize the antimicrobial resistance profiles of the isolated microorganisms, and examine their impact on adverse treatment outcomes.

Materials and Methods

We conducted a systematic review of the literature on fungal and bacterial coinfections in tuberculosis patients in Africa in accordance with the recommendations of the Preferred Reporting Items for Systematic Reviews and Meta-Analyses.

Information sources and search strategy

A systematic search was conducted in PubMed (MEDLINE), ProQuest Central, and African Journals Online (AJOL) to identify relevant studies on fungal and bacterial coinfections in tuberculosis patients in Africa. All database searches were performed on May 5, 2026. The search strategy was developed according to the PECO (Population, Exposure, Comparison, Outcome) framework, combining Medical Subject Headings (MeSH) and free-text keywords using Boolean operators (AND, OR). In addition, the reference lists of relevant studies were manually screened to identify any additional eligible publications.

Study selection and eligibility criteria

This systematic review included original studies conducted in Africa involving patients with tuberculosis who had a bacterial and/or fungal coinfection. The following articles were eligible for inclusion. They had to be published in peer-reviewed journals and written in either French or English. In addition, each article had to report at least one of the specified outcome measures in tuberculosis patients. These outcome measures included the prevalence of bacterial coinfections, the prevalence of fungal coinfections, and the prevalence of mixed coinfections. Mixed coinfections were defined as

tuberculosis occurring together with at least one other bacterial infection (other than *M. tuberculosis*) and/or a fungal infection. Further outcome measures comprised the antimicrobial susceptibility or resistance profiles of bacteria and fungi isolated from patients with tuberculosis coinfections. Adverse treatment outcomes associated with bacterial and/or fungal coinfections were also considered, particularly treatment failure. Finally, mortality associated with bacterial and/or fungal coinfections in tuberculosis patients was included as an outcome measure. Studies were excluded if they were not related to tuberculosis or did not investigate tuberculosis co-infections. We also excluded studies focusing on viral or parasitic co-infections, studies conducted outside Africa, animal or experimental studies, diagnostic tool evaluations, reviews, and study protocols.

Studies were required to report sufficient microbiological, clinical, or epidemiological data to allow for the extraction of prevalence estimates, microbiological profiles, or clinical outcomes of interest. Thus, the identified documents were imported into Zotero for reference management and the removal of duplicates. The references were then imported into the Rayyan.ai platform to facilitate the selection process. Study selection was conducted in two stages by two independent reviewers. First, the titles and abstracts were reviewed. Second, the full texts of the preselected studies were read and evaluated in depth.

Quality assessment

Two reviewers independently assessed the quality of the studies using validated tools appropriate for each study design: the Newcastle-Ottawa Scale (NOS) for the cohort study, the AXIS tool for cross-sectional studies, and the Joanna Briggs Institute (JBI) checklists for case series and case reports (9, 10, 11). Disagreements were resolved by consensus. Quality was categorized into three levels (high, moderate, low).

Data extraction

Data were extracted independently by the investigators using a standardized extraction form developed specifically for this systematic review. For each included study, the following bibliographic and methodological information was collected: first author, year of publication, study title, country of conduct, language of publication, and study type and setting. Data on the characteristics of the study population included the number of participants, the number of tuberculosis patients included, sociodemographic characteristics (mean or median age, gender distribution), HIV status, the presence of multidrug-resistant tuberculosis (MDR-TB), and the diagnostic methods used to confirm tuberculosis.

Detailed epidemiological data on coinfections were also extracted. For bacterial coinfections, the information collected included the number of cases, the prevalence of coinfections, the bacterial species identified, their frequency, and antimicrobial susceptibility profiles when reported. Similarly, for fungal coinfections, the extracted data included the number of cases, prevalence, isolated fungal species, their frequency, and the results of antifungal susceptibility testing. Data on mixed coinfections involving tuberculosis and bacterial and/or fungal infections were also collected, including the number of cases, prevalence, and types of coinfections reported. Finally, key clinical outcomes were extracted, including the proportions of treatment failure and overall mortality or mortality specific to bacterial, fungal, or mixed coinfections. Any other supplementary information deemed relevant to the interpretation of the results was also documented.

Data synthesis and analysis

Given the significant heterogeneity of the included studies, no meta-analysis was performed. The extracted data were synthesized according to predefined thematic areas: (i) bacterial coinfections, including nontuberculous mycobacteria and other opportunistic respiratory bacterial agents; (ii) fungal coinfections; and (iii) antibiotic and antifungal susceptibility profiles. For each area, the results were summarized taking into account the characteristics of the studies, geographic contexts, study populations, diagnostic methods used, and the main reported frequency estimates. Particular attention was paid to identifying inter-study variations that could influence the observed estimates, including differences in methods for confirming tuberculosis (microscopy, culture, GeneXpert, PCR), diagnostic criteria for coinfections, the HIV status of the included populations, and hospital or community settings. Prevalence data were reported descriptively using the numerators and denominators available in the original studies.

Results and Discussion

A total of 455 articles were identified through database

searches, including PubMed (n = 190), African Journals Online (n = 26), and ProQuest Central (n = 239). After removing 70 duplicates, 385 unique records were screened by title and abstract. Of these, 357 were excluded for the following reasons: lack of data on bacterial or fungal coinfection (n = 170), viral coinfection only (n = 107), non-tuberculous foci (n = 38), parasitic coinfections only (n = 13), non-African setting (n = 12), animal models of tuberculosis (n = 4), experimental study designs (n = 4), diagnostic tool evaluation studies (n = 3), review articles (n = 3), and study protocols (n = 3).

The remaining 28 records were retrieved for a full eligibility assessment, of which 15 were excluded because they were conducted outside of Africa. Thirteen studies m*et al.,*l predefined eligibility criteria and were included in the final systematic review (Figure 1).

General characteristics of the study populations

The thirteen (13) included studies were conducted in nine (9) African countries: Uganda (n = 1), a multisite study in sub-Saharan Africa (n = 1), Mali (n = 1), Ghana (n = 1), Nigeria (n = 3), Tanzania (n = 2), Côte d'Ivoire (n = 1), Morocco (n = 1), Kenya (n = 1), and Zambia (n = 1). Study designs included cross-sectional studies (n = 8), prospective cohort studies (n = 2), a case series (n = 1), and two individual case reports (n = 2). Publication dates ranged from 2013 to 2026. The total sample size ranged from 1 participant in the case reports to 6,123 in the largest multicenter study, while the number of confirmed tuberculosis cases per study ranged from 1 to 923 (10). Tuberculosis was microbiologically confirmed using GeneXpert MTB/RIF (3 studies), sputum culture (3 studies), direct microscopy (5 studies), polymerase chain reaction (1 study), and microscopy combined with cytohistological examination (1 study). The proportion of male participants ranged from 29.3% to 68.7%, and the mean or median age of participants ranged from 33 to 49.9 years (13, 14). The prevalence of HIV coinfection varied widely across studies, ranging from 0% in studies limited to HIV-negative populations to 100% in cohorts consisting of HIV-positive participants. The main characteristics of the included studies are summarized in Table 1.

Bacterial coinfections

Bacterial coinfections were documented in eight of the thirteen included studies and covered a broad microbiological spectrum, including nontuberculous mycobacteria, Gram-negative opportunistic bacteria, Gram-positive cocci, and *Nocardia spp*. (Table II).

Nontuberculous mycobacteria: Three studies specifically assessed the prevalence of nontuberculous mycobacteria in patients with confirmed or suspected tuberculosis. The proportion of nontuberculous mycobacteria among tuberculosis cases varied across studies (13.9%, 18.4%, and 36.6%), reflecting significant variation between studies attributable to differences in geographic context, patient selection, and diagnostic methodology(14,15,16).

Other bacterial coinfections: Attah *et al.,* identified bacterial coinfections in 78.4% (40/51) of patients with confirmed tuberculosis. The predominant microorganisms were *Staphylococcus spp*. (35.3%) and *Streptococcus spp*. (35.3%), followed by *Klebsiella spp*. (13.7%) and *Proteus spp*. (2.0%)(14). Mhimbira *et al.,* documented concomitant bacterial respiratory copathogens in 35.0% (171/489) of patients with tuberculosis, with *Haemophilus influenzae* (22.5%) and *Streptococcus pneumoniae* (20.2%) being the most common, and *Legionella pneumophila* (1.8%), *Bordetella pertussis* (0.8%), and *Bordetella parapertussis* (0.6%) detected in lower proportions(18). Sakyi *et al.,* reported coinfection with *Nocardia spp*. in 33.3% (4/12) of confirmed tuberculosis cases(19). In the Malian case series by Meli *et al.,* all four patients with TB-HIV coinfection developed a nosocomial superinfection with *Klebsiella pneumoniae* (100%), one of whom also had a coinfection with *Escherichia coli* (25%)(20).

Fungal coinfections: Fungal coinfections were reported in six of the thirteen included studies and encompassed a clinically diverse range of pathogenic fungi, including *Aspergillus, Candida, Cryptococcus, Blastomyces,* and *Paracoccidioides* (Table 3).

Page *et al.,* reported chronic pulmonary aspergillosis in 3.5% (14/398) of patients who had completed tuberculosis treatment and had residual pulmonary cavitation(21). Similarly, Shiboski *et al.,* reported an oral coinfection with *C. albicans* in 35.0% (19/54) of tuberculosis-seropositive patients enrolled at 11 multinational clinical trial sites(13). Kuria *et al.,* identified dimorphic fungal coinfections, primarily *Blastomyces dermatitidis* and *Paracoccidioides spp*., in 9.2% (37/400) of patients with confirmed

tuberculosis(22). Sani *et al.,* reported pulmonary fungal coinfections, primarily *Aspergillus fumigatus* and *C. albicans*, in 32.5% (14/43) of patients with suspected tuberculosis who had microbiologically confirmed tuberculosis(23). Two isolated case reports have expanded the clinical spectrum to include concomitant neurocryptococcosis and osteoarticular tuberculosis in an immunocompetent patient, as well as invasive systemic non-*Candida albicans* infection complicating spinal tuberculosis in a kidney transplant recipient(24, 25).

Antimicrobial resistance: Data on antimicrobial susceptibility were available from three studies. In the case series by Meli *et al.,* the four *K. pneumoniae* isolates from patients coinfected with HIV and TB showed extensive resistance to beta-lactams (20). Residual susceptibility profiles varied by case: the first isolate was susceptible only to kanamycin, amikacin, chloramphenicol, colistin, and fosfomycin; the second to cefoxitin, gentamicin, colistin, and chloramphenicol; the third to netilmicin, gentamicin, and imipenem; and the fourth to amikacin alone. The co-isolated *E. coli* strain in the fourth case was multidrug-resistant to all quinolones and beta-lactams, with intermediate susceptibility to cefoxitin.

Attah *et al.,* reported high resistance rates among bacterial co-isolates: ampicillin (88.9%), erythromycin (66.7%), ceftriaxone (42.2%), and ofloxacin (37.8%) (14). Meropenem showed the strongest in vitro activity, followed by amoxicillin + clavulanic acid, nitrofurantoin, and ciprofloxacin.

Regarding antifungal resistance, Sani *et al.,* in Nigeria reported that 92.5% of fungal isolates were resistant to fluconazole, while voriconazole and nystatin showed the greatest antifungal activity against the tested isolates (23).

This systematic review synthesized data from 13 studies conducted in nine African countries. This helped clarify that pulmonary TB is part of a complex and often polymicrobial microbiological ecosystem.

The proportion of coinfections with non-tuberculous mycobacteria among confirmed or suspected cases of tuberculosis ranged from 13.9% to 36.6% and poses a major diagnostic and ethical challenge. Indeed, nontuberculous mycobacteria (NTM) can cause pulmonary disease that is clinically and radiologically indistinguishable from tuberculosis. Misidentification of nontuberculous mycobacteria (NTM) as *Mycobacterium tuberculosis* (MTB) may lead to inappropriate antituberculosis treatment, resulting in treatment failure, unnecessary drug exposure, delayed diagnosis, and prolonged patient suffering (26).

In most healthcare facilities in Africa, microscopy remains the primary diagnostic method and cannot distinguish between *Mycobacterium tuberculosis* (MTB) and nontuberculous mycobacteria (NTM). This can lead to systematic misclassification and underestimation of the disease and underscores the urgency of widespread adoption of culture and molecular testing (27). The spectrum of non-mycobacterial bacterial coinfections documented in this review reflects the widespread vulnerability of tuberculosis patients to concomitant respiratory and opportunistic infections.

The high proportions of *H. influenzae* (22.5%) and *S. pneumoniae* (20.2%) in the Tanzanian cohort are consistent with data from other African studies on respiratory diseases and underscore the extent of polymicrobial pulmonary infection among patients with tuberculosis (18). These coinfections can obscure the diagnosis of tuberculosis, precipitate respiratory deterioration, and contribute to early mortality if left untreated. The detection of coinfection with *Nocardia spp*. in 33.3% of confirmed tuberculosis cases in the Ghanaian cohort is particularly noteworthy. *Nocardia* is an actinomycete capable of causing progressive and disseminated pulmonary disease in immunocompromised hosts and exhibits intrinsic resistance to standard antituberculosis regimens, making its co-occurrence therapeutically challenging(19).

Fungal coinfections in this review encompassed a clinically diverse and potentially fatal spectrum of syndromes. Chronic pulmonary aspergillosis complicating tuberculosis-related cavitation—documented in 3.5% of post-tuberculosis patients by Page *et al.,* is increasingly recognized as a significant global sequela of pulmonary tuberculosis (21). A major analysis by Denning *et al.,* estimated that approximately 1.2 million patients develop chronic pulmonary aspergillosis each year as a direct consequence of tuberculosis; and more recent modeling suggests that this figure is greatly underestimated, particularly in Africa(28, 29).

The high proportion of coinfections with *Aspergillus fumigatus* and *Candida albicans* (32.5%) reported by

Sani *et al.,* in Nigeria is consistent with the profound immune dysregulation associated with active tuberculosis, which compromises both innate and adaptive antifungal defenses and facilitates opportunistic fungal colonization and invasion(29).

The 35.0% prevalence of oral candidiasis among HIV-positive tuberculosis patients documented by Shiboski *et al.,* is also consistent with well-established data on oral mycobiome dysbiosis due to immunosuppression in individuals co-infected with HIV and TB(13, 30, 31).

Global estimates indicate that cryptococcal meningitis alone causes approximately 112,000 deaths per year among HIV-positive individuals. However, its co-occurrence with tuberculosis, particularly in non-immunocompromised hosts, as illustrated by the case report by Gbané-Koné, *et al.,* remains poorly quantified and is likely largely underdiagnosed in sub-Saharan Africa(24, 32).

The antimicrobial resistance profiles documented in this review raise profound clinical and public health concerns.

The widespread resistance to beta-lactams observed in all *Klebsiella pneumoniae* isolates from the case series by Meli *et al.,* in which some strains retained susceptibility only to last-resort agents such as colistin, imipenem, and amikacin, is consistent with the global spread of *K. pneumoniae*(33).

K. pneumoniae belongs to the ESKAPE group of pathogens (*Enterococcus faecium*, *Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa, Enterobacter spp*.), which is collectively responsible for the majority of healthcare-associated infections that are refractory to conventional antimicrobial treatments(34).

The high resistance to ampicillin (88.9%) and significant resistance to ceftriaxone (42.2%) reported by Attah *et al.,* also illustrate the progressive erosion of first-line antibiotic activity in these settings.

The convergence of drug-resistant tuberculosis with multidrug-resistant bacterial infections represents a major therapeutic challenge, leading to a considerable reduction in available treatment options.

The near-universal resistance to fluconazole documented by Sani *et al.,* (92.5% of fungal isolates) requires urgent attention.

Table.1 General characteristics of the studies included in the systematic review.

Author	Sample size	Number of tuberculosis patients	TB Confirmation Tests	TB (%)	Men (%)	HIV-positive (%)	Average age (years)
Page ID	398	398	GeneXpert	100	61.1	50	42
Shiboski CH	454	54	Culture	11.9	29.3	100	33
Meli H	4	4	GeneXpert	100	75	100	39.5
Sakyi AS	60	12	PCR	20	56.7	25	43.9
Attah I	220	51	Microscopy	23.2	46.4	38.2	Not reported
Hoza AS	372	36	Microscopy	9.7	52.7	14.2	40
Gbané-Koné M	1	1	Agriculture	100	100	0	39
Bekaoui S	1	1	Microscopy and Cytology/Histology	100	0	Not reported	24
Kuria JK	400	400	Microscopy	100	Not reported	Not reported	Not reported
Sani FM	216	43	GeneXpert	19.9	62	0	34
Aliyu G	1,603	375	Microscopy	23.4	56.2	23.6	37
Chanda-Kapata P	6123	923	Microscopy and Culture	15.1	48.3	Not reported	49.9
Mhimbira F	794	489	Agriculture	61.6	61	21.2	33

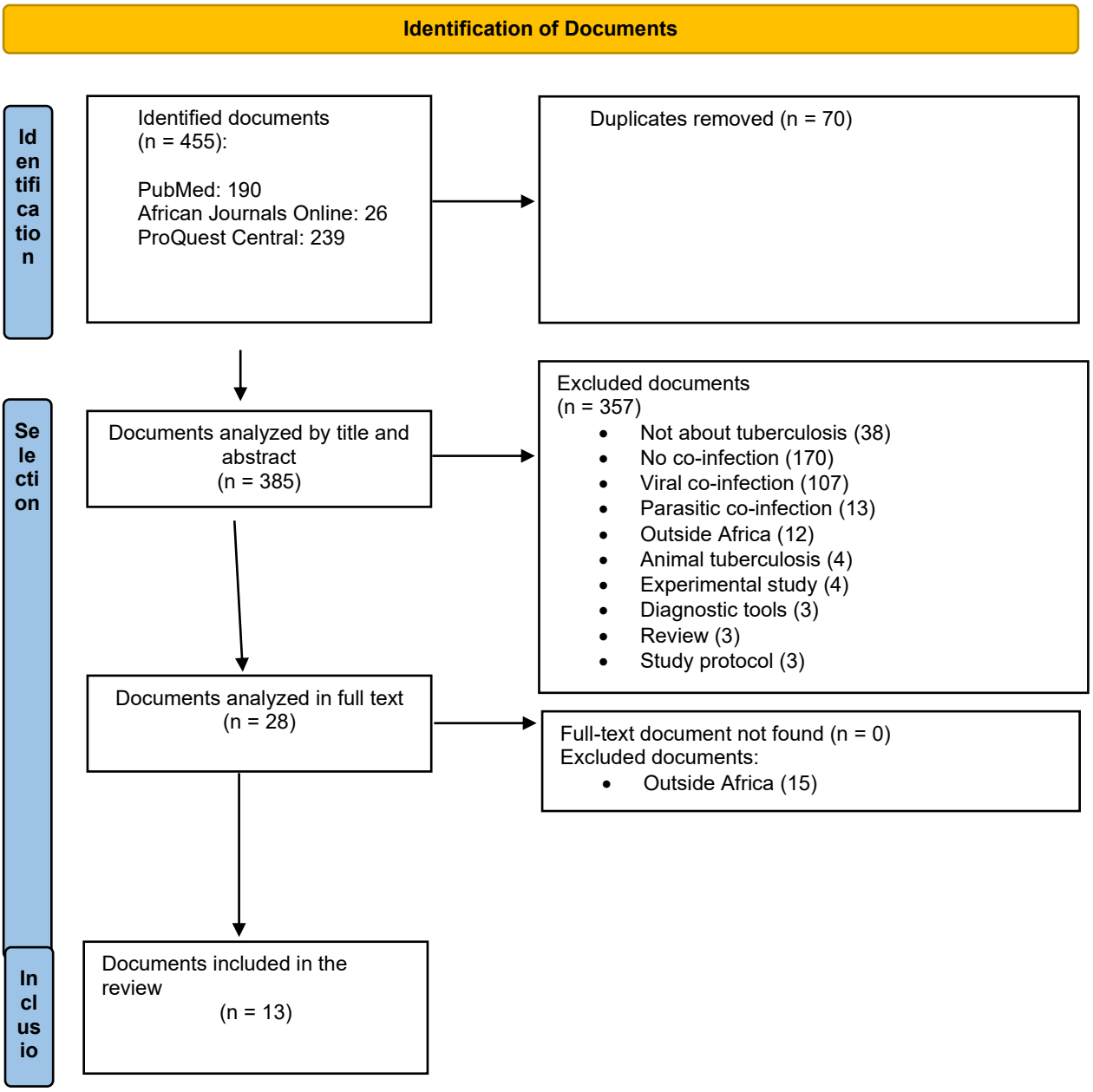
Table.2 Bacterial coinfections in patients with tuberculosis in Africa

Author	Tuberculosis cases	Bacteria	Number of cases	Proportion (%)
Meli H	4	*Klebsiella pneumoniae*	4	100.0
Meli H	4	*Escherichia coli*	1	25.0
Sakyi AS	12	*Nocardia*	4	33.3
Attah I	51	Other bacteria	40	78.4
Attah I	51	*Staphylococcus spp.*	18	35.3
Attah I	51	*Streptococcus spp.*	18	35.3
Attah I	51	*Klebsiella spp.*	7	13.7
Attah I	51	*Proteus spp*	1	2.0
Hoza AS	36	Nontuberculous mycobacteria	5	13.9
Aliyu G	375	Nontuberculous mycobacteria	69	18.4
Chanda-Kapata P	923	Nontuberculous mycobacteria	338	36.6
Mhimbira F	489	Other bacteria	171	35.0
Mhimbira F	489	*Haemophilus influenzae*	110	22.5
Mhimbira F	489	*Streptococcus pneumoniae*	99	20.2
Mhimbira F	489	*Legionella pneumophila*	9	1.8
Mhimbira F	489	*Bordetella parapertussis*	3	0.6
Mhimbira F	489	*Bordetella pertussis*	4	0.8

Table.3 Fungal coinfections in patients with tuberculosis in Africa

Author	Tuberculosis cases	Fungi	Number of cases	Proportion (%)
Page ID	398	*Aspergillus spp*	14	3.5
Shiboski CH	54	*Candida albicans*	19	35
Gbané-Koné M	1	*Cryptococcus spp*	1	100
Bekaoui S	1	*Candida non-albicans*	1	100
Kuria JK	400	*Blastomyces dermatitidis*, *Paracoccidioides*	37	9.2
Sani FM	43	*Aspergillus fumigatus*, *Candida albicans*	14	32.5

Figure.1 Flowchart of the study selection process for the systematic review on tuberculosis and bacterial and fungal coinfections in Africa.



The detailed search strategy is presented in the supplementary materials (Supplementary File 1).

Databases/Search Engines	Search Equations	Filters
PubMed	tuberculosis(mh) AND coinfection(mh) AND (mycoses(mh)) AND africa(mh) tuberculosis(mh) AND coinfection(mh) AND (bacteria(mh)) AND africa(mh)	None
ProQuest Central	subject(tuberculosis) AND abstract(coinfection) AND (Streptococcus OR Streptococcus OR Staphylococcus OR Staphylococcus OR Klebsiella OR Pseudomonas OR Haemophilus OR Burkholderia OR melioidosis OR melioidosis OR Coxiella OR Q fever OR Q fever OR Brucella OR brucellosis OR Francisella tularensis OR tularemia OR tularemia OR Bartonella OR Salmonella OR typhoid fever OR Helicobacter OR Actinomyces OR actinomycosis OR Legionella OR legionellosis OR Listeria OR Neisseria OR meningitis OR meningitis OR Enterobacteriaceae OR enterobacteria OR mycoses OR Candida OR candidiasis OR Aspergillus OR aspergillosis OR Cryptococcus OR cryptococcus OR cryptococcosis OR Histoplasma OR histoplasma OR histoplasmosis OR Talaromyces OR Ppenicilliosis OR Talaromycosis OR Coccidioides OR Coccidioidomycosis OR Paracoccidioides OR Paracoccidioidomycosis OR Blastomyces OR Blastomycosis OR Pneumocystis OR Pneumocystosis OR Sporothrix OR Sporotrichosis OR Mucor OR Rhizopus OR Mucormycosis)	Peer-reviewed
AJOL	+tuberculosis AND +coinfection +tuberculosis AND +Streptococcus +tuberculosis AND +Staphylococcus +tuberculosis AND +Staphylococcus +tuberculosis AND +Klebsiella +tuberculosis AND + Salmonella +tuberculosis AND + Actinomyces +tuberculosis AND +actinomycosis +tuberculosis AND + meningitis +tuberculosis AND + meningitis +tuberculosis AND + fungal infections +tuberculosis AND + candidiasis +tuberculosis AND + Aspergillus +tuberculosis AND + cryptococcosis +tuberculosis AND + histoplasmosis +tuberculosis AND + blastomycosis	None

Supplementary File S1

Author, year	Study title	Country	Study type	Study Setting	Describe the study population	Sample size	Assessment Tool	Methodological Quality
Page ID, 2019	Chronic pulmonary aspergillosis commonly complicates treated pulmonary tuberculosis with residual cavitation	Uganda	Cohort study	Hospital (Gulu Regional Referral Hospital) and community	Adults (≥16 years)	398	NOS	High
Shiboski CH, 2014	Role of oral candidiasis in TB and HIV coinfection: AIDS Clinical Trial Group Protocol A5253	Sub-Saharan Africa	Cross-sectional study	Multicenter (11 ACTG clinical trial sites)	Adults and adolescents (≥13 years) infected with HIV	454	**AXIS**	High
Meli H, 2020	Tuberculosis-HIV coinfection complicated by a nosocomial Klebsiella pneumoniae superinfection: a report of 4 cases in an Infectious Diseases Unit in Mali	Mali	Case series	Point G Hospital	Patients with HIV coinfection	4	**JBI**	Moderate
Sakyi AS, 2018	Evaluating the Contribution of Nocardia spp. and Mycobacterium tuberculosis to Pulmonary Infections among HIV-Positive and HIV-Negative Patients at the Komfo Anokye Teaching Hospital, Ghana	Ghana	Cross-sectional study	Komfo Anokye Hospital	Children and Adults (ages 4–80)	60	**AXIS**	Moderate
Attah I, 2026	Comparison of Bacterial Coinfections and Antibiotic Resistance Patterns in Confirmed and Non-Tuberculosis Patients Presenting with Presumptive Pulmonary TB Symptoms in a Nigerian Tertiary Hospital	Nigeria	Cross-sectional study	Karshi and Kubwa Hospitals	Adults (≥15 years)	220	**AXIS**	Moderate
Hoza AS, 2016	Increased Isolation of Nontuberculous Mycobacteria Among TB Suspects in Northeastern Tanzania: Public Health and Diagnostic Im: Implications for Control Programs	Tanzania	Cross-sectional study	Hospitals in Tanga	Adults	372	**AXIS**	High
Gbané-Koné M, 2015	Neuromeningeal cryptococcosis and bone tuberculosis in an immunocompetent patient: a case report	Ivory Coast	Clinical Case	Cocody Hospital	39-year-old patient not infected with HIV	1	**JBI**	Moderate
Bekaoui S, 2014	Tuberculous spondylodiscitis in a kidney transplant recipient complicated by systemic mycosis	Morocco	Clinical Case	Hospital (Ibn Sina University Hospital, Rabat)	24-year-old female kidney transplant recipient	1	**JBI**	Moderate
Kuria JK, 2020	Coinfection with Dimorphic Fungi in Tuberculosis Patients	Kenya	Cross-sectional study	Laikipia Hospital	Adults	400	**AXIS**	Moderate

	in Kenya							
Sani FM, 2020	Spectrum of Pulmonary Fungal Pathogens, Associated Risk Factors, and Antifungal Susceptibility Patterns Among Persons with Presumptive Tuberculosis in Gombe, Nigeria	Nigeria	Cross-sectional study	Gombe Hospital	Adults (≥15 years)	216	**AXIS**	Moderate
Aliyu G, 2013	Prevalence of Non-Tuberculous Mycobacterial Infections among Tuberculosis Suspects in Nigeria	Nigeria	Cross-sectional study	Hospital (NTBLTC Zaria and Barau Dikko Hospital, Kaduna)	Adults (≥18 years)	1,603	**AXIS**	High
Chanda-Kapata P, 2015	Non-tuberculous mycobacteria (NTM) in Zambia: prevalence, clinical, radiological, and microbiological characteristics	Zambia	Cross-sectional study	Multicenter (national reference laboratories)	Adults (≥15 years)	6,123	**AXIS**	High
Mhimbira F, 2019	Prevalence and clinical significance of respiratory viruses and bacteria detected in tuberculosis patients compared to household contact controls in Tanzania: a cohort study	Tanzania	Cohort study	Temeke Hospital	Children and adults	794	**NOS**	High

This finding is consistent with the global emergence *of* azole-resistant *Aspergillus fumigatus*—partly due to the environmental use of azole fungicides—and with the selection of fluconazole-resistant *Candida* strains following widespread prophylactic and therapeutic use of azoles in populations infected with HIV and co-infected with tuberculosis (35). This finding underscores the critical need for systematic antifungal susceptibility surveillance programs in African settico-infectionngs where fluconazole is used empirically.

A key implication of this review is the likely systematic and substantial underestimation of bacterial and fungal among tuberculosis patients in Africa. The microbiological evidence summarized here was primarily generated in research settings with enhanced diagnostic capacity, which is not routinely available in standard African healthcare facilities.

In most hospitals in sub-Saharan Africa, access to tuberculosis confirmation via culture, automated mycological identification, and antifungal susceptibility testing remains severely limited. Consequently, coinfections are rarely investigated systematically in clinical practice, leading to missed diagnoses, inappropriate treatment, and significant, unquantified mortality.

The various diagnostic methods used in the included studies—ranging from smear microscopy to GeneXpert and culture—have different sensitivities for detecting the disease. This variation can lead to detection bias, with some studies identifying more cases than others, regardless of the actual prevalence of coinfection.

Several methodological limitations of this review must be acknowledged. The relatively small number of included studies and the marked heterogeneity in study design, sample size, patient population, methods for confirming tuberculosis, and strategies for identifying coinfection precluded a formal quantitative meta-analysis. The inclusion of case reports and case series alongside population-based cross-sectional studies introduces selection bias and precludes meaningful pooling of prevalence estimates. Most of the included studies were cross-sectional in design, limiting causal inference. The predominant focus on hospitalized populations and those with pulmonary tuberculosis limits generalizability to community settings and manifestations of extrapulmonary tuberculosis.

In conclusion, this systematic review highlights a significant and likely underestimated burden of bacterial and fungal coinfections among tuberculosis patients in Africa. Nontuberculous mycobacteria, as well as several opportunistic bacterial and fungal pathogens, complicate diagnosis and therapeutic management and may contribute to clinical worsening and mortality. The high levels of antibiotic and antifungal resistance observed also underscore a growing threat to the effectiveness of empirical treatments in these settings. These findings reinforce the urgent need to strengthen microbiological and mycological diagnostic capabilities, to integrate surveillance of antibacterial and antifungal resistance into tuberculosis control programs, and to develop standardized multicenter studies to better characterize the extent and clinical impact of coinfections among tuberculosis patients in Africa.

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Author's contributions

Conceptualization: KD**,** KMSO

Data curation: KMSO, KD

Formal analysis: KMSO, SM, OTR, KD

Investigation: KD, OO, KDS, DSC, ZA

Resources: KD

Supervision: KD**,** OO, KDS, ZC, SA, SM, OTR

Validation: ZA, OO, KDS, DSC, OHG, ZC, SA, SM, OTR, KD

Visualization: PJES, MON, ZA, OO, KDS, ZI, DSC, KJF, TH, SB, ZSD, ST, CTR, SST, TM, OHG, ZC, SA, SM, OTR

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Data Availability

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

Declarations

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