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SYSTEMATIC REVIEW | Article in Press

Prevalence and factors associated with multidrug resistant *Mycobacterium tuberculosis* disease in Cameroon: a systematic review and meta-analysis

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Abstract

Background Multidrug-resistant tuberculosis (MDR-TB) remains a significant public health threat in low- and middle-income countries, including Cameroon. This systematic review and meta-analysis aimed to determine the pooled prevalence of MDR-TB and other anti-tuberculosis drug resistance patterns, and identify factors associated with drug-resistant tuberculosis in Cameroon.

Methods A comprehensive literature search was conducted in PubMed, Scopus, Web of Science, Embase, Cochrane Library, and African Journals Online. Additional studies were identified through Google Scholar and reference list screening. Observational studies (cross-sectional and cohort) reporting drug resistance among bacteriologically confirmed tuberculosis patients in Cameroon were eligible. Joanna Briggs Institute critical appraisal tools assessed study quality. Pooled prevalence estimates used random-effects meta-analysis. A p-value < 0.05 was considered statistically significant.

Results Twenty-seven studies (from 1995 to 2022) were included. Pooled prevalence of MDR-TB was 4.9% (95% CI: 2.5–9.4; 20 studies; $n = 6{,}914$), with significantly higher resistance among previously treated patients (11.2%; 95% CI: 5.6–21.2; 10 studies; $n = 1{,}469$) than new patients (2.0%; 95% CI: 1.1–3.5; 11 studies; $n = 3{,}345$). Multiregion studies revealed a higher pooled prevalence (13.6%; 95% CI: 4.1–36.8; 4 studies; $n = 743$) than Adamawa region (1.6%; 95% CI: 0.9–2.7; 2 studies; $n = 882$), where the lowest pooled prevalence was observed. Any resistance prevalence was 16.0% (95% CI: 10.1–24.3; 27 studies; $n = 9{,}330$), and rifampicin resistance was 4.6% (95% CI: 2.4–8.6; 25 studies; $n = 8{,}728$). Monoresistance was highest for streptomycin (6.4%; 95% CI: 3.7–10.8; 13 studies; $n = 3{,}813$) and isoniazid (4.7%; 95% CI: 3.0-7.4; 15 studies; $n = 4{,}579$). Previous tuberculosis disease was the strongest factor associated with drug resistance (OR = 3.9; 95% CI: 1.8–8.4; 7 studies), followed by alcohol consumption (OR = 1.8; 95% CI: 1.2–2.7; 2 studies) and incarceration history (OR = 1.7; 95% CI: 1.1–2.6; 2 studies). High heterogeneity was observed across most of the pooled estimates.

Conclusions Drug-resistant tuberculosis, particularly MDR-TB, poses a substantial burden in Cameroon. These findings underscore the urgent need to strengthen routine drug susceptibility testing, scale up rapid molecular diagnostics, enhance treatment adherence, and implement targeted interventions for high-risk populations.

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Keywords Tuberculosis · Multidrug-resistance · Drug resistance · Rifampicin resistance · Prevalence · Risk factors · Systematic review · Meta-analysis · Cameroon

Introduction

Tuberculosis (TB) is still a major cause of morbidity and mortality around the world, especially in low- and middle-income countries where the burden has been consistently high over the years. In 2024, the WHO estimated 10.7 million new tuberculosis cases and 1.23 million deaths globally, including cases of multidrug-resistant (MDR-TB) [1, 2].

MDR-TB is a form of TB that shows resistance to at least isoniazid and rifampin. It is a global threat and a challenge for TB control worldwide, particularly in lower- and middle-income countries, where the burden remains high. MDR-TB usually requires longer treatment, costs more, has lower success rates, and leads to more deaths than drug-susceptible TB [3, 4]. According to World Health Organization (WHO) estimates, approximately 410,000 incident cases of MDR/rifampicin-resistant TB (RR-TB) occurred worldwide in 2024, with an estimated 150,000 associated deaths. More than half of the global burden was concentrated in India (32%), China (7.1%), the Philippines (7.1%), and the Russian Federation (6.7%) [5].

Sub-Saharan Africa bears a substantial burden of tuberculosis (TB) and drug-resistant tuberculosis (DR-TB), driven by delayed diagnosis, limited access to drug susceptibility testing, weak health systems, and high rates of HIV co-infection [6, 7]. HIV infection substantially increases the risk of progression from latent to active TB and has been associated with poorer treatment outcomes, including drug resistance [7]. According to recent WHO estimates, the number of individuals diagnosed with drug-resistant tuberculosis in 2024 varied considerably across the region, with approximately 3,662 cases in Nigeria, 2,099 cases in Democratic Republic of the Congo, 835 cases in Ethiopia, and 122 cases in Burkina Faso [8]. History of prior TB treatment remains the most consistently identified predictor of MDR-TB in the region, while other commonly reported associated factors include poor treatment adherence, treatment interruption, contact with known MDR-TB cases, delayed diagnosis, socioeconomic disadvantage [9].

In Cameroon, an estimated 6,810 tuberculosis (TB) deaths were reported in 2024, corresponding to a TB mortality rate of 23 per 100,000 population, while 188 people were diagnosed with drug-resistant TB in the same year [10]. Studies conducted in the country have identified several potential risk factors for MDR-TB, including previous TB treatment, treatment failure, poor adherence to therapy, HIV co-infection, and close contact with individuals diagnosed with MDR-TB [11].

However, these findings are not always consistent across studies due to differences in study design, population characteristics, diagnostic methods, and study settings [10, 11]. This lack of pooled evidence limits informed decision-making for TB control programs, resource allocation, and policy development. This systematic review and meta-analysis therefore aimed to address this gap by providing pooled estimates of MDR-TB prevalence and synthesizing associated risk factors in Cameroon.

Methods

Study design

This review was reported in accordance with the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines. It was registered with the International Prospective Register of Systematic Reviews under the number CRD420261391710 [12].

Eligibility criteria

Inclusion criteria

Studies conducted in Cameroon reporting data on tuberculosis patients with confirmed MDR-TB prevalence were eligible. Participants included individuals of any age or sex diagnosed with tuberculosis, including new and previously treated cases. MDR-TB must have been confirmed using standard diagnostic methods, such as culture and drug susceptibility testing (DST), performed phenotypically or by molecular diagnosis. Eligible study designs were observational studies (cross-sectional and cohort) and randomized controlled trials. Studies published in English or French were considered. There was no restriction on study timeframe

Exclusion criteria

Studies without primary data (reviews, editorials, commentaries), duplicate publications, case-control studies, unpublished grey literature and studies lacking sufficient data (abstract only) to calculate prevalence or assess methodological quality were excluded. Multi-country studies without extractable Cameroon-specific data were disregarded.

Search strategy

Databases

A comprehensive literature search was conducted in PubMed, Embase, Scopus, Web of Science, and African Journals Online (AJOL). Additional studies will be identified through Google Scholar searches and screening the reference lists of included studies.

Search terms

The search strategy combined Medical Subject Headings (MeSH) and free-text terms using Boolean operators: ("multidrug-resistant tuberculosis" OR "MDR-TB" OR "drug-resistant tuberculosis" OR "rifampicin-resistant tuberculosis") AND ("prevalence" OR "epidemiology" OR "risk factors" OR "associated factors" OR "determinants") AND ("Cameroon" OR "Cameroun"). Study selection was performed independently by two reviewers (FZLC and RT) (Table S1). In cases of disagreement, consensus was reached through discussion or by consulting a third reviewer (MNT). The last search was conducted on April 15, 2026.

Data extraction

Data were extracted by two independent reviewers (FZLC and CA) using a standardized extraction form developed in Microsoft Excel. Cases of disagreement were resolved through discussion or by contacting a third reviewer (MNT). For each included study, the following data were extracted: first author surname, publication year, year of study completion, design, region of study, sample size, number of MDR-TB cases, number of monoresistance cases, diagnostic methods, participant characteristics, and reported risk factors with corresponding effect estimates (number of cases among confirmed and control groups for each risk factor). To prevent double-counting of patient samples originating from the same regional reference centers, we performed a thorough de-duplication process by screening for duplicate author groups, overlapping study periods, and identical sampling locations. In case of duplication, the most recent study report was retained for inclusion. In this present systematic review and meta-analysis, multiregion referred to studies conducted in more than one Cameroonian region.

Outcomes measurement

The prevalence was calculated by multiplying the number of positive events (antimicrobial resistance cases) by 100 and dividing by the total number of TB patients screened for drug susceptibility testing using either phenotypic or molecular diagnosis. MDR-TB was defined as a form of TB that shows resistance to at least isoniazid and rifampin [13]. Mono-resistance was resistance to one specific anti-TB drug only. Any antituberculosis drug resistance was defined as any resistance to at least one antituberculosis drug. Any resistance to rifampicin referred to as rifampicin-monoresistance (using phenotypic proportion method on Löwenstein-Jensen medium), and/or MDR-TB patients [14–16].

Risk of bias assessment

Two independent reviewers (FZLC and CA) assessed study quality and risk of bias using the Joanna Briggs Institute (JBI) critical appraisal tools tailored to each study design. Disagreements were resolved through discussion or by consulting a third reviewer (MNT). For the cross-sectional study, the criteria included: a clear definition of inclusion criteria, comprehensive descriptions of study subjects and settings, validity and reliability of exposure measurements, use of objective, standardized criteria for outcome assessment, identification of potential confounding factors, implementation of appropriate strategies to address them, and the appropriateness of statistical methods. Each criterion was scored as 1 (yes) or 0 (no or unclear). In this study, we defined and applied the following categorization of the overall risk of bias: low = 7–9, moderate = 4–6, or high = 0–3.

Statistical analysis

The pooled prevalence estimates were calculated for each study with 95% confidence intervals. A random-effects meta-analysis method was performed to account for potential heterogeneity, as assessed by the I^2 statistic. Subgroup analyses and meta-regression were conducted based on study timeframe (year of study completion), type of study participants, method, geographic region, localization of TB disease, and drug susceptibility. The generalized linear mixed models (GLMM), coupled with the logit transformation (PLOGIT), were utilized for their effectiveness in handling meta-analyses of binary data [17]. Statistical significance was set at a p-value of < 0.05. All analyses were conducted using the 'meta' package in R Statistics version 4.5.3 [18]. Correlates to anti-tuberculosis drug resistance were also computed to generate pooled ORs and their corresponding 95% CIs.

Publication bias and sensitivity analysis

Publication bias was assessed graphically using funnel plots and statistically using Egger's and Begg's tests [19, 20]. A p-value below 0.05 was considered evidence of significant publication bias. In such cases, the trim-and-fill technique was employed to correct the pooled estimate. Furthermore, a leave-one-out sensitivity analysis was performed to determine the influence of individual studies on the overall findings.

Results

Studies selection

A systematic search of electronic databases identified 349 records from PubMed ($n = 16$), Scopus ($n = 43$), Web of Science ($n = 120$), Embase ($n = 43$), Cochrane Library ($n = 11$), and African Journals Online ($n = 116$). After removing 37 duplicate records, 312 unique records were screened based on titles and abstracts. Of these, 274 records were excluded as they did not meet the inclusion criteria.

The full texts of the remaining 38 reports were retrieved and assessed for eligibility. Following full-text review, 16 reports were excluded with reasons. Additionally, 160 records were identified through Google Scholar, and 1,777 records were identified through reference list searching of included studies and five additional studies were identified and included from these sources. Ultimately, 27 studies met the eligibility criteria and were included in the systematic review and meta-analysis (Fig.S1).

Studies characteristics

A total of 27 studies, conducted between 1995 and 2022 and published between 1997 and 2025, were included. Most studies were cross-sectional ($n=22$; 81.5%), followed by cohort ($n=5$; 18.5). The majority of studies were conducted in the Centre ($n=9$; 33.3%) and Littoral ($n=9$; 33.3%) regions, while 4 studies (14.8%) were conducted in the West, South-West, and North-West regions. Twenty studies (74.1%) were conducted in a single region, while 7 studies (25.9%) covered multiple regions. Twenty-three studies (85.2%) included participants from the general population, while 3 studies (11.1%) included retreated TB patients. Twenty-three studies (85.2%) were conducted among patients with pulmonary tuberculosis; 3 studies (11.1%) included a mix of pulmonary and extrapulmonary tuberculosis patients, and one study (3.7%) focused exclusively on extrapulmonary tuberculosis. Nearly half of the studies (44.4%) used the phenotypic proportion method on Löwenstein-Jensen medium, while molecular diagnosis was used for drug susceptibility testing in 8 reports (29.6%); 1 study (3.7%) did not specify the method used. Almost all included studies ($n=26$; 96.3%) had low risk of bias at methodology quality assessment (Table 1).

Prevalence of multidrug-resistant tuberculosis

The pooled prevalence of MDR-TB was 4.9% (95% CI: 2.5–9.4; 20 studies; $n=6,914$), with high heterogeneity among included studies ($I^2=97.2\%$; $p<0.001$), reflecting wide variation in MDR-TB prevalence estimates over time, ranging from as low as 0.6% in some studies to as high as 50.0% in others (Fig. 2). Given the high heterogeneity observed, this pooled estimate should be interpreted with caution.

Subgroup analysis revealed that study timeframe ($p<0.001$), region ($p=0.002$), participant type ($p<0.001$), and drug susceptibility testing methods ($p<0.001$) were significant sources of heterogeneity. The evolution of pooled MDR prevalence in Cameroon was inconsistent. The highest pooled prevalence was observed in the most recent (2020+) studies (38.8%; 95% CI: 33.7–44.2; 2 studies; $n=330$), while the lowest was observed during 2015–2019 (2.7%; 95% CI: 0.4–15.2; 4 studies; $n=2,244$). This difference should be interpreted with caution, as the high prevalence estimates observed in the most recent studies are likely attributable to the small sample sizes and the inclusion of high-risk populations (people living with HIV) among these two studies. Studies conducted in multiple regions revealed a higher pooled prevalence (13.6%; 95% CI: 4.1–36.8; 4 studies; $n=743$) compared to the Adamawa region (1.6%; 95% CI: 0.9–2.7; 2 studies; $n=882$), where the lowest pooled prevalence was observed. Patients enrolled for tuberculosis retreatment showed a higher pooled prevalence (18.3%; 95% CI: 9.9–31.3; 2 studies; $n=314$) compared to patients from the general population (3.7%; 95% CI: 1.8–7.6) (Table 2 and Figs. S2-S7).

The sensitivity analysis showed that our main findings were robust; however, the funnel plot revealed asymmetry, indicating potential publication bias, as reflected by a significant Egger's test ($p=0.040$). The resulting adjusted pooled prevalence from the trim-and-fill analysis raised the pooled estimate to 12.9% (95% CI: 6.2–24.9; 7 imputed studies) (Figs. S8-S10).

The pooled prevalence of MDR-TB among previously treated patients awas significantly higher (11.2%; 95% CI: 5.6–21.2; 10 studies; $n=1,469$) than the prevalence among new patients (2.0%; 95% CI: 1.1–3.5; 11 studies; $n=3,345$) (Figs. 3 and 4). Both pooled estimates were robust in sensitivity analyses and showed no evidence of publication bias (Figs S11-S14).

Table 1 Characteristics of included studies

Author	Study period	Publication	Design	Region	Participant	Type of TB cases	Diagnostic method	Risk of bias	Sample size (*n*)	Number of resistant cases (*n*)								
	(year)[1]	(year)								Any resistance	Any RIF	Mono-resistance					Multidrug resistance		
												RIF	INH	EMB	STM	FLQ	Total	NP	PTP
Bercion, 1995 [16]	1995	1997	CS	CE	PGP	PTB	PLJ	Low	516	164	4	2	11	1	78	NR	3	3/516	NR
Kuaban, 1997 [21]	1997	2000	CS	CE	Retreated TB patient	PTB	PLJ	Low	98	57	27	0	19	1	3	NR	27	NR	27/566
Kuaban, 1998 [22]	1998	2000	CS	WE	PGP	PTB	PLJ	Low	566	152	28	4	47	5	36	NR	23	6/437	17/129
Noeske, 1998 [23]	1998	2002	Cohort	WE	PGP	PTB	PLJ	Low	560	150	28	NR	NR	NR	NR	NR	23	6/436	17/124
Mbacham, 2006 [24]	2006	2011	CS	WE and CE	PGP	PTB	Dot-blot hybridization	Low	112	91	60	3	9	2	12	NR	56	NR	NR
Ane-Anyangwe, 2007 [25]	2007	2016	CS	SW	PGP	PTB	Dot-blot hybridization	Low	59	35	17	NR	NR	NR	32	NR	NR	NR	NR
Assam-Assam, 2009 [11]	2009	2011	CS	CE and WE	PGP	PTB	PLJ	Low	149	16	3	1	4	0	4	NR	5	2/130	3/19
Koro, 2009 [26]	2009	2016	CS	AD	PGP	PTB	PLJ	Low	437	38	5	2	13	0	12	NR	6	6/437	NR
Noeske, 2009 [27]	2009	2012	Cohort	LT	Retreated TB patient	PTB	PLJ	Low	216	51	26	0	NR	NR	NR	NR	26	NR	26/216
Jubulis, 2010 [28]	2010	2015	CS	NW	PGP	PTB	MYCOTB phenotypic assay	Low	65	26	5	0	2	0	5	0	5	NR	NR
Kuaban, 2010 [29]	2010	2014	CS	AD	PGP	PTB	PLJ	Low	445	35	11	3	12	1	10	NR	8	6/426	2/19

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Table 1 (continued)

Author	Study period	Publication	Design	Region	Participant	Type of TB cases	Diagnostic method	Risk of bias	Sample size (*n*)	Number of resistant cases (*n*)									
	(year)[1]	(year)								Any resistance	Any RIF	Mono-resistance					Multidrug resistance		
												RIF	INH	EMB	STM	FLQ	Total	NP	PTP
Sidze, 2011 [30]	2011	2014	CS	CE	PGP	PTB	PLJ	Low	576	63	6	1	27	0	19	1	6	4/517	2/59
Meriki, 2012 [31]	2012	2013	CS	NW and SW	PGP	PTB	PLJ	Low	256	71	20	NR	10	3	25	NR	15	NR	NR
Pefure-Yone, 2012 [32]	2012	2014	Cohort	CE	PGP	PTB	PLJ	Low	46	7	2	0	5	NR	NR	NR	2	2/46	NR
Sidze, 2012 [33]	2013	2012	CS	CE	PGP	PTB	Spoligotyping	Low	298	28	NR	NR	NR	NR	NR	NR	3	NR	NR
Kuaban, 2015 [34]	2015	2020	Cohort	NW, SW, WE, and LT	Retreated TB patient	PTB	Xpert MTB/RIF	Low	753	47	0	0	47	NR	NR	NR	NR	NR	NR
Abanda, 2016 [35]	2016	2017	CS	CE, LT, and NW	PGP	PTB	MTBDRplus assay	Low	226	74	49	0	6	0	14	NR	49	7/79	42/169
Mbuh, 2017_1 [36]	2017	2021	CS	LT	PGP	PTB and EPTB	Xpert MTB/RIF	Low	1665	86	86	11	NR	NR	NR	NR	75	19/435	67/1230
Mbuh, 2017_2 [37]	2017	2019	CS	LT	PGP	EPTB	Xpert MTB/RIF	Moderate	45	0	0	0	NR	NR	NR	NR	0	0/30	0/45
Noeske, 2017 [38]	2017	2018	CS	Multi-region	PGP	PTB	Xpert MTB/RIF	Low	1029	16	16	NR	NR	NR	NR	NR	NR	NR	NR
Pokam, 2017 [39]	2017	2020	CS	LT	PGP	PTB	Xpert MTB/RIF	Low	147	13	13	NR	NR	NR	NR	NR	NR	NR	NR
Motse, 2019 [40]	2019	2020	CS	LT	PGP	PTB and EPTB	Xpert MTB/RIF	Low	119	8	8	NR	NR	NR	NR	NR	NR	NR	NR

Table 1 (continued)

Author	Study period	Publication	Design	Region	Participant	Type of TB cases	Diagnostic method	Risk of bias	Sample size (*n*)	Number of resistant cases (*n*)									
	(year)[1]	(year)								Any resistance	Any RIF	Mono-resistance					Multidrug resistance		
												RIF	INH	EMB	STM	FLQ	Total	NP	PTP
Tiani, 2019 [41]	2019	2022	CS	CE	PGP	PTB	Spoligotyping and Line Probe Assay	Low	308	25	2	0	2	7	12	NR	2	NR	NR
Djuikoue, 2020 [10]	2020	2022	CS	LT	PGP	PTB	NR	Low	304	122	NR	NR	NR	NR	NR	NR	122	NR	NR
Foncha, 2020 [42]	2020	2021	Cohort	LT	PGP	PTB and EPTB	GeneXpert	Low	272	6	6	NR	NR	NR	NR	NR	NR	NR	NR
Djoufack, 2022 [43]	2022	2025	CS	CE	PLHIV	PTB	TB-LAMP	Low	26	13	13	7	7	NR	NR	0	6	NR	NR
Pokam, 2022 [44]	2022	2025	CS	SW	PGP	PTB	GeneXpert MTB/RIF Ultra	Low	37	3	3	NR	NR	NR	NR	NR	NR	NR	NR

1: Year of study completion; TB: Mycobacterium tuberculosis; NP: New patient; PTP: Previously treated patient; RIF: Rifampicin; INH: Isoniazid; EMB: Ethambutol; STM: Streptomycin; FLQ: Fluoroquinolones; CS: Cross-sectional; CE: Centre; LT: Littoral; NW: North-West; AD: Adamawa; SW: South-West; WE: West; PGP: Patient form general population; PTB: Pulmonary tuberculosis; EPTB: Extra-pulmonary tuberculosis; PLJ: Phenotypic proportion method on Löwenstein-Jensen medium; NR: Non reported

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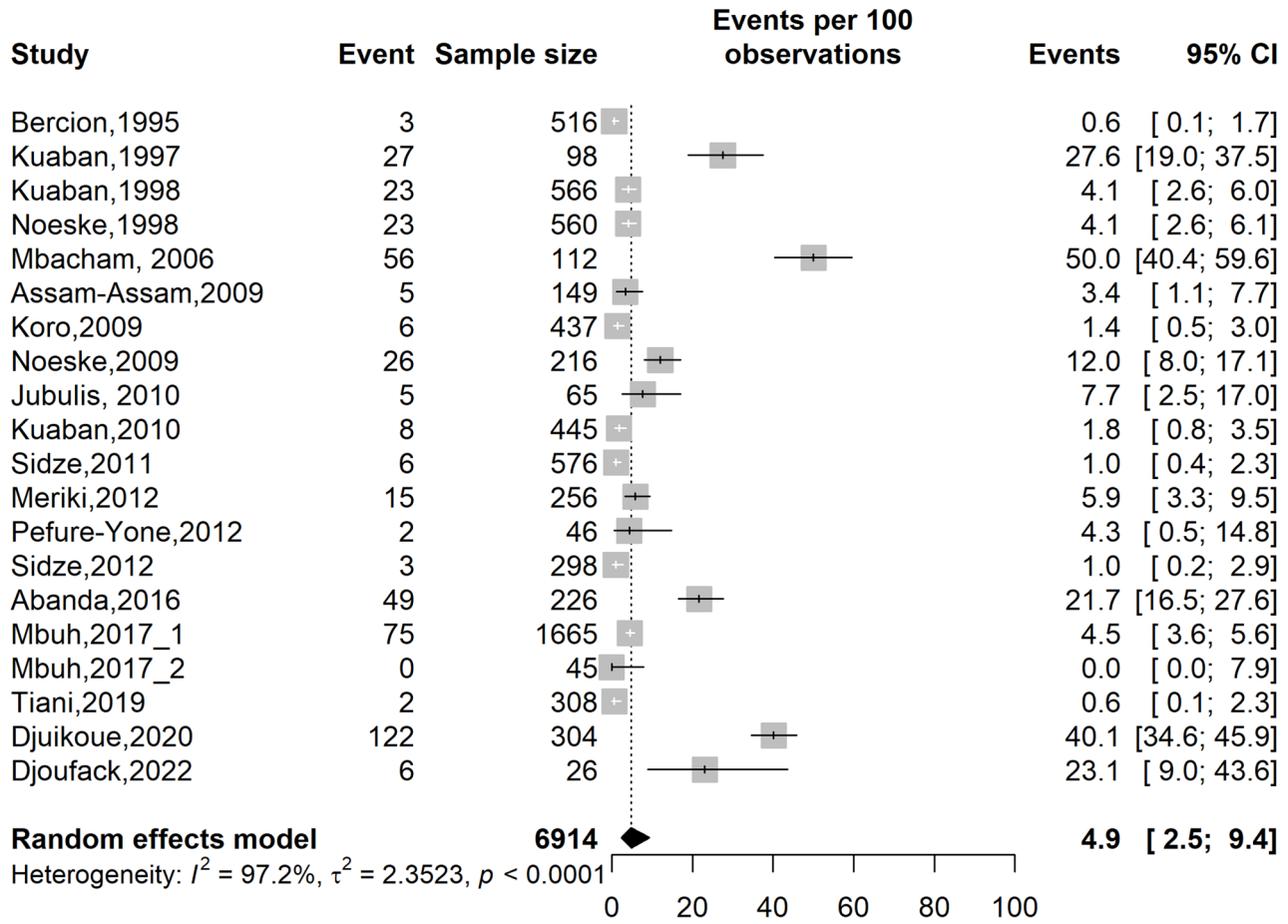

Fig. 2 Pooled prevalence of multidrug-resistant *Mycobacterium tuberculosis* among tuberculosis patients in Cameroon, 1995–2022

Prevalence of any resistance to anti-tuberculosis drugs

The pooled prevalence of any resistance to anti-tuberculosis drugs was 16.0% (95% CI: 10.1–24.3; 27 studies; $n=9,330$), with high heterogeneity across included reports ($I^2=97.5\%$; $p<0.001$). The forest plot reveals wide variation in any anti-TB drug resistance prevalence across Cameroon from 1995 to 2022, ranging from 0.0% to 81.2% (Fig. 5). The substantial heterogeneity observed warrants a cautious interpretation of this pooled estimate.

The subgroup analysis indicated that study timeframe, region, participant type, tuberculosis disease localization, and drug susceptibility testing methods were significant sources of heterogeneity ($p<0.001$). There was an overall decline in prevalence across study periods, reaching its lowest level during 2015–2019 before increasing in studies conducted from 2020 onwards. The highest pooled prevalence was recorded before 2005 (34.6%; 95% CI: 24.0-46.9; 4 studies; $n=1,740$), and the lowest in 2015–2019 (6.1%; 95% CI: 3.0–12.0; 8 studies; $n=4,292$). Significant disparities were observed in any resistance prevalence across Cameroonian regions, the lowest being observed in the Littoral region (7.7%; 95% CI: 2.9–18.6; 7 studies; $n=2,768$) and the highest in the South-West region (27.2%; 95% CI: 4.7–73.8; 2 studies; $n=96$). The prevalence of any resistance to anti-TB drugs was significantly higher among patients with pulmonary tuberculosis (20.3%; 95% CI: 13.2–29.8; 23 studies; $n=7,229$) compared to the group of studies among mixed patients with either extrapulmonary or pulmonary tuberculosis (4.0%; 95% CI: 2.3–6.9; 4 studies; $n=2,101$) (Table 3 and Figs. S15-S20).

Table 2 Subgroup meta-analysis of multidrug-resistant *Mycobacterium tuberculosis* among tuberculosis patients in Cameroon, 1995–2022

Subgroup	Sample size	Prevalence[1] (%)	95% CI limits[1]		Number of studies	Heterogeneity statistic[1]		Subgroup difference
			Lower	Upper		I^2(%)	*p*-value	*p*-value
Study period (year)[2]								<0.001
<2005	1,740	4.3	1.1	16.1	4	96.5	<0.001	
2005–2009	914	8.2	1.7	31.2	4	97.7	<0.001	
2010–2014	1,686	2.5	1.2	5.0	6	79.5	0.002	
2015–2019	2,244	2.7	0.4	15.2	4	96.7	<0.001	
2020+	330	38.8	33.7	44.2	2	64.4	0.094	
Study design								0.546
Cross-sectional	6,092	4.7	2.1	10.0	17	97.5	<0.001	
Cohort	822	6.4	3.3	12.0	3	87.2	<0.001	
Region								0.002
Adamawa	882	1.6	0.9	2.7	2	0.0	0.615	
Centre	1,868	2.7	0.7	9.3	7	95.2	<0.001	
Littoral	2,230	7.8	1.6	30.8	4	98.8	<0.001	
North-West	65	7.7	2.5	17.0	1	-	-	
West	1,126	4.1	3.1	5.4	2	0.0	0.971	
Multi-region	743	13.6	4.1	36.8	4	96.9	<0.001	
Participant								<0.001
Patient from general population	6,574	3.7	1.8	7.6	17	97.5	<0.001	
Retreated tuberculosis patient	314	18.3	9.9	31.3	2	90.9	<0.001	
People living with HIV	26	23.1	9.0	43.6	1	-	-	
Tuberculosis disease localization								0.479
Extrapulmonary or mixed	1,710	4.4	3.5	5.5	2	0.0	0.999	
Pulmonary	5,204	5.4	2.6	10.6	18	96.8	<0.001	
Drug susceptibility method used								<0.001
Phenotypic proportion method on LJ	3,865	3.5	1.8	6.7	11	93.2	<0.001	
Molecular diagnosis	2,745	5.6	1.5	18.3	8	97.2	<0.001	
Not reported	304	40.1	34.6	45.9	1	-	-	

1: Random effects model; 2: Time frame aligns with the development of successive National Strategic Plans against tuberculosis in Cameroon; CI: Confidence interval; HIV: Human immunodeficiency virus; LJ: Lowenstein-Jensen medium; Multiregion included studies conducted in more than one Cameroonian region

The sensitivity analysis demonstrated that no single study significantly influenced the pooled estimate, indicating its robustness. Furthermore, visual inspection showed an almost symmetrical funnel plot, with non-significant *p*-values for the Egger's (0.389) and the Begg's (0.492) tests (Figs. S21-S22).

Prevalence of any resistance to rifampicin

The pooled prevalence of any resistance to rifampicin was 4.6% (95% CI: 2.4–8.6; 25 studies; $n=8{,}728$) with high heterogeneity observed across studies ($I^2=95.6\%$; $p < 0.001$) (Fig. 6). The prevalences varied widely from 0.6% to 53.6%. The resulting pooled estimate should be interpreted with caution, given the high heterogeneity observed across the included reports.

The analysis of potential sources of heterogeneity revealed that the region ($p=0.001$) and the type of participants ($p < 0.001$) were significant sources of observed heterogeneity. The highest prevalence was significantly higher in the South-West region of Cameroon (17.4%; 95% CI: 6.7–38.1; 2 studies; $n=96$), and the lowest in the Adamawa region (1.8%; 95% CI: 1.1-3.0; 2 studies; $n=882$). A single study revealed a high prevalence of any rifampicin resistance of 50.0% among HIV-TB coinfected patients. Much lower prevalences were detected among TB patients from the general population (4.2%; 95% CI: 2.4–7.4; 21 studies; $n=7{,}635$) (Table 4 and Figs. S23-28).

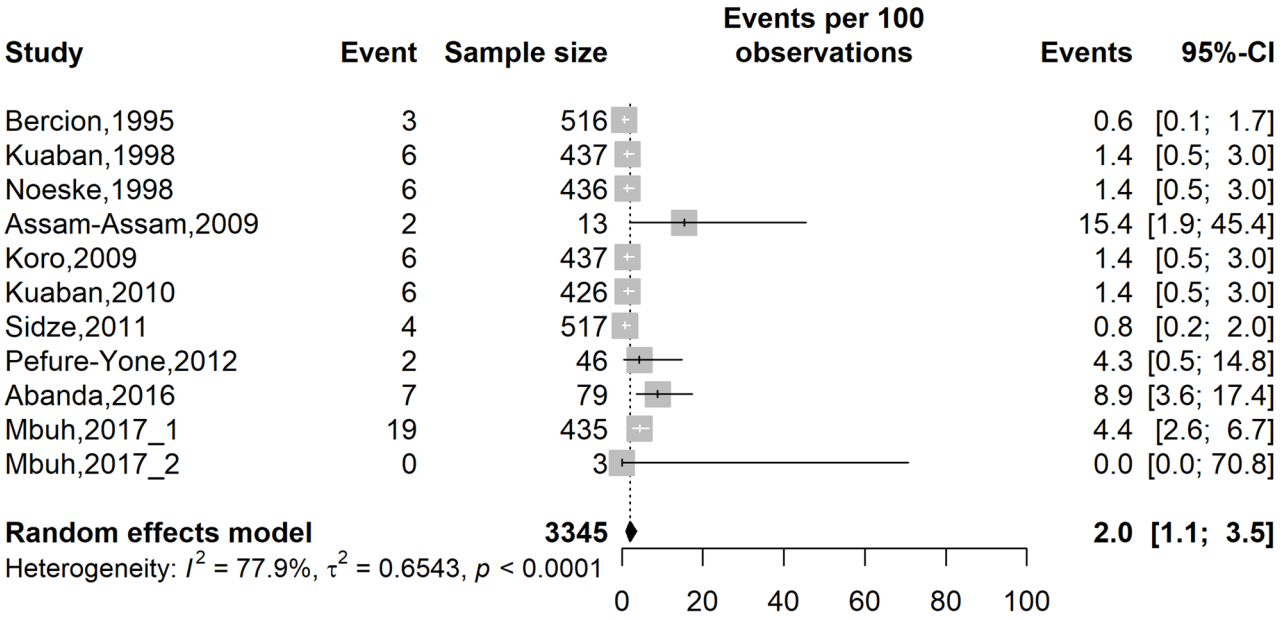

Fig. 3 Pooled prevalence of multidrug-resistant *Mycobacterium tuberculosis* among new patients in Cameroon, 1995–2022

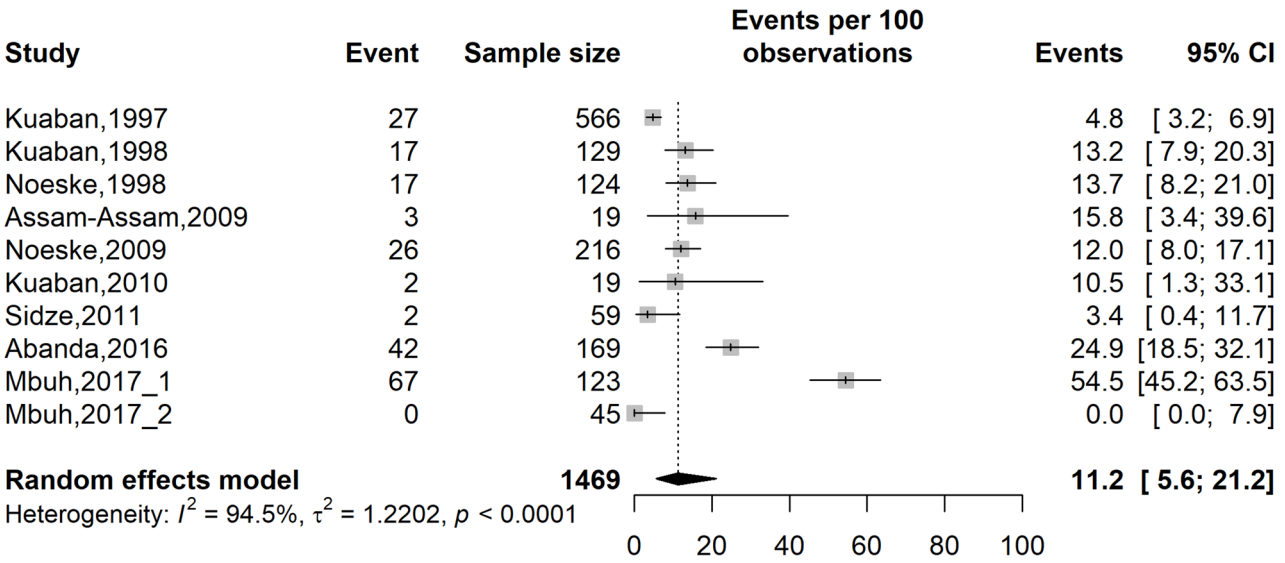

Fig. 4 Pooled prevalence of multidrug-resistant *Mycobacterium tuberculosis* among previously treated patients in Cameroon, 1995–2022

No single study significantly influenced the pooled estimate, suggesting robustness of findings at the sensitivity analysis. In addition, no sign of publication bias was observed on the funnel plot and after performing statistical tests (p-value for Egger's [0.189] and Begg's [0.225] tests) (Figs. S29-S30).

Prevalence of monoresistance to anti-tuberculosis drugs

Higher monoresistance to anti-TB drugs was observed for streptomycin (6.4%; 95% CI: 3.7–10.8; 13 studies, n=3,813) and isoniazid (4.7%; 95% CI: 3.0-7.4; 15 studies; n=4,579). Conversely, much lower monoresistance prevalences were recorded for rifampicin, ethambutol, and fluoroquinolones.

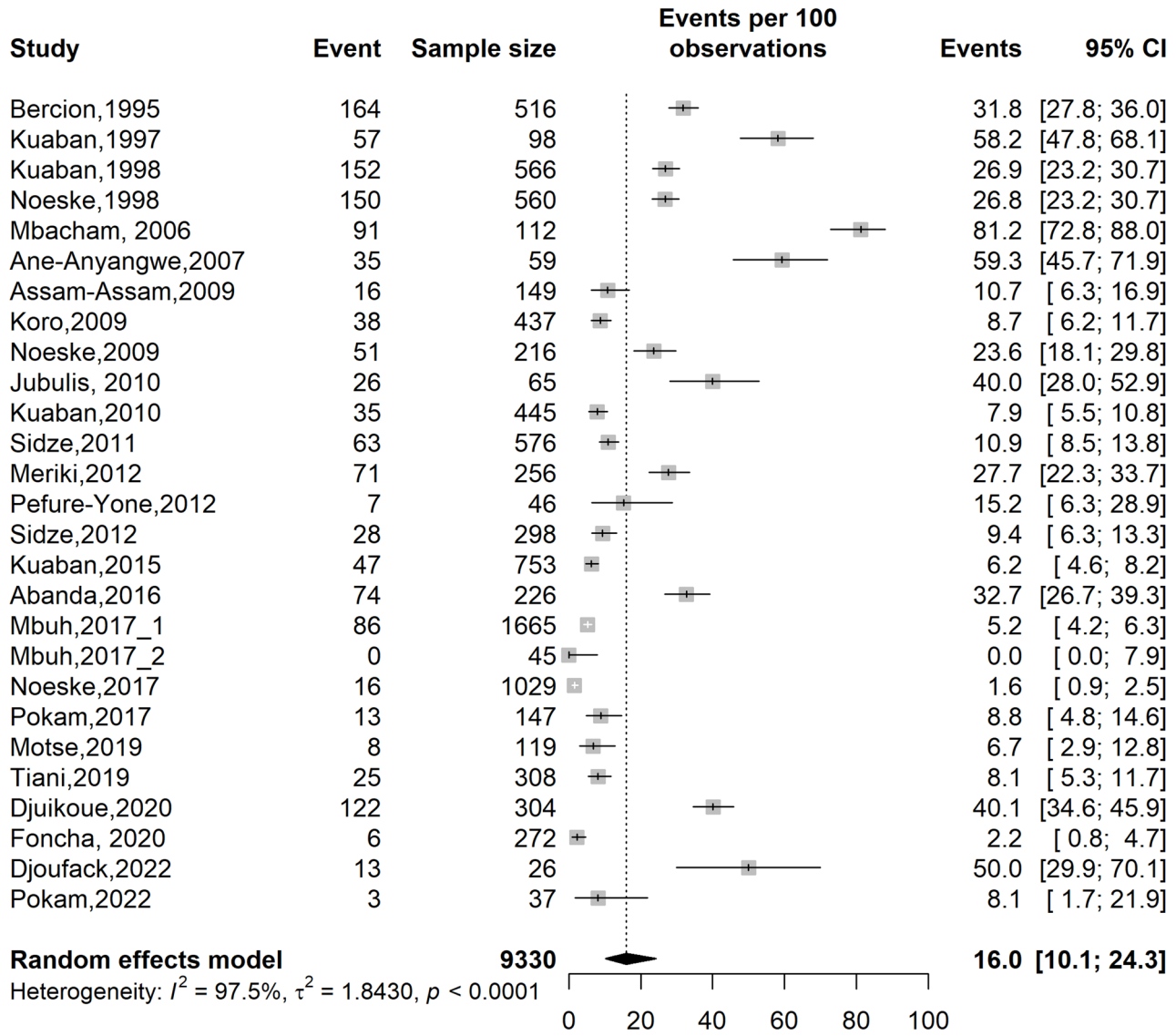

Fig. 5 Pooled prevalence of any resistance to anti-tuberculosis drugs among tuberculosis patients in Cameroon, 1995–2022

Most pooled estimates were robust at sensitivity analysis, with no significant risk of publication bias ($p=0.187$–0.520). However, the pooled prevalence of ethambutol monoresistance revealed a significant risk of publication bias ($p=0.002$ by Egger's test), with an adjusted pooled estimate from the trim-and-fill analysis of 1.4% (95% CI: 0.7–2.6; 6 imputed studies), indicating that the pooled estimate among new TB patients was underestimated (Table 5 and Figs. S31-43).

Determinants of antimicrobial resistance

A synthetic analysis of determinants of the risk of anti-tuberculosis drug resistance identified previous TB disease, alcohol consumption, and a history of incarceration as significant factor associated with the occurrence of antimicrobial resistance. Previous TB disease was associated with a fourfold higher risk of developing resistance to anti-tuberculosis drugs (OR = 3.9; 95% CI: 1.8–8.4; 7 studies). Patients who reported alcohol consumption were 80% more at risk of developing resistance (OR = 1.8; 95% CI: 1.2–2.7; 2 studies), and those with a history

Table 3 Subgroup meta-analysis of the prevalence of any resistance to anti-tuberculosis drugs among tuberculosis patients in Cameroon, 1995–2022

Subgroup	Sample size	Prevalence[1] (%)	95% CI limits[1]		Number of studies	Heterogeneity statistic[1]		Subgroup difference
			Lower	Upper		I^2(%)	*p*-value	*p*-value
Study period (year)[2]								<0.001
<2005	1,740	34.6	24.0	46.9	4	92.3	<0.001	
2005–2009	973	31.7	11.2	62.9	5	98.1	<0.001	
2010–2014	1,686	15.8	9.3	25.5	6	94.4	<0.001	
2015–2019	4,292	6.1	3.0	12.0	8	96.7	<0.001	
2020+	639	15.9	3.8	47.3	4	95.9	<0.001	
Study design								0.365
Cross-sectional	7,483	17.3	10.3	27.7	22	97.7	<0.001	
Cohort	1,847	11.2	4.8	23.9	5	96.8	<0.001	
Region								<0.001
Adamawa	882	8.3	6.6	10.3	2	0.0	0.655	
Centre	1,868	21.4	11.1	37.3	7	96.4	<0.001	
Littoral	2,768	7.7	2.9	18.6	7	97.9	<0.001	
North-West	65	40.0	28.0	52.9	1	-	-	
South-West	96	27.2	4.7	73.8	2	94.5	<0.001	
West	1,126	26.8	24.3	29.5	2	0.0	0.979	
Multi-region	2,525	17.7	5.0	46.8	6	98.7	<0.001	
Participant								0.001
Patient from general population	8,237	14.3	8.6	22.7	23	97.5	<0.001	
Retreated tuberculosis patient	1,067	23.2	6.9	55.4	4	98.0	<0.001	
People living with HIV	26	50.0	29.9	70.1	1	-	-	
Tuberculosis disease localization								<0.001
Extrapulmonary or mixed	2,101	4.0	2.3	6.9	4	40.5	0.169	
Pulmonary	7,229	20.3	13.2	29.8	23	97.2	<0.001	
Drug susceptibility method used								<0.001
Phenotypic proportion method on LJ	3,865	19.9	13.3	28.6	11	95.9	<0.001	
Molecular diagnosis	5,161	12.2	5.4	25.0	16	97.8	<0.001	
Not reported	304	40.1	34.6	45.9	1	-	-	

1: Random effects model; 2: Time frame aligns with the development of successive National Strategic Plans for the fight against tuberculosis in Cameroon; CI: Confidence interval; HIV: Human immunodeficiency virus; LJ: Lowenstein-Jensen medium; Multiregion included studies conducted in more than one Cameroonian region

of incarceration were 70% more likely to present resistance to anti-TB drugs (OR = 1.7; 95% CI: 1.1–2.6; 2 studies) (Table 6 and Figs. S44-S53).

Discussion

This systematic review and meta-analysis provide a comprehensive synthesis of the burden and determinants of MDR-TB and anti-tuberculosis drug resistance in Cameroon. In our analysis, the pooled prevalence of MDR-TB was 5.2%, while the prevalence of any resistance to anti-tuberculosis drugs was 16.0%. Rifampicin resistance was observed in 4.6% of patients with tuberculosis. Furthermore, history of prior active TB disease or treatment, alcohol consumption, and a history of incarceration were identified as significant factors associated with anti-tuberculosis drug resistance. These findings indicate that drug-resistant tuberculosis remains an important public health challenge in Cameroon despite ongoing efforts to strengthen tuberculosis prevention, diagnosis, and treatment services.

The pooled MDR-TB rate found in our review is higher than the global average for new tuberculosis cases, showing that drug-resistant TB remains a major global threat in general and Cameroon in particular. The World

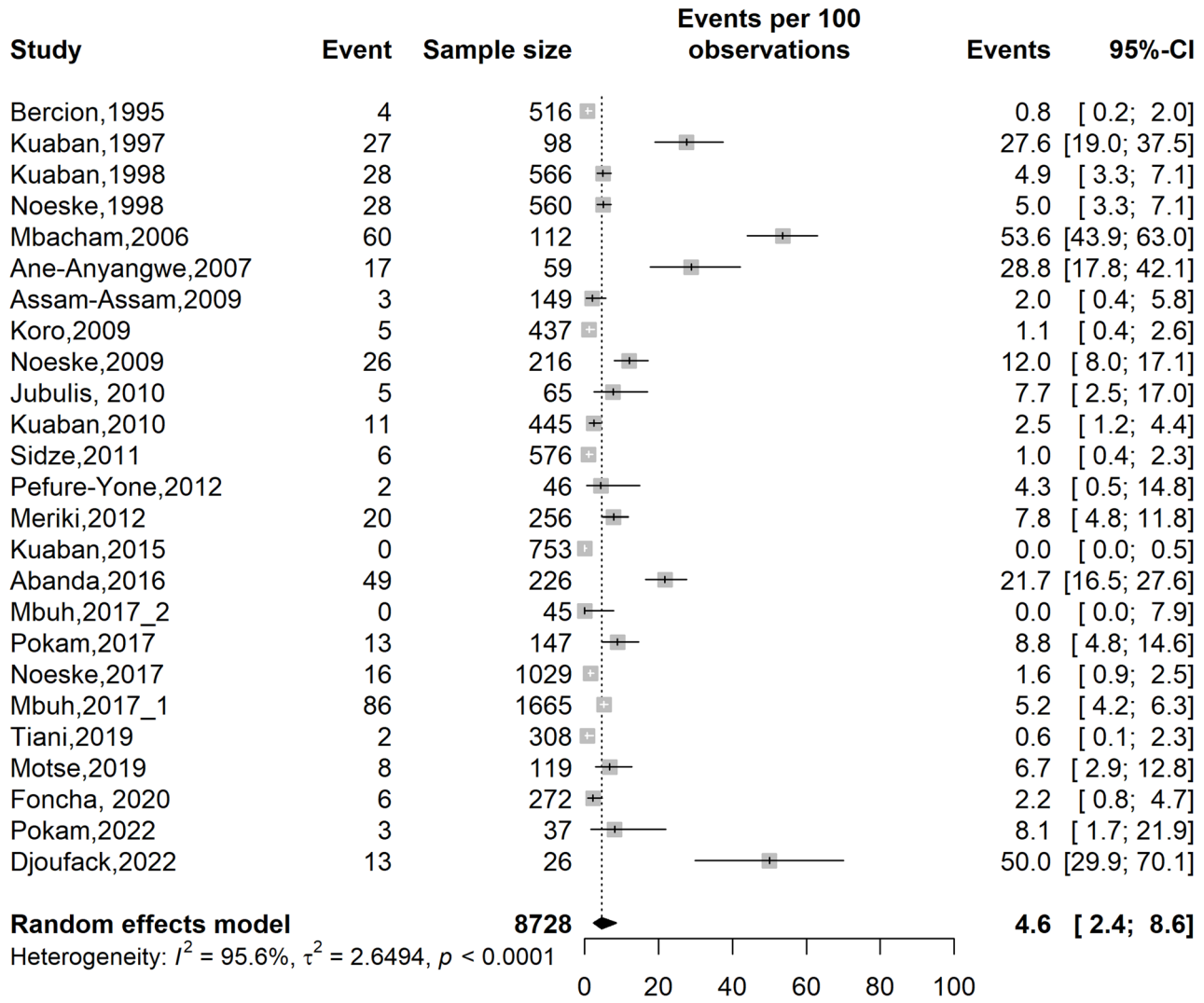

Fig. 6 Pooled prevalence of any-resistance to rifampicin among tuberculosis patients in Cameroon, 1995–2022

Health Organization (WHO) estimates that 10.7 million people developed tuberculosis and 1.23 million died from it in 2024, with about 410,000 cases of MDR/RR-TB worldwide [2, 45]. Similar MDR-TB rates have been reported in other sub-Saharan African countries. For instance, Musa et al. in 2017 reported a pooled prevalence of 2.1% [46]. Cameroon, like many other sub-Saharan African countries, faces ongoing challenges in TB care such as delayed diagnosis, gaps in treatment monitoring, treatment interruptions, high burden of HIV, and limited access to drug resistance testing that may still be driving the spread of resistant tuberculosis strains in Cameroon [47].

One of the major key findings of our review was that MDR-TB among previously treated patients was much more prevalent than MDR-TB among new patients. Our results support earlier evidence that previous anti-tuberculosis treatment is a strong risk factor for drug resistance [48]. Poor treatment adherence, interruptions, incorrect prescriptions, and delays in spotting treatment failure can all lead to more resistant strains [49]. The analysis showed that people with a history of TB disease were almost four times more likely to develop drug resistance. This result is consistent with previous studies carried out in sub-Saharan Africa, where history of prior active TB disease or treatment was highlighted as one of the major risk factors [43].

Table 4 Subgroup meta-analysis of the prevalence of any-resistance to rifampicin among tuberculosis patients in Cameroon, 1995–2022

Subgroup	Sample size	Prevalence[1] (%)	95% CI limits[1]		Number of studies	Heterogeneity statistic[1]		Subgroup difference
			Lower	Upper		I^2(%)	*p*-value	*p*-value
Study period (year)[2]								0.431
<2005	1,740	5.1	1.4	17.0	4	96.2	<0.001	
2005–2009	973	9.8	2.2	34.1	5	97.1	<0.001	
2010–2014	1,388	3.5	1.7	7.1	5	84.1	<0.001	
2015–2019	4,292	2.0	0.5	8.1	8	94.4	<0.001	
2020+	335	10.6	1.8	43.4	3	95.6	<0.001	
Study design								0.280
Cross-sectional	6,881	5.5	2.8	10.6	20	96.3	<0.001	
Cohort	1,847	2.1	0.4	10.4	5	80.3	<0.001	
Region								0.001
Adamawa	882	1.8	1.1	3.0	2	51.9	0.149	
Centre	1,570	4.1	0.8	18.3	6	96.4	<0.001	
Littoral	2,464	5.4	3.1	9.2	6	78.9	<0.001	
North-West	65	7.7	2.5	17.0	1	-	-	
South-West	96	17.4	6.7	38.1	2	80.8	0.023	
West	1,126	5.0	3.8	6.4	2	0.0	0.967	
Multi-region	2,525	3.8	0.5	24.3	6	97.7	<0.001	
Participant								<0.001
Patient from general population	7,635	4.2	2.4	7.4	21	95.6	<0.001	
Retreated tuberculosis patient	1,067	1.9	0.0	63.4	3	81.8	0.004	
People living with HIV	26	50.0	29.9	70.1	1	-	-	
Tuberculosis disease localization								0.642
Extrapulmonary or mixed	2,101	4.0	2.3	6.9	4	40.5	0.169	
Pulmonary	6,627	5.0	2.4	10.1	21	95.9	<0.001	
Drug susceptibility method used								0.574
Phenotypic proportion method on LJ	3,865	3.7	1.9	7.1	11	93.0	<0.001	
Molecular diagnosis	4,863	5.3	1.8	14.3	14	96.5	<0.001	

1: Random effects model; 2: Time frame aligns with the development of successive National Strategic Plans for the fight against tuberculosis in Cameroon; CI: Confidence interval; HIV: Human immunodeficiency virus; LJ: Lowenstein-Jensen medium; Multiregion included studies conducted in more than one Cameroonian region

Table 5 Prevalence of anti-tuberculosis drug monoresistance among tuberculosis patients in Cameroon, 1995–2022

Drug	Sample size	Prevalence[1] (%)	95% CI limits[1]		Number of studies	Heterogeneity statistic[1]		Egger's and Begg's tests	Sensitivity
			Lower	Upper		I^2(%)	*p*-value	*p*-value	
Rifampicin	6,249	0.3	0.1	0.9	17	78.9	< 0.001	0.209 0.187	Robust
Isoniazid	4,579	4.7	3.0	7.4	15	86.0	< 0.001	0.318 0.520	Robust
Ethambutol	3,754	0.3	0.1	0.9	12	0.0	0.540	0.002 0.273	Robust
Streptomycin	3,813	6.4	3.7	10.8	13	94.0	< 0.001	0.174 0.464	Robust
Fluoroquinolones	667	0.1	0.0	1.1	3	0.0	1.000	NA	Robust

1: Random effects model; CI: Confidence interval; NA: Not applicable

Table 6 Factors associated with anti-tuberculosis drug resistance among tuberculosis patients in Cameroon, 1995–2022

Risk factor	Modality	OR [1]	95% Confidence interval		Reports included	Heterogeneity	
			Lower	Upper		I^2 (%)	*p*-value
Gender	Female vs. Male	1.2	0.8	1.7	5	0.0	0.660
Age (years)	< 25 vs. 25+	1.6	0.9	3.0	3	55.0	0.108
Marital status	Single vs. Married	1.1	0.5	2.2	4	80.1	0.002
HIV status	Positive vs. Negative	1.1	0.8	1.4	4	0.0	0.692
History of TB disease	Yes vs. No	3.9	1.8	8.4	7	82.9	< 0.001
Alcohol consumption	Yes vs. No	1.8	1.2	2.7	2	0.0	0.957
Notion of incarceration	Yes vs. No	1.7	1.1	2.6	2	0.0	0.850

[1]*Random effect model; TB: Mycobacterium tuberculosis; HIV: Human immunodeficiency virus*

Nevertheless, resistance to anti-tuberculosis drugs in our study generally dropped over time, from 34.6% before 2005 to 6.1% between 2015 and 2019. This may likely reflect better national TB programs, more directly observed treatment, improved drug availability, and better access to diagnostics [50]. Other African countries observed similar drops after improving surveillance, labs, and treatment adherence [46, 51]. An increase was observed in studies conducted in 2020+, suggesting that drug resistance remains a concern. However, this increase should be interpreted with caution, as the 2020 + subgroup is based on only two small, highly enriched cross-sectional studies conducted in hospital and HIV settings during the COVID-19 pandemic, a period characterized by healthcare disruptions.

Drug resistance rates vary widely across regions in Cameroon. These differences may reflect disparities in healthcare access, laboratory resources, socioeconomic factors, treatment adherence, population movement, and the level of TB control program implementation and management [52]. Urban areas in Cameroon have many specialized TB treatment centers with well-equipped laboratories that offer molecular testing, whereas rural areas rely heavily on sputum AFB microscopy for TB diagnosis, which contributes to poor characterization of resistance genes. These results underscore the need to strengthen local surveillance to identify high-burden areas and guide targeted actions. Better surveillance is especially important in resource-constrained settings, where access to diagnostics and specialized TB services can vary widely.

The pooled rate of rifampicin resistance was 4.6%, indicating that resistant strains remain in the population. This is important because rifampicin resistance is often used as a marker for MDR-TB and is typically detected by rapid molecular tests such as GeneXpert MTB/RIF [53]. RR-TB leads to worse treatment outcomes, longer treatment duration, higher costs, and more deaths than drug-sensitive TB [54]. Therefore, improving access to rapid diagnostics and initiating appropriate treatment promptly are key components of TB control in Cameroon.

Streptomycin and isoniazid had the highest rates of monoresistance among first-line TB drugs. The high rate of isoniazid resistance is concerning because isoniazid is a key component of TB treatment and prevention. Studies show that failing to detect isoniazid resistance can lead to treatment failure, relapse, and more cases of MDR-TB [55, 56]. The higher rate of streptomycin resistance may reflect its past widespread use and the continued presence of resistant strains [57].

This review also found that prior TB disease, alcohol use, and incarceration are important factors linked to drug resistance. Prior TB disease is a strong risk factor for MDR-TB worldwide [48, 58]. Alcohol use can lead to an impaired immune system, which subsequently weakens the overall effect of drugs on the infectious agent and favors the emergence of resistant strains [59, 60]. Other reviews have also found a strong link between alcohol use and poor TB treatment outcomes [61]. Incarceration is another key risk factor, as prisons often have overcrowding, poor ventilation, late diagnosis, and weak infection control [62]. These findings underscore the need to strengthen TB treatment follow-up, integrate alcohol counseling and adherence support for those with regular alcohol consumption, and decongest prisons with routine screening and rapid molecular testing at entry [63].

Limitations

This review has some limitations. There was substantial heterogeneity across several analyses due to differences in study design, study populations, geographic coverage, and diagnostic methods. The predominance of data from the Centre and Littoral regions (>65%), with a notable absence of studies from the northern regions, introduces a selection bias that limits the national generalizability of these findings to Cameroon's diverse epidemiological and ecological contexts. In addition, publication bias was detected in the MDR-TB prevalence analysis. Therefore, the pooled estimates should be interpreted as national weighted average rather than precise measures of disease burden. However, sensitivity analyses showed that the findings were robust and not unduly influenced by any single study.

Conclusions

In summary, this review shows that drug-resistant tuberculosis remains a major challenge to tuberculosis control in Cameroon. The results highlight a high rate of MDR-TB and drug resistance, especially in patients with history of prior active TB disease or treatment. Importantly, national strategies for scaling up drug susceptibility testing must account for existing gaps in regional laboratory infrastructure. To reduce the impact of MDR-TB and stop the spread of resistant strains, it is important to strengthen routine drug susceptibility testing, make rapid molecular diagnostics more widely available, improve treatment adherence, strengthen surveillance systems, and focus on high-risk groups.

Abbreviations

AD	Adamawa region (Cameroon)
AIDS	Acquired Immunodeficiency Syndrome
AJOL	African Journals Online
CE	Centre region (Cameroon)
CI	Confidence interval
CS	Cross-sectional
DST	Drug susceptibility testing
EMB	Ethambutol
EPTB	Extrapulmonary tuberculosis
FLQ	Fluoroquinolones
GLMM	Generalized linear mixed models
HIV	Human Immunodeficiency Virus
INH	Isoniazid
JBI	Joanna Briggs Institute
LJ	Löwenstein-Jensen medium
LT	Littoral region (Cameroon)
MDR-TB	Multidrug-resistant tuberculosis
NR	Not reported
NW	North-West region (Cameroon)
OR	Odds Ratio
PGP	Patient from general population
PLHIV	People living with HIV
PLJ	Phenotypic proportion method on Löwenstein-Jensen medium
PLOGIT	Probit-Logit transformation

PRISMA	Preferred Reporting Items for Systematic Reviews and Meta-Analyses
PTB	Pulmonary tuberculosis
RIF	Rifampicin
STM	Streptomycin
SW	South-West region (Cameroon)
TB	Tuberculosis
WE	West region (Cameroon)
WHO	World Health Organization

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Data availability All data generated in this study are available in the main manuscript and its supplementary material.

Declarations

Ethical approval and consent to participate Not applicable.

Consent for publication Not applicable.

Competing interests The authors declare no competing interests.

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