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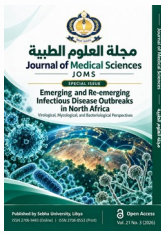

Drug-Resistant Tuberculosis Along the Trans-Saharan Corridor: A Systematic Review and Meta-Analysis of Resistance, Mutation and Lineage Data from Libya and Seven North African and Sahelian Countries, 1991–2025

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A B S T R A C T

Libya receives large numbers of people travelling north from Sudan, Chad, Niger and the Sahel, yet the drug-resistance profile of the tuberculosis (TB) moving along this route has never been assembled. Following PRISMA 2020, we reviewed human TB studies published between 1991 and 2025 from Libya and seven North African and Sahelian countries and pooled the proportion of multidrug-resistant (MDR) isolates with a random-effects model. Of 107 included studies, 64 reported drug-resistance data, 35 resistance mutations and 19 strain typing. Libya contributed ten studies, nine on migrant patients, but none characterised a Libyan isolate at the molecular level. Across 12 unselected series (2623 isolates), pooled MDR was 6.0% (95% CI 3.6–9.9), from 1.9% in Libya to 11.4% in Sudan. The rpoB S531L (S450L) substitution accounted for 66.8% of characterised rifampicin-resistance mutations, and 20.5% of MDR or rifampicin-resistant isolates were also resistant to fluoroquinolones. Clonal MDR transmission was documented in Tunisia, eastern Sudan and Chad. The countries that supply most of Libya's migrant TB patients carry the region's highest MDR burden, while Libya has no genotypic surveillance. Drug-susceptibility testing of previously treated and migrant patients, fluoroquinolone testing of every rifampicin-resistant case and a first genomic survey of isolates from southern Libya are now the priorities.

السل المقاوم للأدوية على امتداد الممر العابر للصحراء الكبرى: مراجعة منهجية وتحليل تجميعي لبيانات المقاومة والطفرات والسلالات من ليبيا وسبع دول في شمال إفريقيا والساحل، 1991–2025

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الكلمات المفتاحية:
السل
المقاومة للأدوية المتعددة
الجين rpoB
الهجرة
الوبائيات الجزيئية
ليبيا
التحليل التجميعي

الملخص

تستقبل ليبيا أعداداً كبيرة من القادمين شمالاً من السودان وتشاد والنيجر والساحل الإفريقي، غير أن صورة مقاومة الأدوية لدى السل المنتقل عبر هذا الممر لم تُجمع من قبل. أجرينا، وفق إرشادات PRISMA 2020، مراجعة منهجية لدراسات السل البشري المنشورة بين عامي 1991 و2025 من ليبيا وسبع دول في شمال إفريقيا والساحل، وجمعنا نسبة العزلات المقاومة للأدوية المتعددة (MDR) بنموذج التأثيرات العشوائية. من بين 183 تقريراً كاملاً أُدرجت 107 دراسات؛ قدّمت 64 منها بيانات عن مقاومة الأدوية، و35 عن طفرات المقاومة، و19 عن تنميط السلالات. أسهمت ليبيا بعشر دراسات تناولت تسع منها المرضى المهاجرين، لكن لم تُوصِّف أيٌّ منها عزلة ليبية على المستوى الجزيئي. وبلغت النسبة المجمّعة للعزلات المقاومة للأدوية المتعددة في 12 سلسلة 6.0% (فترة الثقة 95%: 3.6–9.9، I^2 = 88%)، وتراوحت بين 1.9% في ليبيا و11.4% في السودان. وشكّل الاستبدال S531L (S450L) في الجين rpoB نسبة 66.8% من طفرات مقاومة الريفاميسين الموصَّفة، وكانت 20.5% من العزلات المقاومة للأدوية المتعددة أو للريفاميسين مقاومة أيضاً للفلوروكينولونات. ووُثّق الانتقال النسيلي للسل المقاوم للأدوية المتعددة في تونس وشرق السودان وتشاد. وعليه فإن الدول التي يأتي منها معظم مرضى السل المهاجرين إلى ليبيا تحمل أعلى عبء للسل المقاوم في المنطقة، في حين تفتقر ليبيا إلى أي ترصد جيني. والأولوية الآن هي إجراء اختبار الحساسية الدوائية لكل مريض سبق علاجه ولكل مريض مهاجر، واختبار الحساسية للفلوروكينولونات لكل حالة مقاومة للريفاميسين، وإجراء أول مسح جينومي لعزلات جنوب ليبيا.

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1. Introduction

Tuberculosis remains the leading cause of death from a single infectious agent. In 2024 an estimated 10.7 million people fell ill with TB and 1.23 million died, and the global decline in incidence since 2015 stands at only 12.3%, far short of the End TB milestones [1]. Across North Africa and the Sahel, programme capacity ranges from national reference laboratories with molecular and genomic expertise, as in Morocco and Tunisia [2,3], to services in which diagnosis still rests largely on smear microscopy, as in parts of Chad and Mauritania [4,5].

Libya sits at the centre of this map. It shares land borders with Egypt, Sudan, Chad, Niger, Algeria and Tunisia, and since 2011 it has served both as a destination for labour migrants and as a transit point for people trying to reach Europe. The country hosts more than half a million migrants, many from TB-endemic countries and many living in crowded and unsanitary conditions [6]. A recent regional meta-analysis confirmed that migrants in the Middle East and North Africa carry a higher TB burden and poorer treatment outcomes than host populations [7]. Libyan surveillance has long shown the same pattern locally: immigrants made up a large share of pulmonary cases in the north-west and fared worse on treatment than Libyan nationals [8], and a national spatiotemporal analysis of 26,478 notified cases from 2015 to 2024 found an annual notification rate of 40.3 per 100,000 with marked regional clustering [9]. In Sebha, the main referral centre of the south, monthly notifications fell by 57.5% at the onset of the COVID-19 pandemic and treatment non-completion exceeded 50% in 2022–2023 [10].

What remains unknown is the drug-resistance profile of the TB that travels along this corridor. Drug resistance in Libya has been described mainly in single-hospital series from Tripoli and Benghazi [11,12], and a 2026 national meta-analysis of antimicrobial resistance pooled TB data together with Gram-negative pathogens rather than examining TB in its regional setting [13]. The Sudanese evidence has been synthesised separately and points to a high MDR burden [14], while molecular studies in Tunisia, Algeria and Morocco describe resistance mutations and clonal outbreaks that have never been read alongside the data from Libya's southern neighbours. This fragmentation matters for a practical reason. The rapid molecular assays now used to detect rifampicin resistance interrogate a short region of *rpoB*, and their performance depends on which mutations circulate locally [15,16]. A country without its own genotypic data can borrow that information only if the neighbouring evidence is assembled and found to be consistent.

Recent commentary from southern Libya has argued that many infections described as emerging in North Africa are better understood as newly detected, because surveillance and laboratory capacity lag behind transmission [17], and a parallel review concluded that malaria in Libya is sustained by importation from Niger, Chad and Sudan rather than by local transmission [18]. Tuberculosis has not been examined through this lens. We therefore conducted a systematic review of TB studies from Libya and seven connected countries published over 35 years, with three aims: to map where and how the evidence has been generated, to estimate the proportion of MDR TB and the frequency of the principal resistance mutations, and to describe the lineages and transmission networks that link these countries to Libya.

2. Methods

2.1. Search strategy and eligibility criteria

This systematic review followed the PRISMA 2020 statement [19]. The review covered eight countries chosen because they border Libya or share its principal migration routes and cross-border networks: Libya, Egypt, Sudan, Chad, Tunisia, Algeria, Morocco and Mauritania. South Sudan was not included because it became a separate state in 2011 and its data are not reported within Sudanese national series after that year.

We searched PubMed/MEDLINE, Embase, Scopus, Web of Science and the Cochrane Library for reports published from 1 January 1991 to 2025. Because much of the regional literature appears in journals that these databases do not index, the electronic search was supplemented by Google Scholar, by hand-searching of regional medical journals, including Libyan university journals, and by screening the reference lists of included studies. The search combined three blocks with Boolean operators: disease terms (“tuberculosis”, “*Mycobacterium tuberculosis*”, “MDR-TB”, “XDR-TB”, “rifampicin resistance”), molecular terms (“genotyping”, “spoligotyping”, “MIRU-VNTR”, “whole-genome sequencing”, “mutation”) and geographical terms (each country name, “North Africa”, “Maghreb”, “Sahel”), with truncation where appropriate. Reports in English or French were eligible.

Studies were included if they reported primary data, or a systematic synthesis, on human TB in at least one of the eight countries and described epidemiological, clinical, microbiological, drug-resistance, molecular, diagnostic or programme outcomes. We excluded studies limited to animals or food products, single-case reports, studies of latent infection alone, archaeological material, laboratory or *in vitro* work without patient data, studies of host genetic polymorphisms, purely mathematical or forecasting models, narrative reviews, conference abstracts, studies of non-tuberculous mycobacteria and reports published before 1991. Because every included study had to be cited in a form that readers could retrieve, reports whose bibliographic record could not be traced in Crossref,

OpenAlex or the publishing journal were also excluded.

2.2. Study selection and data extraction

Two reviewers screened titles and abstracts independently, assessed full texts, and resolved disagreements by discussion, with a third reviewer available when consensus was not reached. Data were extracted into a piloted Microsoft Excel form that recorded the study title, authors, year, country, design, population, sample size, genes analysed, mutations identified, drug-resistance profile, any discussion of migration or population movement, and the phenotypic or molecular methods used. The form was tested on ten studies before full extraction. Each included study was then coded for five evidence domains: drug-resistance data of any kind, resistance-mutation data, strain typing or lineage assignment, whole-genome sequencing, and explicit treatment of migration or cross-border movement. Every bibliographic record was checked against Crossref or OpenAlex before citation.

2.3. Risk of bias and statistical analysis

Risk of bias in the drug-resistance studies used for pooling was appraised with items adapted from the Joanna Briggs Institute checklist for prevalence studies [20]: whether patients were enrolled consecutively or without selection on resistance, whether a phenotypic reference method was used for drug-susceptibility testing, whether at least 100 isolates were tested, and whether results were reported separately for new and previously treated patients. Studies that enrolled only patients referred for suspected drug resistance, only retreatment patients or only known MDR cases were not pooled with unselected series, because their proportions answer a different question.

The primary quantitative outcome was the proportion of tested isolates that were MDR, defined as resistant to at least isoniazid and rifampicin. Proportions were logit-transformed, with 0.5 added to cells containing zero, and pooled with the DerSimonian–Laird random-effects model; 95% confidence intervals for single studies used the Wilson method. Heterogeneity was quantified with Cochran's Q and the I^2 statistic. Pre-specified subgroups were country and region (Libya, Tunisia and Algeria versus Sudan and Chad), and a sensitivity analysis removed the series with the highest proportion. The same model was used to pool the share of characterised rifampicin-resistance mutations located at *rpoB* codon 531 (S450L in the *Mycobacterium tuberculosis* numbering system [21]) and the proportion of MDR or rifampicin-resistant isolates resistant to fluoroquinolones. Mutation data from the Moroccan systematic review [22] were reported but not pooled, to avoid counting the same isolates twice. Lineage and transmission findings were synthesised narratively. Analyses were run in Python 3. The review used published data only and did not require ethical approval.

3. Results

3.1. Study selection and characteristics

The searches returned 828 records. After removal of duplicates and screening of titles and abstracts, 183 full-text reports were assessed and 107 studies were included (Figure 1). The most frequent reasons for exclusion were an untraceable bibliographic record (n = 25) and the use of animal or food samples alone (n = 22). Six of the 25 untraceable reports came from Libya; most had appeared in local journals without digital object identifiers.

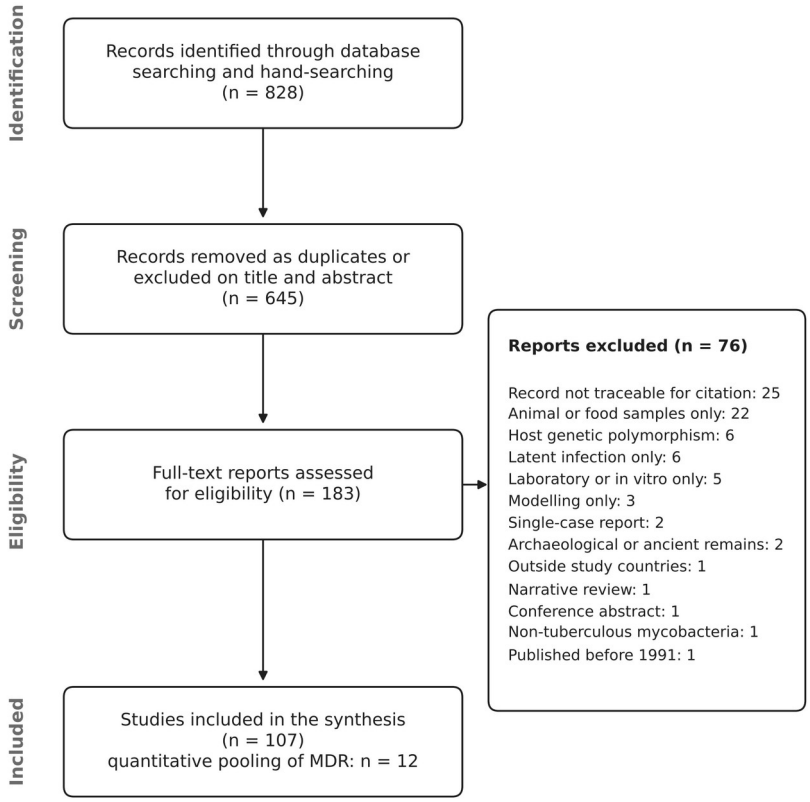

Fig. 1. PRISMA 2020 flow diagram of record identification, screening and inclusion.

The included studies were published between 1993 and 2025, and research activity rose steeply after 2010: one study appeared in 1991–2000, ten in 2001–2010, 54 in 2011–2020 and 42 in 2021–2025, with 15 published in 2024 alone. Morocco (n = 22) and Sudan (n = 21) contributed the most studies, followed by Tunisia (n = 17), Egypt (n = 12), Algeria (n = 12), Libya (n = 10), Chad (n = 9) and Mauritania (n = 4) (Table 1). Cross-sectional designs (n = 27) and retrospective record reviews (n = 21) predominated, followed by molecular or genomic epidemiology (n = 21), diagnostic evaluations (n = 11), case–control studies (n = 9), cohorts (n = 7), surveillance analyses (n = 6), interventions (n = 3) and systematic reviews (n = 2). The characteristics of every included study are listed in Supplementary Table S1.

Table 1. Characteristics of the 107 included studies by country

Country	Studies	Years	Most frequent designs	DR data	Mutations	Typing	WGS	Migration
Libya	10	2011–2025	retrospective (4); cross-sectional (3)	3	0	0	0	9
Egypt	12	2003–2024	cross-sectional (3); diagnostic (2)	7	2	3	1	1
Sudan	21	2011–2025	cross-sectional (12); case–control (4)	19	9	3	1	8
Chad	9	2012–2025	cross-sectional (8); retrospective (1)	4	3	2	0	3
Tunisia	17	1993–2024	molecular (10); diagnostic (3)	13	9	8	4	5
Algeria	12	2006–2025	molecular (4); retrospective (3)	5	3	3	2	2
Morocco	22	2008–2025	retrospective (6); molecular (4)	12	9	0	0	1
Mauritania	4	2016–2019	retrospective (3); cross-sectional (1)	1	0	0	0	1
Total	**107**	**1993–2025**	**cross-sectional (27); molecular (21)**	**64**	**35**	**19**	**8**	**30**

Domain columns give the number of studies contributing data to each domain; a study can contribute to more than one domain. DR, drug-resistance data; WGS, whole-genome sequencing; Migration, migration or nationality addressed.

The distribution of evidence across domains was uneven (Figure 2). Sixty-four studies reported drug-resistance data, 35 reported resistance mutations, 19 typed strains or assigned lineages, eight used whole-genome sequencing, and 30 discussed migration or population movement. Molecular work was concentrated in Tunisia, Morocco and Sudan. Libya presented the inverse profile: nine of its ten studies addressed migrant patients, but only three reported any drug-resistance data and none reported a resistance mutation, a strain type or a genome. The only molecular information on isolates from Libyan patients came indirectly from a Tunisian reference laboratory, where 14 of 103 patients with rifampicin-resistant TB were foreign nationals, including patients from Libya [23].

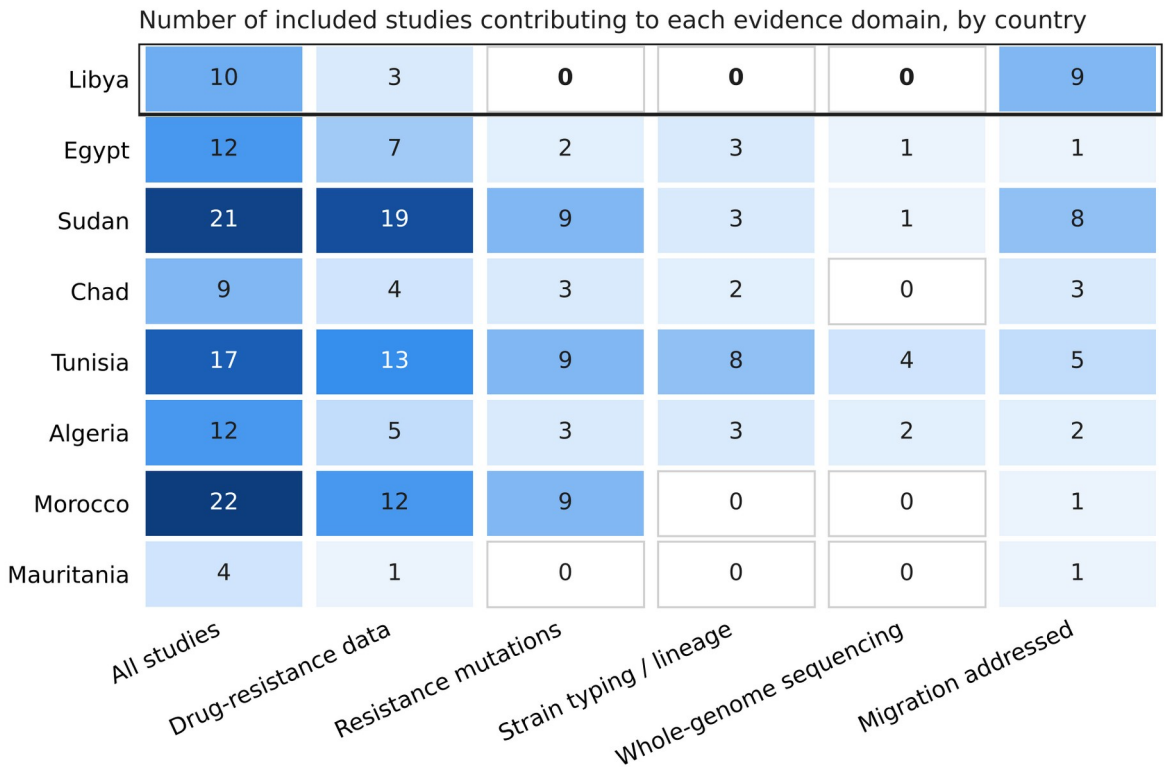

Fig. 2. Evidence map of the 107 included studies by country and evidence domain. Cell values are numbers of studies; darker shading indicates more studies. The Libya row is outlined.

3.2. Proportion of multidrug-resistant tuberculosis

Twelve series enrolled patients without selection on resistance and reported both the number of isolates tested and the number that were MDR (Table 2, Figure 3). Together they tested 2623 isolates, of which 138 were MDR. The pooled proportion was 6.0% (95% CI 3.6–9.9), with substantial heterogeneity (I^2 = 88%). Libya had the lowest subtotal, 1.9% (0.5–6.6), drawn from a Tripoli series of 261 isolates tested on the BACTEC MGIT 960 system [11] and a Benghazi series of 430 patients [12]. Chad followed at 3.8% (2.1–6.8) [24,25], then Tunisia at 4.2% (0.9–18.3) [26,27]. The single Algerian series reached 12.2% (6.8–21.0) [28], and the Sudanese subtotal was the highest at 11.4% (6.0–20.6), based on five series from Port Sudan, Wad Madani, Kassala and eastern Sudan [29-33]. Removing the Kassala series, which reported 30% MDR among 60 isolates [31], lowered the overall estimate to 5.1% (3.3–7.9) without reducing heterogeneity to an acceptable level (I^2 = 82%). Grouped by region, the Sudanese and Chadian series pooled at 8.2% (4.3–15.0) against 3.9% (1.6–9.0) for Libya, Tunisia and Algeria. Three of the 12 series tested fewer than 100 isolates [28,31,32], one relied on Xpert MTB/RIF for resistance detection [30], and only four reported results by treatment history.

Table 2. Series included in the pooled estimate of multidrug-resistant tuberculosis

Study	Setting and population	Resistance testing	MDR / tested	MDR, % (95% CI)
Albarouni 2014 [11]	Tripoli, Libya; consecutive pulmonary TB (217 new, 44 previously treated)	MGIT 960 (phenotypic)	9/261	3.4 (1.8–6.4)
Abbar 2014 [12]	Benghazi, Libya; pulmonary TB inpatients, 2009–2010	LJ culture and MGIT 960	4/430	0.9 (0.4–2.4)
Soudani 2007 [26]	Tunis, Tunisia; university hospital, 2004–2006	Phenotypic; INNO-LiPA Rif.TB	10/544	1.8 (1.0–3.4)
Namouchi 2008 [27]	Bizerte, Tunis and Zaghouan, Tunisia	Phenotypic; spoligotyping, MIRU-VNTR	34/378	9.0 (6.5–12.3)
Benremila 2023 [28]	Algeria; pulmonary TB isolates	Whole-genome sequencing	10/82	12.2 (6.8–21.0)
Hassan 2012 [29]	Port Sudan, Sudan; new untreated patients	Phenotypic; MAS-PCR	6/100	6.0 (2.8–12.5)
Alfaham 2022 [30]	Wad Madani, Sudan; new and retreated presumptive TB	Xpert MTB/RIF	10/103	9.7 (5.4–17.0)
Abdul-Aziz 2013 [31]	Kassala, Sudan; smear-positive patients	Phenotypic; PCR-SSCP	18/60	30.0 (19.9–42.5)
Khalid 2015 [32]	Kassala, Sudan; pulmonary TB	Phenotypic; *rpoB* sequencing	5/53	9.4 (4.1–20.3)
Shuaib 2020 [33]	Eastern Sudan, 2014 and 2016	Phenotypic; whole-genome sequencing	15/166	9.0 (5.6–14.4)
Diallo 2017 [24]	Seven cities, Chad, 2007–2012; consecutive patients	Phenotypic; MIRU-VNTR, spoligotyping	14/311	4.5 (2.7–7.4)

Study	Setting and population	Resistance testing	MDR / tested	MDR, % (95% CI)
Abdelhadi 2012 [25]	Chad; smear-positive patients	Phenotypic	3/135	2.2 (0.8–6.3)
Pooled (random effects)	**12 series, 2623 isolates**		**138/2623**	**6.0 (3.6–9.9); I² = 88%**

MDR, multidrug-resistant (resistant to at least rifampicin and isoniazid); CI, confidence interval; LJ, Löwenstein–Jensen; MGIT, Mycobacteria Growth Indicator Tube. Confidence intervals for single series are Wilson intervals; the pooled estimate is a DerSimonian–Laird random-effects proportion on the logit scale.

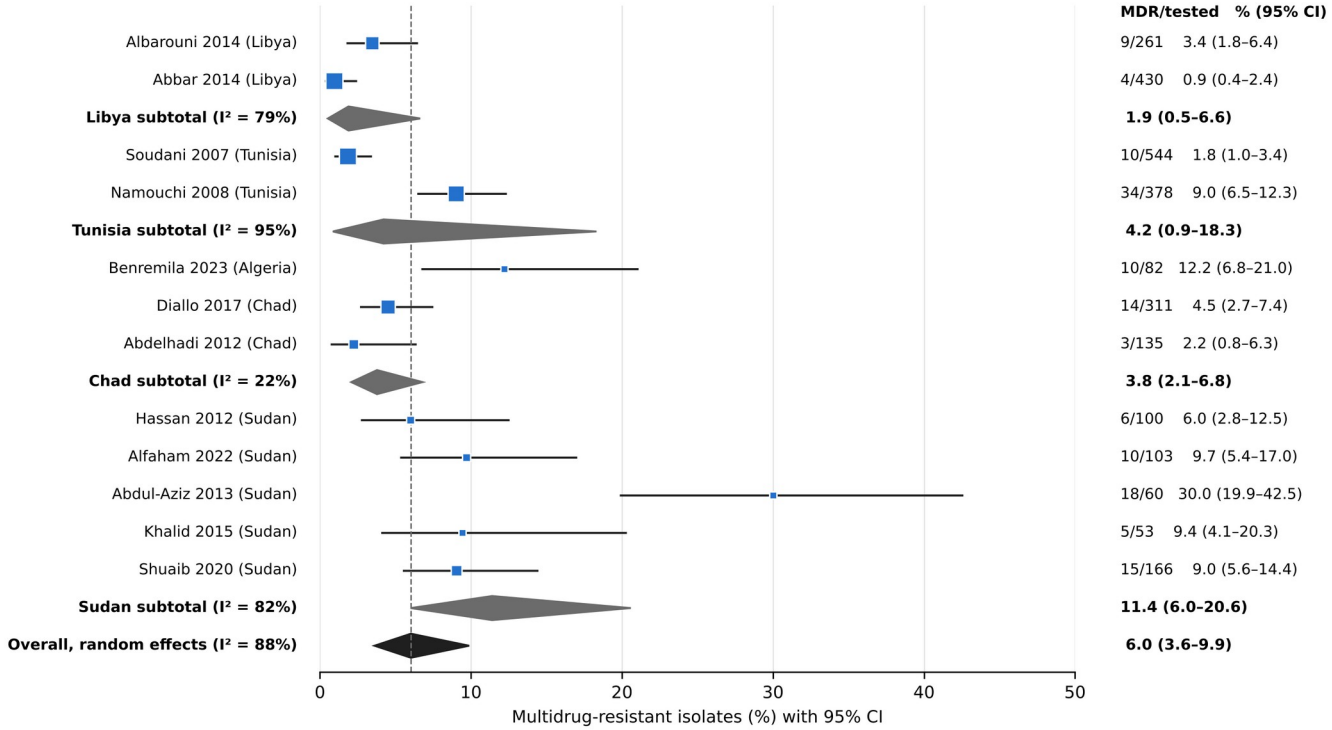

Fig. 3. Forest plot of the proportion of multidrug-resistant tuberculosis in 12 series without selection on resistance, grouped by country. Pooled estimate from a DerSimonian–Laird random-effects model on the logit scale.

Where treatment history was reported, it separated the burden sharply. In Tripoli, none of 217 isolates from new patients was MDR (0%; 95% CI 0–1.7), whereas 9 of 44 isolates from previously treated patients were (20.5%; 11.2–34.5) [11]. Sudanese data showed the same gradient at a higher level: 5% of new and 24% of previously treated patients in a multicentre study [34], 5.3% and 14.7% in Khartoum [35], and 1.8% and 19% in the national survey cited by the Sudanese programme review [36]. A Sudanese meta-analysis estimated MDR at 22.8% across mixed populations [14]. Series restricted to previously treated or defaulting patients reached higher values still: 38.3% of isolates from Sudanese retreatment patients were MDR [37], and case–control analyses identified previous treatment as a principal determinant of MDR in Sudan [38,39]. Referral-laboratory series from Morocco reported MDR in 12.8% of 703 isolates from Casablanca [40] and 24.6% of 187 isolates at the national reference laboratory [2], and a Moroccan systematic review found rifampicin resistance in 24.3% and MDR in 13.1% of 1792 isolates [22]. In Algeria, 42% of 50 patients with suspected MDR TB had rifampicin resistance on Xpert [41]. Among flood-displaced people in N'Djamena, 8 of 76 TB cases (10.5%) were rifampicin resistant [42].

3.3. Resistance mutations and second-line resistance

The molecular data showed a consistent resistance signature (Table 3). In the four studies that counted mutations among rifampicin-resistant isolates from Algeria, Morocco and Sudan, codon 531 accounted for 67 of 100 characterised mutations, a pooled 66.8% (57.0–75.4) with no detectable heterogeneity (I² = 0%) [29,43-45]. The Moroccan systematic review reported the same share, 70.3% at codon 531, followed by codons 516 (8.3%) and 526 (8.1%) [22]. S531L also dominated in the Tunisian MDR outbreak strain [46-48] and was reported alongside H526D and H526Y substitutions in Chad and Sudan [24,35]. Mutations outside the 81-bp rifampicin-resistance-determining region were uncommon but present, including the *rpoB* V615M secondary-site mutation that compensates for the fitness cost of S531L in the Tunisian outbreak clone [49], and codon 488–498 changes in Kassala [32]. Isoniazid resistance was driven mainly by *katG* S315T, found in 77.3% of isoniazid-resistant isolates at the Moroccan reference laboratory [50] and in 9 of 11 Algerian isoniazid-resistant isolates [43], while *inhA* promoter mutations accounted for 37% of isoniazid-resistant isolates in a Moroccan hospital series [51].

Table 3. Resistance mutations, second-line resistance and lineages reported by country

Country	Rifampicin resistance (*rpoB*)	Isoniazid resistance (*katG* / *inhA*)	Second-line resistance	Lineages and transmission
Tunisia	S531L and V615M in outbreak clone; S531W, H526C [26,46,47,49]	*katG* S315T; novel *katG* T326D; *inhA* −15C→T [47,52]	*gyrA* A90V; XDR in 4/68 outbreak isolates; FQ resistance in 14/103 RR isolates [23,48]	Haarlem L4.1.2.1 MDR clone since about 1974, prison-linked spread; 65.2% of MDR isolates clustered [3,27,48,53]
Morocco	Codon 531 in 70.3% of 436 RR isolates; S531L 71.1% and 60.5% in two series [22,44,45]	*katG* S315T in 77.3% of INH-resistant isolates; *inhA* in 37% [50,51]	Ofloxacin resistance 22.2% of MDR (*gyrA* D94A most frequent); *gyrA* mutations in 30% of MDR [40,54]	No lineage data in included studies
Algeria	S531L 7/10; H526D/Q; novel 9-bp deletion (codons 512–514) [43]	*katG* S315T 9/11; rare S315R [43]	4 pre-XDR among 82 isolates [28]	Beijing strain circulating in Blida after arrival of Chinese workers; *M. bovis* pulmonary TB [55,56]
Sudan	Codon 531 in 5/7; S531L, H526D; codons 512, 528 and outside RRDR (488–498) [29,32,35]	*katG* 315 in 90% of INH-resistant isolates; *inhA* −15 in 10% [29]	Second-line resistance in 10% of MDR; 1 XDR [57]	Lineage 3 in 73.4% of 166 genomes; 10/15 MDR strains in one network [33]
Chad	H526Y, H526D, S531L [24]	*katG* S315T; *inhA* C−15T [24]	Not reported	Clonal MDR transmission; Cameroon-family (SIT61) strains near the Cameroonian border [24]
Egypt	Codons 516, 522, 526, 531 [58]	*katG* S315T [58]	*gyrA*/*gyrB* variants in *M. bovis* genomes [59]	Human *M. bovis* genomes related to Algerian human strains [59]
Libya	No data	No data	No data	No data
Mauritania	No data	No data	No data	No data

Codon numbers follow the *Escherichia coli* convention used by the source studies (*rpoB* S531L corresponds to S450L in *Mycobacterium tuberculosis* numbering). FQ, fluoroquinolone; INH, isoniazid; RR, rifampicin-resistant; RRDR, rifampicin-resistance-determining region; XDR, extensively drug-resistant.

Resistance beyond the first-line drugs was documented in every country with molecular data. Across three studies of MDR or rifampicin-resistant isolates from Morocco and Tunisia, 43 of 223 were resistant to fluoroquinolones or carried *gyrA* resistance mutations, a pooled 20.5% (13.1–30.5; I^2 = 57%) [23,40,54]. In Casablanca, ofloxacin resistance reached 22.2% of MDR isolates, with *gyrA* D94A the most frequent change [40]. Sudanese retreatment patients carried second-line resistance in 10% of MDR isolates and one XDR strain [57]. Whole-genome sequencing in Algeria identified four pre-XDR isolates among 82 [28], and by about 2008 the Tunisian outbreak clone had acquired *gyrA* A90V, producing an XDR phenotype in 4 of 68 isolates [48].

3.4. Lineages and transmission networks

Lineage data were available from five countries and pointed to several distinct transmission systems (Table 3). In northern Tunisia, a Haarlem L4.1.2.1 MDR clone emerged in the Bizerte region around 1974, spread to other regions by 1992 and was carried from prisons into the general population, where incarceration-linked cases were connected to 22 later outbreak cases [48,53]; whole-genome sequencing of 46 MDR isolates from 2012–2016 placed 30 (65.2%) in three clusters dominated by the same clone [3]. In eastern Sudan, 122 of 166 sequenced strains (73.4%) belonged to lineage 3, and 10 of the 15 MDR strains formed a single transmission network [33]. In Chad, MDR strains showed clonal transmission, and Cameroon-family strains were concentrated in cities near the Cameroonian border [24]. In Algeria, a Beijing strain had circulated in the Blida region for about a decade after the arrival of Chinese workers, and *Mycobacterium bovis* was confirmed as a cause of pulmonary TB [55]; Egyptian *M. bovis* genomes from human disease were related to Algerian human strains [59]. No study typed isolates from Libya or Mauritania.

3.5. Evidence from Libya

The Libyan studies converged on a single theme (Table 4). In north-western Libya, immigrant men accounted for 92% of non-Libyan pulmonary cases, the most frequent nationalities were Sudanese (38%), Chadian (17.6%) and Nigerian (15.3%), and treatment success was 68.1% among Libyans against 48.6% among immigrants [8]. At Misurata Chest Hospital, 344 of 743 patients (46.3%) came from 15 sub-Saharan countries [60]. In Benghazi, three of the four MDR patients were from Chad or Sudan [12], and in Tripoli, 38 of 261 patients (14.6%) were foreign nationals and two of the nine MDR patients were foreign-born [11]. Reports from Ajdabiya linked rising incidence to Sudanese migration through Kufra [61], eastern Libyan clinicians attributed rising head-and-neck TB to arrivals from Niger, Sudan and Chad [62], and a nurse-training study described a concentration of TB among prison inmates in Sabha associated with undocumented migration [63]. The national spatiotemporal analysis found high-rate clusters in the north-east and north-west and low-rate clusters in the centre and south [9]. Treatment safety was examined in a single Tripoli cohort, which recorded no MDR TB after six months of therapy [64], and one Tripoli series described primary tuberculous pleural effusion in 32 patients, five of whom were hospital doctors [65].

Table 4. Libyan studies included in the review

Study	Setting	Design, sample	Findings relevant to the corridor
Ben Ramadan 2011 [8]	North-western Libya, national TB centre	Retrospective, 1559 pulmonary cases	Immigrant men 92% of non-Libyan cases; Sudanese 38%, Chadian 17.6%, Nigerian 15.3%; treatment success 68.1% (Libyans) vs 48.6% (immigrants)
Dow 2023 [60]	Misurata Chest Hospital, 2005–2007	Cross-sectional, 743 patients	344 (46.3%) from 15 sub-Saharan countries; patients were young
Albarouni 2014 [11]	Tripoli, national TB laboratory	Cross-sectional, 261 isolates	MDR 3.4%, all in previously treated patients (9/44); 14.6% foreign nationals; 2/9 MDR foreign-born
Abbar 2014 [12]	Benghazi, Quefia Chest Hospital, 2009–2010	Retrospective, 430 patients	4 MDR cases, 3 from Chad or Sudan
Fnaish 2024 [61]	Ajdabiya, 2010–2020	Retrospective, 536 patients	Pleural TB most frequent extrapulmonary form; Sudanese migration through Kufra linked to rising incidence
Abdulkarim 2025 [62]	Benghazi, Ajdabiya and Kwifia, 2021–2023	Cross-sectional, 168 patients	49 with head and neck TB; arrivals from Niger, Sudan and Chad cited as a driver
Daw 2025 [9]	National surveillance, 2015–2024	Spatiotemporal, 26,478 cases	40.3 per 100,000 per year; high-rate clusters north-east and north-west, low-rate clusters centre and south
Amer 2023 [63]	Six prison clinics	Educational intervention, 102 nurses	Baseline knowledge good in 31.4%; TB concentrated among Sabha inmates linked to undocumented migration
Buargub 2024 [65]	Three Tripoli hospitals, 2007–2009	Retrospective, 32 patients	Primary tuberculous pleural effusion; 5 patients were hospital doctors
Hadida 2013 [64]	Tripoli, Abu-Setta hospital	Prospective, 75 inpatients	Liver function changes on treatment; no MDR after 6 months

MDR, multidrug-resistant; TB, tuberculosis.

4. Discussion

This review brings together 35 years of TB research from Libya and seven connected countries and shows a striking mismatch between where drug-resistant TB is best documented and where it is least examined. The countries from which most of Libya's migrant TB patients come, Sudan and Chad above all, have the highest MDR proportions in the region, the clearest gradient between new and previously treated patients and the best-documented MDR transmission networks. Libya, which receives these patients in large numbers, has three drug-resistance studies, no genotypic data and no lineage data. The regional resistance signature, however, is consistent enough to support practical decisions in Libya while that deficit is corrected.

The low MDR proportion in Libya should be read with care. Both Libyan series in the pooled analysis came from northern referral hospitals and predate the post-2014 escalation of conflict and migration [11,12]. The Tripoli data show that MDR was confined entirely to previously treated patients, which suggests that resistance there was mainly acquired during treatment rather than transmitted. The same was not true further south. In eastern Sudan, two-thirds of MDR strains belonged to one lineage 3 transmission network [33], and in Chad MDR strains spread clonally [24]. A patient who acquires MDR TB through transmission in Sudan or Chad and travels north will arrive in Libya as a "new" case with resistant disease. That is precisely the patient whom a programme that tests only retreatment cases will miss. The Sudanese gradient between new and previously treated patients, from about 2–5% to 15–24% [34-36], matches the pooled East African estimates of 4% and 21% [66], which supports the view that Libya's southern neighbours belong epidemiologically to the Horn and Sahel rather than to the Maghreb.

The national spatiotemporal analysis gives further reason for caution. Its low-rate clusters lay in the centre and south of the country [9], the regions that border Chad, Niger and Sudan and receive overland migration first. A low notification rate in a region with weak laboratory coverage more probably reflects under-detection than low transmission, an interpretation consistent with the argument that apparent emergence in North Africa often reflects late detection [17]. A review of two decades of evidence from Fezzan reached the same conclusion for TB, noting that the south combines high mobility with diagnostics limited largely to microscopy and rapid tests [67]. A medical-geography study of pulmonary TB in Sebha relied on health-centre records alone [68], and only one included study, a nurse-training evaluation, described TB in Sabha at all [63]. Treatment outcomes in the south add to the concern, because incomplete treatment is the setting in which resistance is acquired: in Sebha, the odds of an unsuccessful outcome were 3.4 times higher during the pandemic than before it [10]. The analogy with malaria is instructive: in Libya malaria is sustained by importation from Niger, Chad and Sudan [18], and the southern part of the country is where importation first becomes visible. For TB, the same geography means that southern Libya is the place where migrant patients enter the health system, and where resistance testing would intercept the largest number of patients carrying strains acquired elsewhere.

The resistance signature itself is reassuring for diagnosis. Two-thirds of characterised rifampicin-resistance mutations sat at codon 531, with no heterogeneity between Algeria, Morocco and Sudan, and the Moroccan review reported the same 70% share across 436 resistant isolates [22]. Mutations at codons 526 and 516 made up most of the remainder. All three codons lie in the region targeted by Xpert MTB/RIF and by line-probe assays, so rapid molecular testing

introduced in Libya should detect most rifampicin resistance carried along the corridor [15,16]. Two qualifications apply. Mutations outside the core region were reported in Kassala [32], and the Tunisian outbreak strain carries a secondary-site *rpoB* mutation that restores fitness [49]. Compensated S531L strains of this kind spread efficiently between hosts [69], which helps explain why a single Haarlem clone has persisted in Tunisia for five decades [48,53]. The Haarlem and other lineage 4 sublineages that dominate the Maghreb include both globally distributed and geographically restricted forms [70], whereas lineage 3 dominates eastern Sudan [33]. A first genomic survey of Libyan isolates would show whether Libya's strains resemble its Maghreb neighbours, its Sahelian neighbours, or both.

Fluoroquinolone resistance deserves particular attention. One in five MDR or rifampicin-resistant isolates in the pooled studies was also resistant to fluoroquinolones [23,40,54], and XDR or pre-XDR strains were documented in Tunisia, Algeria and Sudan [28,48,57]. Current short MDR regimens depend on a fluoroquinolone. A Libyan programme that confirms rifampicin resistance but does not test fluoroquinolone susceptibility risks starting patients from these countries on regimens that are already compromised. Rapid line-probe testing for second-line resistance has performed well in the region [23], and its use for every rifampicin-resistant patient in Libya is a modest and achievable step.

The evidence map also explains why Libya's situation has stayed invisible. Six of the 25 untraceable reports were Libyan, and most Libyan studies that could be traced appeared in local journals without indexing or persistent identifiers. Research on the corridor has also been organised along national lines. Tunisian, Moroccan and Sudanese groups have produced detailed molecular work on their own isolates, but no study has followed strains or patients across a border, and only a Tunisian reference laboratory has reported resistance data on patients from Libya [23]. A regional meta-analysis of antimicrobial resistance in Libya pooled TB together with other pathogens [13], and the regional migrant meta-analysis did not examine resistance mutations [7]. The present review is, to our knowledge, the first to read resistance proportions, mutations and lineages from both sides of the Sahara against the Libyan data.

Several limitations follow from the evidence base. Heterogeneity in the pooled MDR estimate was high and persisted in sensitivity analysis, reflecting differences in setting, period, sampling and laboratory method. Only 12 series qualified for pooling, two of them Libyan, and both Libyan series came from the north. Few studies reported results by treatment history or nationality, so we could not estimate MDR among migrants directly. Mutation pooling rested on four studies and 100 characterised mutations. Excluding reports whose bibliographic record could not be traced made every citation verifiable, but it removed six Libyan reports, and their findings could not be weighed. Restricting the search to English and French may also have missed Arabic-language reports. Risk of bias was appraised only for the studies used in pooling, and many of the remaining studies were small single-centre series.

The findings point to four actions for Libya. Drug-susceptibility testing should cover every previously treated patient and every patient who has recently arrived from Sudan, Chad or Niger, whatever the reported treatment history. Every rifampicin-resistant isolate should be tested for fluoroquinolone resistance. Isolates from southern Libya, where migrant patients first enter the health system, should be sequenced to establish which lineages circulate and whether they link to the Sudanese, Chadian or Maghreb networks. Libyan TB research should be published with persistent identifiers and reported by nationality and treatment history, so that future syntheses can measure what this review could only infer.

5. Conclusions

Drug-resistant TB along the trans-Saharan corridor is concentrated in the countries that supply most of Libya's migrant patients, and it spreads there through documented clonal networks. Libya's own data show a low MDR proportion confined to previously treated patients, but they come from northern hospitals and include no molecular characterisation. The shared dominance of *rpoB* S531L means that rapid molecular tests can serve Libya well. Testing migrants and retreatment patients, testing every rifampicin-resistant isolate for fluoroquinolone resistance and sequencing isolates from southern Libya would turn an inferred risk into measured evidence.

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Declarations

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Data availability: The data-extraction sheet, the coded study inventory and the analysis code are available from the corresponding author on reasonable request. All primary data synthesised in this review are contained in the published sources cited in the reference list.

Supplementary material: Table S1 lists the 107 included studies with country, design, sample size and evidence domains.

References

[1] World Health Organization. Global tuberculosis report 2025. Geneva: World Health Organization; 2025.

[2] Sabouni R, Kourout M, Chaoui I, Jordaan A, Akrim M, Victor TC, et al. Molecular analysis of multidrug resistant *Mycobacterium tuberculosis* isolates from Morocco. Ann Microbiol. 2008;58(4):749-754. doi:10.1007/BF03175585

[3] Bouzouita I, Cabibbe AM, Trovato A, Daroui H, Ghariani A, Midouni B, et al. Whole-genome sequencing of drug-resistant *Mycobacterium tuberculosis* strains, Tunisia, 2012-2016. Emerg Infect Dis. 2019;25(3):538-546. doi:10.3201/eid2503.181370

[4] Ndeikoundam Ngangro N, Ngarhounoum D, Ngangro MN, Rangar N, Siriwardana MG, Halley des Fontaines V, et al. Pulmonary tuberculosis diagnostic delays in Chad: a multicenter, hospital-based survey in Ndjamena and Moundou. BMC Public Health. 2012;12:513. doi:10.1186/1471-2458-12-513

[5] Aw B, Ade S, Hinderaker SG, Dlamini N, Takarinda KC, Chiaa K, et al. Childhood tuberculosis in Mauritania, 2010-2015: diagnosis and outcomes in Nouakchott and the rest of the country. Public Health Action. 2017;7(3):199-205. doi:10.5588/pha.16.0123

[6] World Health Organization. Revitalization of TB services in Libya following the COVID-19 pandemic. WHO Results Report 2022, country story [Internet]. Geneva: World Health Organization; 2023 [cited 2026 Nov 26]. Available from: https://www.who.int/about/accountability/results/who-results-report-2022-mtr/country-story/2022/revitalization-of-tb-services-in-libya-following-the-covid-19-pandemic

[7] Maatoug T, Seedat F, Elafef E, Ouahchi A, Mtiraoui A, Evangelidou S, et al. Burden, clinical outcomes, and characteristics of tuberculosis in migrant populations in the Middle East and North African region: a systematic review and meta-analyses. Travel Med Infect Dis. 2025;66:102872. doi:10.1016/j.tmaid.2025.102872

[8] Ben Ramadan AA, Shambesh MK, Abusnena OI, Al-Baccush M. Estimation of the incidence of pulmonary tuberculosis in Northwestern Libya. Ibnosina J Med Biomed Sci. 2011;3(2):53-58. doi:10.4103/1947-489X.210871

[9] Daw MA, El-Bouzedi AH, Abumahara SA, Najjar AK, Ben Ashur NR, Grebi A, et al. Geographic mapping and spatiotemporal patterns of tuberculosis in Libya within ten years' period (2015 to 2024). Front Epidemiol. 2025;5:1571065. doi:10.3389/fepid.2025.1571065

[10] Shamsi SS, Eltaher A, Al-Fakhri A, Al-Griw H. Divergent trends in tuberculosis notifications and treatment outcomes: an interrupted time series analysis in southern Libya (2019–2023). Int J Mycobacteriol. 2026;15(Suppl):S14-S15. doi:10.4103/ijmy.ijmy_40_26

[11] Albarouni AS, Aboguttaia NB, Alamri WM, Fungi AM, Furjani M, Zorgani A. Drug susceptibility patterns of *Mycobacterium tuberculosis* isolated from patients with pulmonary tuberculosis in Tripoli-Libya. Mycobact Dis. 2014;4(3):154. doi:10.4172/2161-1068.1000154

[12] Abbar MF, Sherif YM, Majbri HJ, Osman MEM, Konozy EHE. Multidrug resistant tuberculosis (MDR-TB): a lethal risk in Benghazi City, Libya. Int J Pharm. 2014;4(13):22-27.

[13] Bleiblo FA, El-Awamie MW, Elsharif NA, Feetouri MM, Alogali IS, et al. Burden of bacterial antimicrobial resistance in Libya, 1970–2024: a systematic meta-analysis with projections to 2050. Antibiotics (Basel). 2026;15(1):92. doi:10.3390/antibiotics15010092

[14] Hajissa K, Marzan M, Idriss MI, Islam MA. Prevalence of drug-resistant tuberculosis in Sudan: a systematic review and meta-analysis. Antibiotics (Basel). 2021;10(8):932. doi:10.3390/antibiotics10080932

[15] World Health Organization. WHO consolidated guidelines on tuberculosis. Module 3: diagnosis. Rapid diagnostics for tuberculosis detection, 2024 update. Geneva: World Health Organization; 2024.

[16] World Health Organization. Catalogue of mutations in *Mycobacterium tuberculosis* complex and their association with drug resistance. 2nd ed. Geneva: World Health Organization; 2023.

[17] Shamsi SS. Emerging or newly detected? Rethinking infectious disease outbreaks in North Africa. J Med Sci (Sebha). 2026;21(3):1-4. doi:10.51984/642cxt20

[18] Yousuf SAA. Malaria in Libya: re-emergence or importation? A short literature review. J Med Sci (Sebha). 2026;21(3):38-43. doi:10.51984/zh47cq70

[19] Page MJ, McKenzie JE, Bossuyt PM, Boutron I, Hoffmann TC, Mulrow CD, et al. The PRISMA 2020 statement: an updated guideline for reporting systematic reviews. BMJ. 2021;372:n71. doi:10.1136/bmj.n71

[20] Munn Z, Moola S, Riitano D, Lisy K. The development of a critical appraisal tool for use in systematic reviews addressing questions of prevalence. Int J Health Policy Manag. 2014;3(3):123-128. doi:10.15171/ijhpm.2014.71

[21] Andre E, Goeminne L, Cabibbe A, Beckert P, Kabamba Mukadi B, Mathys V, et al. Consensus numbering system for the rifampicin resistance-associated *rpoB* gene mutations in pathogenic mycobacteria. Clin Microbiol Infect. 2017;23(3):167-172. doi:10.1016/j.cmi.2016.09.006

[22] Eddabra R, Neffa M. Mutations associated with rifampicin resistance in *Mycobacterium tuberculosis* isolates from Moroccan patients: systematic review. Interdiscip Perspect Infect Dis. 2020;2020:5185896. doi:10.1155/2020/5185896

[23] Bouzouita I, Draoui H, Cabibbe AM, Essalah L, Bejaoui S, Trovato A, et al. Performance of the GenoType MTBDRsl V 2.0 for detecting second-line drugs resistance of *Mycobacterium tuberculosis* isolates in Tunisia. Res Microbiol. 2021;172(3):103816. doi:10.1016/j.resmic.2021.103816

[24] Diallo AB, Ossoga GW, Daneau G, Lo S, Ngandolo R, Djaibe CD, et al. Emergence and clonal transmission of multi-drug-resistant tuberculosis among patients in Chad. BMC Infect Dis. 2017;17(1):579. doi:10.1186/s12879-017-2671-7

[25] Abdelhadi O, Ndokain J, Moussa Ali M, Friocourt V, Mortier E, Heym B. Etude de la resistance de *Mycobacterium tuberculosis* chez les patients bacilliferes au Tchad. Bull Soc Pathol Exot. 2012;105(1):16-22. doi:10.1007/s13149-011-0186-9

[26] Soudani A, Hadjfredj S, Zribi M, Masmoudi A, Messaoud T, Tiouri H, et al. Characterization of Tunisian *Mycobacterium tuberculosis* rifampin-resistant clinical isolates. J Clin Microbiol. 2007;45(9):3095-3097. doi:10.1128/JCM.00643-07

[27] Namouchi A, Karboul A, Mhenni B, Khabouchi N, Haltiti R, Ben Hassine R, et al. Genetic profiling of *Mycobacterium tuberculosis* in Tunisia: predominance and evidence for the establishment of a few genotypes. J Med Microbiol. 2008;57(7):864-872. doi:10.1099/jmm.0.47483-0

[28] Benremila D, Djoudi F, Gharout-Sait A, Kheloufi S, Spitaleri A, Battaglia S, et al. Comprehensive drug resistance characterization of pulmonary tuberculosis in Algeria: insights on *Mycobacterium tuberculosis* strains by whole-genome sequencing. Microb Drug Resist. 2023;29(7):280-295. doi:10.1089/mdr.2022.0321

[29] Hassan SO, Musa MT, Elsheikh HM, Eleragi AMS, Saeed NS. Drug resistance in *Mycobacterium tuberculosis* isolates from Northeastern Sudan. Br J Med Med Res. 2012;2(3):424-433. doi:10.9734/BJMMR/2012/1404

[30] Alfaham ZH, Ahmed EA, Ibrahim EM, Mohamed MS, Mohamed AA, Mahjob A, et al. A study on pulmonary tuberculosis and risk factors in new and re-treated presumptive patients at Wad Madani Tuberculosis Center, Sudan (2018-2019): a cross-sectional study. J Tuberc Res. 2022;10(1):18-27. doi:10.4236/jtr.2022.101002

[31] Abdul-Aziz AA, Elhassan MM, Abdulsalam SA, Mohammed EO, Hamid ME. Multi-drug resistance tuberculosis (MDR-TB) in Kassala State, Eastern Sudan. Trop Doct. 2013;43(2):66-70. doi:10.1177/0049475513490421

[32] Khalid FA, Hamid ZA, Mukhtar MM. Tuberculosis drug resistance isolates from pulmonary tuberculosis patients, Kassala State, Sudan. Int J Mycobacteriol. 2015;4(1):44-47. doi:10.1016/j.ijmyco.2014.11.064

[33] Shuaib YA, Khalil EAG, Wieler LH, Schaible UE, Bakheit MA, Mohamed-Noor SE, et al. *Mycobacterium tuberculosis* complex lineage 3 as causative agent of pulmonary tuberculosis, Eastern Sudan. Emerg Infect Dis. 2020;26(3):427-436. doi:10.3201/eid2603.191145

[34] Sharaf Eldin GS, Fadl-Elmula I, Ali MS, Ali AB, Salih ALGA, Mallard K, et al. Tuberculosis in Sudan: a study of *Mycobacterium tuberculosis* strain genotype and susceptibility to anti-tuberculosis drugs. BMC Infect Dis. 2011;11:219. doi:10.1186/1471-2334-11-219

[35] Sabeel SMA, Salih MA, Ali M, El-Zaki SE, Abuzeid N, Elgadi ZAM, et al. Phenotypic and genotypic analysis of multidrug-resistant *Mycobacterium tuberculosis* isolates from Sudanese patients. Tuberc Res Treat. 2017;2017:8340746. doi:10.1155/2017/8340746

[36] Hassanain SA, Edwards JK, Venables E, Ali E, Adam K, Hussien H, et al. Conflict and tuberculosis in Sudan: a 10-year review of the National Tuberculosis Programme, 2004-2014. Confl Health. 2018;12:18. doi:10.1186/s13031-018-0154-0

[37] Adam MAM, Ali HMH, Khalil EAG. First-line drug resistance patterns of *Mycobacterium tuberculosis* complex isolates from re-treatment patients from Sudan. J Tuberc Res. 2016;4(3):98-104. doi:10.4236/jtr.2016.43012

[38] Ali MH, Alrasheedy AA, Hassali MA, Kibuule D, Godman B. Predictors of multidrug-resistant tuberculosis (MDR-TB) in Sudan.

Antibiotics (Basel). 2019;8(3):90. doi:10.3390/antibiotics8030090

[39] Elduma AH, Holakouie-Naieni K, Almasi-Hashiani A, Rahimi Foroushani A, Ali HMH, Adam MAM, et al. The targeted maximum likelihood estimation to estimate the causal effects of the previous tuberculosis treatment in multidrug-resistant tuberculosis in Sudan. PLoS One. 2023;18(1):e0279976. doi:10.1371/journal.pone.0279976

[40] Oudghiri A, Karimi H, Chetioui F, Zakham F, Bourkadi JE, Elmessaoudi MD, et al. Molecular characterization of mutations associated with resistance to second-line tuberculosis drug among multidrug-resistant tuberculosis patients from high prevalence tuberculosis city in Morocco. BMC Infect Dis. 2018;18(1):98. doi:10.1186/s12879-018-3009-9

[41] Guenaoui K, Harir N, Ouardi A, Zeggai S, Sellam F, Bekri F, et al. Use of GeneXpert *Mycobacterium tuberculosis*/rifampicin for rapid detection of rifampicin resistant *Mycobacterium tuberculosis* strains of clinically suspected multi-drug resistance tuberculosis cases. Ann Transl Med. 2016;4(9):168. doi:10.21037/atm.2016.05.09

[42] Djimenan B, Togde GLD, Nadlaou B, Keloumta MC, Rimtebaye K. Epidemiological and clinical profile of rifampicin-sensitive and -resistant pulmonary tuberculosis in sites of displaced persons due to the 2022-2024 floods in N'Djamena, Chad. J Drug Deliv Ther. 2025;15(1):101-111. doi:10.22270/jddt.v15i1.6962

[43] Bouziane F, Allem R, Sebaihia M, Kumanski S, Mougari F, Sougakoff W, et al. First genetic characterisation of multidrug-resistant *Mycobacterium tuberculosis* isolates from Algeria. J Glob Antimicrob Resist. 2019;19:301-307. doi:10.1016/j.jgar.2019.05.010

[44] Bentaleb EM, El Messaoudi MD, Abid M, Messaoudi M, Yetisen AK, Sefrioui H, et al. Plasmid-based high-resolution melting analysis for accurate detection of *rpoB* mutations in *Mycobacterium tuberculosis* isolates from Moroccan patients. BMC Infect Dis. 2017;17(1):548. doi:10.1186/s12879-017-2666-4

[45] Karimi H, En-Nanai L, Oudghiri A, Chaoui I, Laglaoui A, Bourkadi JE, et al. Performance of GenoType MTBDRplus assay in the diagnosis of drug-resistant tuberculosis in Tangier, Morocco. J Glob Antimicrob Resist. 2018;12:63-67. doi:10.1016/j.jgar.2017.09.002

[46] Mardassi H, Namouchi A, Haltiti R, Zarrouk M, Mhenni B, Karboul A, et al. Tuberculosis due to resistant Haarlem strain, Tunisia. Emerg Infect Dis. 2005;11(6):957-961. doi:10.3201/eid1106.041365

[47] Dekhil N, Meftahi N, Mhenni B, Ben Fraj S, Haltiti R, Belhaj S, et al. MDR-TB outbreak among HIV-negative Tunisian patients followed during 11 years. PLoS One. 2016;11(4):e0153983. doi:10.1371/journal.pone.0153983

[48] Dekhil N, Mardassi H. On the onset and dispersal of a major MDR TB clone among HIV-negative patients, Tunisia. Antimicrob Resist Infect Control. 2024;13(1):18. doi:10.1186/s13756-023-01360-7

[49] Meftahi N, Namouchi A, Mhenni B, Brandis G, Hughes D, Mardassi H. Evidence for the critical role of a secondary site *rpoB* mutation in the compensatory evolution and successful transmission of an MDR tuberculosis outbreak strain. J Antimicrob Chemother. 2016;71(2):324-332. doi:10.1093/jac/dkv345

[50] Elmzibri M, Chaoui I, Sabouni R, Kourout M, Jordaan AM, Lahlou O, et al. Analysis of isoniazid, streptomycin and ethambutol resistance in *Mycobacterium tuberculosis* isolates from Morocco. J Infect Dev Ctries. 2009;3(4). doi:10.3855/jidc.125

[51] Amri A, Benaissa E, Benlahlou Y, Bsaibis F, Maleb A, Chadli M, et al. Genotypic study of isolated resistance to isoniazid in the *Mycobacterium tuberculosis* complex in a Moroccan hospital. Access Microbiol. 2025;7(8). doi:10.1099/acmi.0.000928.v5

[52] Soudani A, Hadjfredj S, Zribi M, Messaadi F, Messaoud T, Masmoudi A, et al. Genotypic and phenotypic characteristics of Tunisian isoniazid-resistant *Mycobacterium tuberculosis* strains. J Microbiol. 2011;49(3):413-417. doi:10.1007/s12275-011-0268-1

[53] Dekhil N, Mardassi H. Delineating the evolutionary pathway to multidrug-resistant outbreaks of a *Mycobacterium tuberculosis* L4.1.2.1/Haarlem sublineage. Int J Infect Dis. 2024;144:107077. doi:10.1016/j.ijid.2024.107077

[54] Chaoui I, Oudghiri A, El Mzibri M. Characterization of *gyrA* and *gyrB* mutations associated with fluoroquinolone resistance in *Mycobacterium tuberculosis* isolates from Morocco. J Glob Antimicrob Resist. 2018;12:171-174. doi:10.1016/j.jgar.2017.10.003

[55] Tazerart F, Saad J, Niar A, Sahraoui N, Drancourt M. *Mycobacterium bovis* pulmonary tuberculosis, Algeria. Emerg Infect Dis. 2021;27(3):972-974. doi:10.3201/eid2703.191823

[56] Ifticene M, Kaidi S, Khechiba MM, Yala D, Boulahbal F. Genetic diversity of *Mycobacterium tuberculosis* strains isolated in Algeria. Int J Mycobacteriol. 2015;4(4):290-295. doi:10.1016/j.ijmyco.2015.06.004

[57] Adam MAM, Ali HMH, Khalil EAG. Initial second-line drug resistance of *Mycobacterium tuberculosis* isolates from Sudanese retreatment-patients. J Clin Tuberc Other Mycobact Dis. 2017;9:21-23. doi:10.1016/j.jctube.2017.10.001

[58] Abdelaal A, El-Ghaffar HA, Zaghloul MHE, El Mashad N, Badran E, Fathy A. Genotypic detection of rifampicin and isoniazid resistant *Mycobacterium tuberculosis* strains by DNA sequencing: a randomized trial. Ann Clin Microbiol Antimicrob. 2009;8:4. doi:10.1186/1476-0711-8-4

[59] Soliman NS, Soliman MS, Khairat SM, Gad MA, Shawky S, Elkholy AA. Genetic diversities and drug resistance in *Mycobacterium bovis* isolates from zoonotic tuberculosis using whole genome sequencing. BMC Genomics. 2024;25(1):1024. doi:10.1186/s12864-024-10909-8

[60] Dow MA, Amar F. Gender, age and origin distributions among tuberculosis patients in Misurata Chest Hospital. Sirte Univ Sci J. 2023;4(2).

[61] Fnaish SG, Bulgasem BY, Alshelmani MI. Retrospective study of tuberculosis cases in Ajdabiya City, Libya during period of 2010-2020. Int Sci Technol J. 2024;35(1):1-17. doi:10.62341/sgbm1129

[62] Abdulkarim YH, Fadallah MM. The frequency of ear, nose, throat, head and neck lesions of tuberculosis in the eastern district of Libya. Libyan J Sci Technol. 2025;15(1):176-180. doi:10.37376/ljst.v15i1.7217

[63] Amer K, Elbahloul M, Alghennai S, Abuhajer S. The impact of tuberculosis educational program on knowledge among nurses working in prison clinics in Libya. Zenodo [Preprint]. 2023. doi:10.5281/zenodo.8052956

[64] Hadida M, Abo-Smhadana A, Draid MM. Effects of anti-tuberculous drugs on liver function profile in Libyan patients with tuberculosis. Egypt J Hosp Med. 2013;52:740-751. doi:10.12816/0000611

[65] Buargub MA, Elshamli I, Alazabi M, Algmizi M, Elazzabi M, Elshatew A, et al. Primary tuberculous pleural effusion: a retrospective study of 32 patients from Tripoli-Libya. Tripolitana Med J. 2024;6(1).

[66] Alem K, Reta MA, Yimam Y. Prevalence of multidrug-resistant tuberculosis in East Africa: a systematic review and meta-analysis. PLoS One. 2022;17(6):e0270272. doi:10.1371/journal.pone.0270272

[67] Abdulsalam FA, Mansour GF. Infectious disease threats and outbreak preparedness in southern Libya (Fezzan): a narrative review of two decades of local evidence. J Med Sci (Sebha). 2026;21(3):63-72. doi:10.51984/a1gc4y41

[68] Al-Baghdadi MSA, Mina KS. Pulmonary tuberculosis in the Sebha City, Libya (study in medical geography) 2010-2016. J Hum Sci (Sebha). 2018;17(1). doi:10.51984/johs.v17i1.495

[69] Comas I, Borrell S, Roetzer A, Rose G, Malla B, Kato-Maeda M, et al. Whole-genome sequencing of rifampicin-resistant *Mycobacterium tuberculosis* strains identifies compensatory mutations in RNA polymerase genes. Nat Genet. 2012;44(1):106-110. doi:10.1038/ng.1038

[70] Stucki D, Brites D, Jeljeli L, Coscolla M, Liu Q, Trauner A, et al. *Mycobacterium tuberculosis* lineage 4 comprises globally distributed and geographically restricted sublineages. Nat Genet. 2016;48(12):1535-1543. doi:10.1038/ng.3704

[71] El-Agroudy AE, Refaie AF, Moussa OM, Ghoneim MA. Tuberculosis in Egyptian kidney transplant recipients: study of clinical course and outcome. J Nephrol. 2003;16(3):404-411.

[72] El-Masry S, Khalil M, Al-Badrawey M, Shokhba M. Determination of matrix metalloproteinases-9 in Egyptian patients with pulmonary *Mycobacterium tuberculosis*. Bull Egypt Soc Physiol Sci. 2009;29(2):219-228. doi:10.21608/besps.2009.36724

[73] AbdelRehim KAA, Soltan EM, Ali AM. RAPD analysis and antibiotic susceptibility for *Mycobacterium tuberculosis* strains isolated from different locations in Egypt. Malays J Microbiol. 2011. doi:10.21161/mjm.30111

[74] Hafez SA, Elhefnawy AM, Hatata EA, El Ganady AA, Ibrahiem MI. Detection of extensively drug resistant pulmonary tuberculosis. Egypt J Chest Dis Tuberc. 2013;62(4):635-646. doi:10.1016/j.ejcdt.2013.07.012

[75] Abd-El Aal AM, Agha SA, Zaghloul MHE, Elshahawy HA, Abdel Azim DM, Fathy A. DNA fingerprinting and drug resistance patterns of active pulmonary *Mycobacterium tuberculosis* in Mansoura hospitals, Egypt. Egypt J Chest Dis Tuberc. 2014;63(2):369-375. doi:10.1016/j.ejcdt.2014.01.014

[76] Saad-Hussein A, Mohammed AM. Trend of application of World Health Organization control strategy of tuberculosis in Egypt. J Epidemiol Glob Health. 2014;4(3):195. doi:10.1016/j.jegh.2014.01.003

[77] Sadek SH, Farghaly S, Abdou MAA, Abdel-Rahim MHM. Bedside inflammatory mediators in pulmonary tuberculosis. Egypt J Bronchol. 2017;11(3):260-267. doi:10.4103/1687-8426.211402

[78] Ghazy RM, Sallam M, Ashmawy R, Elzorkany AM, Reyad OA, Hamdy NA, et al. Catastrophic costs among tuberculosis-affected households in Egypt: magnitude, cost drivers, and coping strategies. Int J Environ Res Public Health. 2023;20(3):2640. doi:10.3390/ijerph20032640

[79] Afifi M, Amin W, Helal D, Ashmawy R, El-Maradny YA, Khalifa N, et al. Impact of bedaquiline regimen on the treatment success rates of multidrug-resistant tuberculosis patients in Egypt. Sci Rep. 2024;14(1):16247. doi:10.1038/s41598-024-65063-8

[80] Soliman N, Soliman M, Shawky SM, Rashed H, Gadalmawla M, Khairat S, et al. Drug resistance trends of *Mycobacterium tuberculosis* before and after the COVID-19 pandemic in an Egyptian Cairo University tertiary-care hospital. Microbes Infect Dis. 2024. doi:10.21608/mid.2024.280803.1873

[81] Zaki AM, Ibrahim NY, Abdelsalam AM, Osman MM. A study on prevalence of drug resistance in drug default pulmonary tuberculosis. Sudan J Med Sci. 2011;6(2). doi:10.4314/sjms.v6i2.72462

[82] Abdelhadi MA, Mahdi TE, Soghaier MA, Awadalla HM, Ahmed AE, Khalid FA. Factors associated with default from treatment among tuberculosis patients in Kassala State, Sudan 2013. J Public Health Epidemiol. 2015;7(6):183-188. doi:10.5897/JPHE2015.0740

[83] Ali AOA, Prins MH. Patient non adherence to tuberculosis treatment in Sudan: socio demographic factors influencing non adherence to tuberculosis therapy in Khartoum State. Pan Afr Med J. 2016;25:80. doi:10.11604/pamj.2016.25.80.9447

[84] Sirelkhatim M, Sharaf Eldin GS, Almula IF, Babiker A, Omer RA. Tuberculosis in Sudan: efficiency of diagnostic techniques commonly used and investigation of some sociodemographic factors which may influence the disease prevalence. Sudan Med Monit. 2016;11(3):71. doi:10.4103/1858-5000.189559

[85] Elegail A, Mohamed NYI, Nour EOM, Hoffner S, Haile M. Molecular characterization of *Mycobacterium tuberculosis* isolates from pulmonary tuberculosis patients in Khartoum, Sudan. Int J Mycobacteriol. 2018;7(3):236. doi:10.4103/ijmy.ijmy_82_18

[86] Ali MH, Alrasheedy AA, Kibuule D, Godman B, Hassali MA, Ali HMH. Assessment of multidrug-resistant tuberculosis (MDR-TB) treatment outcomes in Sudan; findings and implications. Expert Rev Anti Infect Ther. 2019;17(11):927-937. doi:10.1080/14787210.2019.1689818

[87] Hamed MAI, Hammad M, Idris A. Prevalence of rifampicin resistance among tuberculous patients in Khartoum State, Sudan. Microbes Infect Dis. 2024. doi:10.21608/mid.2024.248984.1663

[88] Mohammed AKY, Humida EHM, Ali AMO, Ahmed HG. Burden of tuberculosis in Western Sudan during the Sudan armed conflict. Cureus. 2025;17:e76944. doi:10.7759/cureus.76944

[89] Ngandolo BNR, Didi L, Diguimbaye-Djaibe C, Taddio S, Addo KK, Kazwala RR, et al. Tuberculosis suspicion in Chadian health centers: evaluation of the management system and zoonotic aspect of the disease. PAMJ One Health. 2021;5:6. doi:10.11604/pamj-oh.2021.5.6.25872

[90] Bolti MA, Ngakoutou R, Ahmet A, Joseph MT, Dieudonne D, Mbainadji L, et al. The management problem of miliary tuberculosis in the service of pneumo-phtisiology at the National Reference University Teaching Hospital of N'Djamena (Chad): about 103 cases. J Tuberc Res. 2022;10(3):160-169. doi:10.4236/jtr.2022.103012

[91] Doungous DM, Djimbaye TGL, Djimenan B, Nadlaou B, Rangar N, Ngandolo RNB, et al. Molecular diagnosis of resistant tuberculosis against rifampicin to the patients of the Centre Hospitalier Universitaire de Reference Nationale (CHU-RN): preliminary study during the COVID-19 pandemic period in N'Djamena, Chad. J Clin Med Res. 2024:1-6. doi:10.46889/JCMR.2024.5208

[92] Didi L, Abakar MF, Ngandolo BNR, Djane A, Kessely H, Issaka Y, et al. Assessment of the knowledge, attitudes, and practices toward human tuberculosis amongst rural communities in Chad. Front Vet Sci. 2024;11:1334303. doi:10.3389/fvets.2024.1334303

[93] Ahmat AI, Hassan MTN, Ngandolo BNR, Adoudou MA, Javeres MNL, Yacoubou H, et al. Tuberculosis in the carceral environment in Chad due to the circulating *Mycobacterium tuberculosis* complex. J Biosci Med. 2024;12(2):214-224. doi:10.4236/jbm.2024.122016

[94] Chevrel-Dellagi D, Abderrahman A, Haltiti R, Koubaji H, Gicquel B, Dellagi K. Large-scale DNA fingerprinting of *Mycobacterium tuberculosis* strains as a tool for epidemiological studies of tuberculosis. J Clin Microbiol. 1993;31(9):2446-2450. doi:10.1128/jcm.31.9.2446-2450.1993

[95] Kammoun S, Smaoui S, Marouane C, Slim L, Messadi-Akrout F. Drug susceptibility testing of *Mycobacterium tuberculosis* by a nitrate reductase assay applied directly on microscopy-positive sputum samples. Int J Mycobacteriol. 2015;4(3):202-206. doi:10.1016/j.ijmyco.2015.04.005

[96] Siala M, Smaoui S, Taktak W, Hachicha S, Ghorbel A, Marouane C, et al. First-time detection and identification of the *Mycobacterium tuberculosis* complex members in extrapulmonary tuberculosis clinical samples in south Tunisia by a single tube tetraplex real-time PCR assay. PLoS Negl Trop Dis. 2017;11(5):e0005572. doi:10.1371/journal.pntd.0005572

[97] Ben Ayed H, Koubaa M, Gargouri L, Ben Jemaa M, Trigui M, Hammemi F, et al. Epidemiology and disease burden of tuberculosis in south of Tunisia over a 22-year period: current trends and future projections. PLoS One. 2019;14(7):e0212853. doi:10.1371/journal.pone.0212853

[98] Hammami F, Koubaa M, Chakroun A, Rekik K, Feki W, Marrakchi C, et al. Comparative analysis between tuberculous meningitis and other forms of extrapulmonary tuberculosis. Germs. 2021;11(1):23-31. doi:10.18683/germs.2021.1237

[99] Melki S, Mizouni G, Chebil D, Ben Abdelaziz A. Tuberculosis epidemiological trend in Sousse, Tunisia during twenty years (2000-2019). Libyan J Med. 2022;17(1):2003968. doi:10.1080/19932820.2021.2003968

[100] Tritar F, Ben Saad S, Ferchichi M, Ben Mansour A, Slim A, Naffati O, et al. Risk factors for treatment failure in multidrug resistant tuberculosis in Tunisia: an analytic study. Tunis Med. 2024;102(1). doi:10.62438/tunismed.v102i1.4521

[101] Nateche F, Martin A, Baraka S, Palomino JC, Khaled S, Portaels F. Application of the resazurin microtitre assay for detection of multidrug resistance in *Mycobacterium tuberculosis* in Algiers. J Med Microbiol. 2006;55(7):857-860. doi:10.1099/jmm.0.46513-0

[102] Selmane S, L'Hadj M. Epidemiology and clinical characteristics of tuberculosis in Leon Bernard tuberculosis unit in Algeria. Int J Mycobacteriol. 2020;9(3):254. doi:10.4103/ijmy.ijmy_78_20

[103] Selmane S, L'Hadj M. Spatiotemporal analysis and seasonality of tuberculosis in Algeria. Int J Mycobacteriol. 2021;10(3):234-242. doi:10.4103/ijmy.ijmy_111_21

[104] Guenaoui K, Ouardi A, Kanoun K, Ouali S, Harir N. Multi-resistant tuberculosis in Western Algeria: about 36 cases. Egypt Acad J Biol Sci C Physiol Mol Biol. 2021;13(1):149-157. doi:10.21608/eajbsc.2021.178245

[105] Hamri WH, Diaf M, Hamadouche FZ. A five-year epidemiological study of tuberculosis and its related risk factors in northwestern Algeria. South Sudan Med J. 2024;17(4):173-178. doi:10.4314/ssmj.v17i4.4

[106] Ghermi M, Messedi M, Adida C, Belarbi K, Djazouli MEA, Berrazeg ZI, et al. TubIAgnosis: a machine learning-based web application for active tuberculosis diagnosis using complete blood count data. Digit Health. 2024;10:20552076241278211. doi:10.1177/20552076241278211

[107] Abderrahim S, Taright S. Risk factors for pulmonary tuberculosis in an urban area of Algeria. Int J Mycobacteriol. 2025;14(1):48-55. doi:10.4103/ijmy.ijmy_11_25

[108] Ottmani S, Zignol M, Bencheikh N, Laasri L, Blanc L, Mahjour J. TB contact investigations: 12 years of experience in the National TB Programme, Morocco 1993-2004. East Mediterr Health J. 2009;15(3):494-503. doi:10.26719/2009.15.3.494

[109] Dooley KE, Lahlou O, Ghali I, Knudsen J, Elmessaoudi MD, Cherkaoui I, et al. Risk factors for tuberculosis treatment failure, default, or relapse and outcomes of retreatment in Morocco. BMC Public Health. 2011;11:140. doi:10.1186/1471-2458-11-140

[110] Slama K, Tachfouti N, Obtel M, Nejjari C. Factors associated with treatment default by tuberculosis patients in Fez, Morocco. East Mediterr Health J. 2013;19(8):687-693. doi:10.26719/2013.19.8.687

[111] Tachfouti N, Slama K, Berraho M, Elfakir S, Benjelloun MC, El Rhazi K, et al. Determinants of tuberculosis treatment default in Morocco: results from a national cohort study. Pan Afr Med J. 2013;14:121. doi:10.11604/pamj.2013.14.121.2335

[112] Chaoui I, Atalhi N, Sabouni R, Akrim M, Abid M, Amzazi S, et al. Rifoligotyping assay: an alternative method for rapid detection of rifampicin resistance in *Mycobacterium tuberculosis* isolates from Morocco. Biotechnol Biotechnol Equip. 2014;28(6):1095-1102. doi:10.1080/13102818.2014.975569

[113] El Azbaoui S, Sabri A, Ouraini S, Hassani A, Asermouh A, Agadr A, et al. Utility of the QuantiFERON-TB Gold In-Tube assay for the diagnosis of tuberculosis in Moroccan children. Int J Tuberc Lung Dis. 2016;20(12):1639-1646. doi:10.5588/ijtld.16.0382

[114] El Hamdouni M, Bourkadi JE, Benamor J, Hassar M, Cherrah Y, Ahid S. Treatment outcomes of drug resistant tuberculosis patients in Morocco: multi-centric prospective study. BMC Infect Dis. 2019;19(1):316. doi:10.1186/s12879-019-3931-5

[115] Park S, Moon N, Oh B, Park M, Kang K, Sentissi I, et al. Improving treatment adherence with integrated patient management for TB patients in Morocco. Int J Environ Res Public Health. 2021;18(19):9991. doi:10.3390/ijerph18199991

[116] El Bardai G, Kabbali N, Baba H, Chouhani BA, Sqalli Houssaini T. Tuberculosis in dialysis patients in the central region of Morocco: what is the health-care delay? Cureus. 2022;14:e30369. doi:10.7759/cureus.30369

[117] Aachari I, Tahiri L, Elolemy G, Taik FZ, Afilal S, Fellous S, et al. Active tuberculosis infection in Moroccan patients with rheumatic diseases under biologic therapy. Int J Mycobacteriol. 2022;11(2):175-182. doi:10.4103/ijmy.ijmy_153_20

[118] Yang J, Kim HY, Park S, Sentissi I, Green N, Oh BK, et al. Cost-effectiveness of a medication event monitoring system for tuberculosis management in Morocco. PLoS One. 2022;17(4):e0267292. doi:10.1371/journal.pone.0267292

[119] Ait Ouaaziz N, El Bakkali M, El Yahyaoui O, Bouabid B, Derdaki M, Arfaoui A, et al. Risk factors and the evolution of tuberculosis cases in the Laayoune and Tarfaya provinces of Morocco. Tanzan J Health Res. 2023;25(1):511-523. doi:10.4314/thrb.v25i1.2

[120] Bejja F, Hami H, Aboulhoda F, Hadrya F, Mokhtari A, Soulaymani A. Severity of neuromeningeal tuberculosis in Morocco: a critical evaluation of epidemiological trends and treatment efficacy. Pan Afr Med J. 2024;47:216. doi:10.11604/pamj.2024.47.216.42573

[121] Ez-Zari A, Farouk L, Vilaplana C, Mezzoug N, Bouti K, El Mtili N. A longitudinal prospective study of active tuberculosis among patients in Tetouan, Morocco. Cureus. 2025;17:e81838. doi:10.7759/cureus.81838

[122] Lo A, Tall-Dia A, Bonfoh B, Schelling E. Tuberculosis among transhumant pastoralist and settled communities of south-eastern Mauritania. Glob Health Action. 2016;9:30334. doi:10.3402/gha.v9.30334

[123] Boushab BM, Savadogo M, Sow MS. Prevalence de la tuberculose pulmonaire a bacilloscopie positive dans un centre hospitalier d'Aioun (Hodh El Gharbi). Rev Pneumol Clin. 2016;72(4):243-247. doi:10.1016/j.pneumo.2015.09.007

[124] Boushab BM, Kone N, Basco LK. Contribution of computed tomography scan to the diagnosis of spinal tuberculosis in 14 cases in Assaba, Mauritania. Radiol Res Pract. 2019;2019:7298301. doi:10.1155/2019/7298301

Table S1. Studies included in the systematic review (n = 107), with country, design, sample size and evidence domains

Study	Country	Design	Sample	Domains
Ben Ramadan 2011 [8]	Libya	retrospective	1,559	Mig
Hadida 2013 [64]	Libya	cohort	75	DR
Abbar 2014 [12]	Libya	retrospective	430	DR, Mig
Albarouni 2014 [11]	Libya	cross-sectional	261	DR, Mig
Amer 2023 [63]	Libya	intervention	102	Mig
Dow 2023 [60]	Libya	cross-sectional	743	Mig
Fnaish 2024 [61]	Libya	retrospective	536	Mig
Buargub 2024 [65]	Libya	retrospective	32	Mig
Abdulkarim 2025 [62]	Libya	cross-sectional	168	Mig
Daw 2025 [9]	Libya	surveillance	26,478	Mig
El-Agroudy 2003 [71]	Egypt	retrospective	1,200	—
Abdelaal 2009 [58]	Egypt	diagnostic	153	DR, Mut
El-Masry 2009 [72]	Egypt	case–control	89	—
AbdelRehim 2011 [73]	Egypt	molecular	72	Typ
Hafez 2013 [74]	Egypt	diagnostic	40	DR
Abd-El Aal 2014 [75]	Egypt	cross-sectional	123	DR, Typ
Saad-Hussein 2014 [76]	Egypt	surveillance	NR	—
Sadek 2017 [77]	Egypt	case–control	170	—
Ghazy 2023 [78]	Egypt	cross-sectional	276	DR
Afifi 2024 [79]	Egypt	cohort	84	DR
Soliman 2024 [59]	Egypt	molecular	112	DR, Mut, Typ, WGS, Mig
Soliman 2024 [80]	Egypt	cross-sectional	100	DR
Zaki 2011 [81]	Sudan	cross-sectional	111	DR
Sharaf Eldin 2011 [34]	Sudan	cross-sectional	235	DR, Typ, Mig
Hassan 2012 [29]	Sudan	cross-sectional	100	DR, Mut
Abdul-Aziz 2013 [31]	Sudan	cross-sectional	90	DR, Mut
Khalid 2015 [32]	Sudan	cross-sectional	113	DR, Mut
Abdelhadi 2015 [82]	Sudan	case–control	102	Mig
Ali 2016 [83]	Sudan	case–control	2,727	Mig
Sirelkhatim 2016 [84]	Sudan	cross-sectional	243	DR, Mig
Adam 2016 [37]	Sudan	cross-sectional	239	DR
Sabeel 2017 [35]	Sudan	cross-sectional	100	DR, Mut
Adam 2017 [57]	Sudan	cross-sectional	239	DR, Mut
Hassanain 2018 [36]	Sudan	surveillance	64,957	DR, Mig
Elegail 2018 [85]	Sudan	molecular	406	DR, Mut, Typ
Ali 2019 [38]	Sudan	case–control	183	DR, Mig
Ali 2019 [86]	Sudan	cohort	156	DR, Mig
Shuaib 2020 [33]	Sudan	cross-sectional	383	DR, Mut, Typ, WGS
Hajissa 2021 [14]	Sudan	systematic review	1,786	DR
Alfaham 2022 [30]	Sudan	cross-sectional	300	DR, Mut
Elduma 2023 [39]	Sudan	case–control	1,290	DR
Hamed 2024 [87]	Sudan	cross-sectional	75	DR, Mut
Mohammed 2025 [88]	Sudan	retrospective	751	DR, Mig
Ndeikoundam Ngangro 2012 [4]	Chad	cross-sectional	286	—
Abdelhadi 2012 [25]	Chad	cross-sectional	135	DR
Diallo 2017 [24]	Chad	cross-sectional	593	DR, Mut, Typ, Mig
Ngandolo 2021 [89]	Chad	cross-sectional	478	Typ
Bolti 2022 [90]	Chad	retrospective	103	—
Doungous 2024 [91]	Chad	cross-sectional	680	DR, Mut
Didi 2024 [92]	Chad	cross-sectional	139	Mig
Ahmat 2024 [93]	Chad	cross-sectional	50	—
Djimenan 2025 [42]	Chad	cross-sectional	418	DR, Mut, Mig
Chevrel-Dellagi 1993 [94]	Tunisia	molecular	201	Typ, Mig
Mardassi 2005 [46]	Tunisia	molecular	193	DR, Mut, Typ, Mig
Soudani 2007 [26]	Tunisia	molecular	544	DR, Mut
Namouchi 2008 [27]	Tunisia	molecular	378	DR, Typ
Soudani 2011 [52]	Tunisia	molecular	43	DR, Mut
Kammoun 2015 [95]	Tunisia	diagnostic	111	DR

Study	Country	Design	Sample	Domains
Dekhil 2016 [47]	Tunisia	molecular	48	DR, Mut, Typ
Meftahi 2016 [49]	Tunisia	molecular	45	DR, Mut, Typ
Siala 2017 [96]	Tunisia	diagnostic	170	—
Bouzouita 2019 [3]	Tunisia	molecular	46	DR, Mut, Typ, WGS
Ben Ayed 2019 [97]	Tunisia	surveillance	2,771	—
Bouzouita 2021 [23]	Tunisia	diagnostic	103	DR, Mut, WGS, Mig
Hammami 2021 [98]	Tunisia	retrospective	519	DR
Melki 2022 [99]	Tunisia	surveillance	2,606	—
Dekhil 2024 [48]	Tunisia	molecular	68	DR, Mut, Typ, WGS, Mig
Tritar 2024 [100]	Tunisia	retrospective	140	DR
Dekhil 2024 [53]	Tunisia	molecular	250	DR, Mut, Typ, WGS, Mig
Nateche 2006 [101]	Algeria	diagnostic	136	DR
Ifticene 2015 [56]	Algeria	molecular	129	Typ
Guenaoui 2016 [41]	Algeria	diagnostic	50	DR, Mut
Bouziane 2019 [43]	Algeria	molecular	11	DR, Mut
Selmane 2020 [102]	Algeria	retrospective	1,375	—
Tazerart 2021 [55]	Algeria	molecular	98	Typ, WGS, Mig
Selmane 2021 [103]	Algeria	surveillance	654,658	—
Guenaoui 2021 [104]	Algeria	retrospective	36	DR
Benremila 2023 [28]	Algeria	molecular	82	DR, Mut, Typ, WGS, Mig
Hamri 2024 [105]	Algeria	retrospective	NR	—
Ghermi 2024 [106]	Algeria	case–control	1,649	—
Abderrahim 2025 [107]	Algeria	case–control	669	—
Sabouni 2008 [2]	Morocco	molecular	187	DR, Mut
Ottmani 2009 [108]	Morocco	retrospective	1,000,000	—
Elmzibri 2009 [50]	Morocco	molecular	199	DR, Mut
Dooley 2011 [109]	Morocco	cohort	291	DR
Slama 2013 [110]	Morocco	case–control	320	—
Tachfouti 2013 [111]	Morocco	cohort	1,039	—
Chaoui 2014 [112]	Morocco	diagnostic	500	DR, Mut
El Azbaoui 2016 [113]	Morocco	diagnostic	109	—
Bentaleb 2017 [44]	Morocco	diagnostic	67	DR, Mut
Oudghiri 2018 [40]	Morocco	molecular	703	DR, Mut
Karimi 2018 [45]	Morocco	diagnostic	70	DR, Mut, Mig
Chaoui 2018 [54]	Morocco	molecular	50	DR, Mut
El Hamdouni 2019 [114]	Morocco	cohort	101	DR
Eddabra 2020 [22]	Morocco	systematic review	1,792	DR, Mut
Park 2021 [115]	Morocco	intervention	3,605	DR
El Bardai 2022 [116]	Morocco	retrospective	94	—
Aachari 2022 [117]	Morocco	retrospective	130	—
Yang 2022 [118]	Morocco	intervention	347	—
Ait Ouaaziz 2023 [119]	Morocco	retrospective	1,333	—
Bejja 2024 [120]	Morocco	retrospective	33	—
Amri 2025 [51]	Morocco	retrospective	464	DR, Mut
Ez-Zari 2025 [121]	Morocco	cohort	125	—
Lo 2016 [122]	Mauritania	cross-sectional	500	Mig
Boushab 2016 [123]	Mauritania	retrospective	320	DR
Aw 2017 [5]	Mauritania	retrospective	948	—
Boushab 2019 [124]	Mauritania	retrospective	14	—

Domains: DR, drug-resistance data; Mut, resistance mutations; Typ, strain typing or lineage assignment; WGS, whole-genome sequencing; Mig, migration or nationality addressed; —, epidemiological or clinical data only; NR, not reported. Bracketed numbers refer to the main reference list.