



Research Article

Double Burden of Tuberculosis-HIV Co-infection and Drug Resistance in the Post-Conflict Far-North Region of Cameroon

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Abstract

In Cameroon, the Far-north region counts as one of the ten regions that lacks data's concerning tuberculosis dynamics. Subject to national insecurity few years ago, some of the direct consequences include promiscuity, poverty, under diagnosis, treatment absence, leading to high burden of tuberculosis (TB). The present research was conducted across the Far-North Region of Cameroon for the first time, to investigate pulmonary tuberculosis among affected TB patients. Sputum specimens were collected following a rigorous questionnaire-based investigation and HIV screening test. The specimens were subjected to microscopic examination, followed by culture. Strains of *M. tuberculosis* (MTB) complex isolated were tested for susceptibility to antibiotics and molecular detection of drug resistance (DR) was performed with MTB/DRplus. Between May 2022 to December 2025, 213 questionnaires were administered to randomly selected participants at the Maroua Regional Hospital, Mokolo and Koza District Hospitals, Koza Adventist Hospital and Minawao Health Center. Among these included participants, 146 of the 191 sputum samples were confirmed positive for *M. tuberculosis* complex, yielding a TB positivity rate of 76.4%. HIV seroprevalence of 13.6%, was noted and TB-HIV co-infection rate was 9.9%. Tuberculosis was significantly associated to male sex ($p = 0.007$), urban residence ($p = 0.049$), occupational activity primarily in the agricultural sector ($p = 0.021$) and infection status ($p < 0.001$). 40 randomly selected culture-positive LJ strains of MTBC were subjected to the GenoType MTBDRplus test. While 80% of these strains were susceptible to both rifampicin and isoniazid, 20% exhibited at least one resistance with 7.5% classified as rifampicin monoresistance, 5% isoniazid monoresistance and 7.5% multi-resistant to both drugs. The mutation associated with rifampicin resistance was D516V in *rpoB* gene. for isoniazid resistance, mutation was identified at *katG* gene (S315T) and the *inhA* promoter region (C-15T and A-16G). These findings underscore the need to target sociodemographic determinants of TB in healthcare access and diagnostic delay (male sex, rural residence, agricultural occupation, infection status). The lack of association between HIV status and smear positivity, combined with the well-established risk of paucibacillary disease in HIV-

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positive individuals, represents an important limitation to acknowledge, and supports advocating need for the use of more sensitive conventional and molecular diagnostics interventions (e.g., Xpert MTB/RIF, LPA) in HIV-positive presumptive TB cases in this setting.

Keywords

Tuberculosis, Mycobacterium Tuberculosis Complex, Drug Resistance, Co-infection, Post-Conflict, Far- North, Cameroon

1. Introduction

Tuberculosis (TB) still remains one of the most devastating infectious diseases worldwide. It is an infectious and contagious disease caused by *Mycobacterium tuberculosis* complex strains [1]. With 25% of new cases, TB represents the second highest disease burden in African countries. Claiming millions of lives each year and disproportionately affecting vulnerable populations with an estimated 10.7 million people who fell ill with TB in 2024 and 1.23 million deaths registered worldwide [2]. As a public health dilemma, drug resistance has been an obstacle to achieve the goal of effective TB control. Multi-drug-resistant (MDR) tuberculosis may arise by inadequate antituberculosis treatment or by direct transmission of drug-resistant strains from one individual to another [3]. The worldwide increase in MDR-TB rate (resistance to at least rifampicin [RMP] and isoniazid [INH]) has made the timely identification of resistant *Mycobacterium tuberculosis* complex (MTBC) strains to achieve effective disease management and to prevent their spread extremely important.

In Cameroon, the burden of tuberculosis is still heavily present with a total TB incidence of 38 000 cases recorded in 2024 [2] to unfolds against the backdrop of a prolonged insecurity sanitary situation of crisis as is the case in the Far-North region. Over the past decade, violence and displacement have profoundly weakened local health services, disrupted disease surveillance systems, troubled access to diagnosis and weaken treatment access and follow-up. Entire communities have been displaced, healthcare facilities destroyed or abandoned, and routine TB control activities severely compromised. In such contexts, the silent spread of tuberculosis is often overshadowed by the visible consequences of conflict, allowing the disease to persist and potentially evolve unnoticed.

Compounding this challenge is the intersection of TB with HIV/AIDS infection (which impairs immune system that makes the body able to fight diseases). This justifies why TB is the leading cause of death of people with HIV [4]. With 150 000 deaths among people with HIV suffering from tuberculosis, indeed HIV is a well-established driver of TB morbidity [5]. The coexistence of these two diseases amplifies clinical severity, complicates treatment outcomes, and underscores the urgent need for integrated epidemiological and microbiological investigations. The Core Group (2013) [6] reports that in 2010, 13% of all TB deaths were in people who were HIV infected. According WHO/UNAIDS (2004) [7]. cited in

Noeske et al., (2006) [8]., 5.5% (4.8-9.8%) of sexually active adults (15 - 49 years old) in Cameroon are living with HIV/AIDS and easily die from TB.

In recent years, molecular typing methods have been widely used in epidemiological studies to aid the control of TB, but this usage has not been the case with many African countries, including Cameroon [9]. Several areas of Cameroon, particularly the Far-North remain largely unexplored in terms of pathogen diversity and resistance patterns. This lack of genomic and microbiological data represents a critical gap in our understanding of TB transmission dynamics, drug resistance emergence, and the effectiveness of current therapeutic approaches.

The prevalence of TB in large urban areas is complicated by the close human-to-human contacts and potential multiple sources of MTB strains from different ethnic and migratory populations. Leading to increase in strains resistant rate which is the main problem in TB control. INH and RMP are the most important first-line antituberculosis drugs, and resistance to these drugs often results in treatment failures and fatal clinical outcome [10]. Against this backdrop, the present research was conducted across the Far-North Region of Cameroon to investigate pulmonary tuberculosis among affected patients using a comprehensive approach integrating clinical, epidemiological, microbiological and genetic data. By combining patient questionnaire data, HIV testing results, microscopy and culture findings, as well as antibiotic susceptibility profiles, with Line Probe Assay (LPA) results. This research aimed to shed light on the epidemiological and biological landscape of TB in a region that has not been exploited due to conflict.

2. Materials and Methods

2.1. Study Design

A cross-sectional research study was conducted from May 2022 to December 2025. During this period, 213 well-designed study questionnaires were randomly administered to patients selected for the study to obtain clinical and epidemiological data. Were included all consented smear-positive pulmonary tuberculosis patients aged 15 years and above, and consulting at our five Tuberculosis Diagnosis and Treatment

Centers (CDT) in the Far-North region (Maroua Regional Hospital, the Mokolo and Koza District Hospitals, the Koza

Adventist Hospital and the Minawao Health Center) as shown in Figure 1.

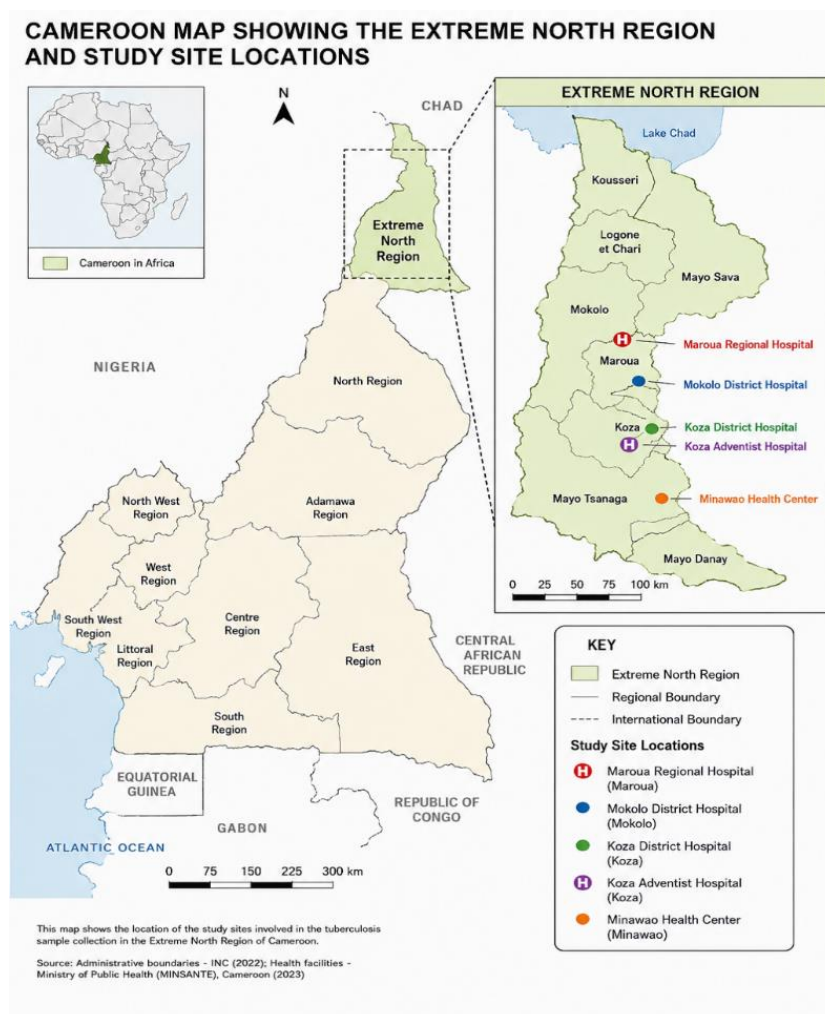


Figure 1. Study area location sites involved in tuberculosis sample collection in the Far-North region of Cameroon [10].

2.2. Sample Processing

Each participant with productive cough provided sputum on two successive days, following HIV testing with respect to routine sampling procedures. Smear-positive sputa were held at +4 °C and transported twice weekly to the Laboratory for Tuberculosis Research and Pharmacology (LTRP) of the Biotechnology Center of the University of Yaoundé 1 (BTC UYI), where culture, drug susceptibility testing, molecular analysis and quality control (internal and external) were realized. Ziehl-Neelsen or auramine smears [11] were performed at the recruitment site. Only the highest-grade smear-positive specimens were forwarded in a cooler within 24 hours to the LTRP for confirmation microscopy and culture. Every specimen underwent decontamination using the cetylpyridinium chloride/NaCl.

2.3. HIV Diagnosis

HIV screening of recruited participants relied on the Determine™ HIV-1/2 rapid assay as a first-line test. Reactive results were confirmed with a second independent test, the OraQuick ADVANCE Rapid HIV-1/2 assay (OraSure Technologies Inc, Bethlehem, PA, USA) [12]. Only participants reactive to both assays were classified as HIV-positive.

2.4. Culture and Identification

On arrival at the LTRP, sputum sediments were rinsed three times in sterile distilled water by successive 20 minutes centrifugation cycles, with the supernatant discarded after each spin. Three to four drops of the resulting decontaminated pellet were used to seed three Lowenstein Jensen (LJ)

slants. Two of these slants contained 0.75% glycerol (pyruvate free) and one contained 0.4% pyruvate, each received approximately 0.1-0.3ml of sediment and was incubated at 37°C. Absence of visible colonies after eight weeks of incubation defines a negative culture, and slants were kept inclined throughout. Isolates that grew were further characterized for drug susceptibility by the indirect proportion method on Löwenstein Jensen at the following critical concentrations: INH (H1: 1 mg/ml and H2: 2 mg/ml), Streptomycin (STM- S: 4 mg/ml), RIF (R: 40 mg/ml), Ethambutol (EMB) -E: 2 mg/ml) [13, 14].

2.5. DNA Extraction

Bacterial DNA was extracted by scraping a loopful of mycobacterial colonies from Lowenstein-Jensen slants into Tris-EDTA (10 mM, 1 mM, pH 8) and heating the suspension for 30 minutes at 90°C. Following centrifugation at 13,000 ×g, the resulting supernatant was transferred to a fresh tube and stored at -20°C until further use [15].

2.6. Molecular Detection of Drug Resistance by LPA

Drug resistance genotyping was performed with MTB/DRplus line-probe assay (Hain Diagnostics), which interrogate wild-type sequences and known mutations at rpoB codons 516, 526 and 531 (rifampicin resistance), and katG codon 315 and inhA promoter position-16 (isoniazid resistance) [16], strictly following the manufacturer's instructions [17], with kit version 1.0. Isolate were scored susceptible when every wild-type band was present and no mutation band appeared, resistance was called whenever at least one wild-type band was absent and/or any mutation band was detected. Strains showing an intact wild-type pattern together with a mutation band at the same locus were classified as heteroresistant, reflecting a mixed population of susceptible and resistant *M. tuberculosis* [18].

2.7. Ethical Considerations

The study received administrative clearance from the Institutional Ethics Committee Research on Human Health in Cameroon (No: 3541CEI-Udo/03/2023/T). All study procedures were explained before and during the study to participants. Written, informed and signed consent (provided in

French and English languages) was obtained from each enrolled patient who incurred no cost for sample processing. Data collection was conducted in a hybrid manner, combining physical (paper -based) and digital administration of questionnaires to maximize participation rates. All drug susceptibility test results were reported to the respective health facilities for further management of the patients.

2.8. Data Analysis

The sample size was calculated by the formula $n = z^2 \times p(1-p)/m^2$. With $p = 0.27$, $z = 1.96$, $m =$ margin which yielded a target of 303 participants. In practice, logistical and security constraints inherent to the post-conflict setting limited enrollment to 213 administered questionnaires, of which 191 were complete and exploitable. Socio-demographic and clinical data obtained through questionnaires and the results of laboratory tests were entered, cleaned and analyzed using the statistical software for social sciences (SPSS) version 22.1. Categorical variables were summarized as frequencies and percentage. Associations between sociodemographic characteristics and HIV status, smear microscopy result, and infection status were assessed using the chi-square test of independence, with Fisher's exact test applied where expected cell counts were below 5. Pearson's chi-square test was used for the 2x2 comparison between HIV status and smear microscopy result. A P-values < 0.05 was considered statistically significant.

3. Results

3.1. Epidemiological Results of Study Population

Sociodemographic Characteristics of the Study Population

From the study population, chosen 191 readily available participants information from the Maroua Regional Hospital, the Mokolo and Koza District Hospitals, the Koza Adventist Hospital and the Minawao Health Center were selected. The rest being incompletely filled. The sociodemographic characteristics described below cover age, sex, area of residence, main occupation and infectious status (Table 1).

Table 1. Sociodemographic characteristics of the study population (n = 191).

Variables	Numbers	Frequencies (%)
Age		
15-30 years	61	31.9
30-45 years	75	39.3

Variables	Numbers	Frequencies (%)
45-60 years	33	17.3
60-75 years	18	9.4
Under 15 years	1	0.5
Over 75 years	3	1.6
Sex		
Female	50	26.2
Male	141	73.8
Residence		
Rural	47	24.6
Urban	144	75.4
Main occupation		
Farmer/herder	49	25.7
Butcher	8	4.2
Trader	30	15.7
Student (school)	8	4.2
Employee	3	1.6
Civil servant	17	8.9
Informal - porter	2	1.0
Informal - pusher	1	0.5
Mason	2	1.0
Mechanic	8	4.2
Housewife	37	19.4
Moto-taxi/driver	16	8.4
Prisoner	10	5.2
HIV test result		
Negative	165	86.4
Positive	26	13.6
Infection status		
No infection	38	19.9
Co-infection	19	9.9
TB mono-infection	127	66.5
HIV mono-infection	7	3.7

Regarding age distribution, the most represented age group was 30–45 years (39.3%), followed by 15–30 years (31.9%). These two groups together accounted for 71.2% of the sample, indicating that the affected population is predominantly composed of young adults of working age. Other age range Participants constituted only 28.8% of the total.

In terms of sex, our study population comprised 191 individuals, predominantly male (141/191, 73.8%), yielding a male-to-female ratio of approximately 2.8:1. Regarding area of residence, three-quarters of participants (75.4%) lived in urban areas, with only 24.6% residing in rural settings, reflecting the predominance of tuberculosis in densely populated ur-

ban environments. With respect to educational level, the majority had attained secondary education (50.3%), 35.1% had primary education, and 13.1% were illiterate. Only 1.6% had reached university level. As for occupation, farmers and livestock keepers constituted the largest occupation.

3.2. Paraclinical and Clinical Characteristics — TB and HIV Prevalence

Figure 2 presents the results of paraclinical and clinical examinations performed on all 191 participants of the study population. Two tests were conducted: sputum smear microscopy

for the detection of mycobacteria (tuberculosis), and an HIV serological screening test.

Regarding tuberculosis, 146 out of 191 participants tested positive by sputum smear microscopy, yielding a prevalence of 76.4%. With respect to HIV serological status, 26 participants were HIV-positive (13.6%), while 165 were HIV-negative (86.4%). The cross-tabulation of both results revealed that among the 146 TB-positive participants, 19 were also HIV-positive, representing a co-infection rate of 13.0% among TB patients (19/146) and 9.9% across the entire study sample (19/191).

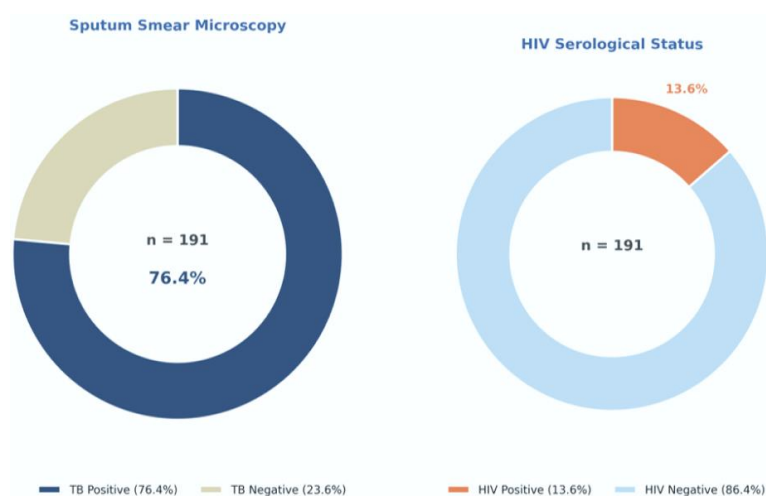


Figure 2. Sputum smear microscopy result (left) and HIV serological status (right) (n = 191). TB prevalence: 76.4%; HIV seroprevalence: 13.6%.

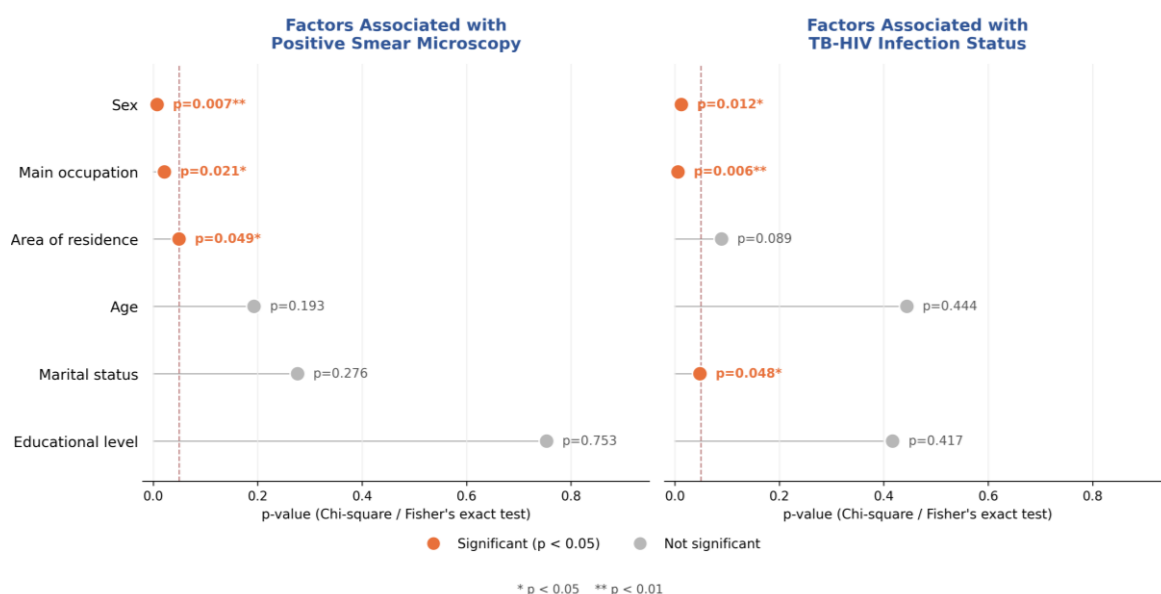


Figure 3. Sociodemographic factors associated with TB and TB-HIV co-infection (n = 191).

Sociodemographic factors associated with positive smear microscopy (left) and TB-HIV infection status (right), n = 191. * p < 0.05; ** p < 0.01.

Sociodemographic Factors Associated with TB and TB-HIV Co-infection

The analysis of factors associated with tuberculosis and TB-HIV infection status was conducted using cross-tabulations with the chi-square test of independence and Fisher's exact test applied according to expected cell counts. A p-value below 0.05 was considered statistically significant.

Sex, main occupation, and area of residence were significantly associated with positive smear microscopy ($p=0.007$, $p=0.021$, and $p=0.049$, respectively), while age, marital status, and educational level showed no significant association. For TB-HIV infection status, sex, main occupation, and marital status were significantly associated ($p=0.012$, $p=0.006$, and $p=0.048$, respectively), whereas area of residence, age, and educational level were not significant.

3.3. Results of Tuberculous Mycobacteria Cultures and Resistance Pattern to First Line Anti-Tb Drugs

From our study population of 119 positive cultures, 108 *Mycobacterium tuberculosis* isolates were analyzed for susceptibility to first-line anti-tuberculosis drugs (11 cultures being contaminated) including isoniazid (INH), rifampicin (RIF), streptomycin (STM), and ethambutol (EMB). Resistance to isoniazid was detected at 1.9% (2/108) at low concentration

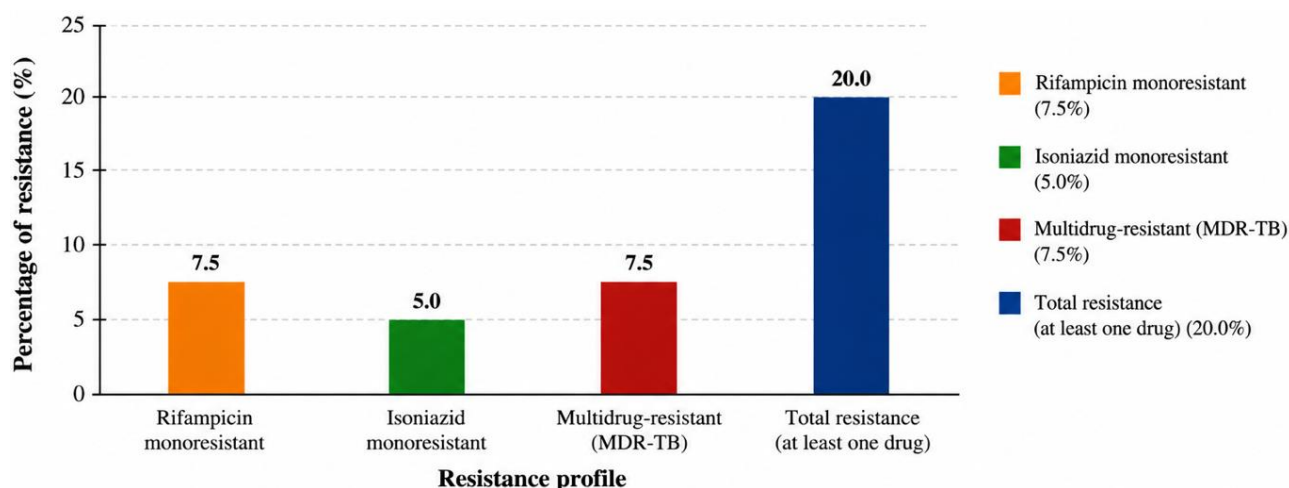
(INH0.2) and 3.7% (4/108) at high concentration (INH1). Rifampicin resistance was identified 1.9% (2/108). The highest resistance rate was observed for streptomycin at 10.2% (11/108), followed by ethambutol at 5.6% (6/108). Importantly, 2.7% were (MDR-TB).

3.4. Drug Resistance Profile Results to Molecular Hybridization Using the Line Probe Assay (Lpa)

Forty culture strains were subjected to Hybridization and detection performed with LPA (MTB/DRplus version 1.0 kit). Thirty-two (80%) isolates were found to be sensitive to both rifampicin (RIF) and isoniazid (INH), while 8 (20%) isolates exhibited resistance to at least one of these first-line anti-tuberculosis drugs, (*rpoB* gene (rifampicin resistance): 6 (75%) isolates harbored the D516V mutation at codon 516, among which 3/6 were associated with multidrug resistance. 1 (12.5%) isolate in both *katG* gene (isoniazid resistance) with S315T mutation at codon 315, associated with multidrug resistance and *inhA* promoter region (isoniazid resistance) combined mutations C-15T and A-16G, associated with multidrug resistance were observed. Three (7.5%) isolates showed rifampicin monoresistance, 2(5%) isolates showed isoniazid monoresistance and 3 (7.5%) isolates exhibited multidrug resistance (MDR-TB). Two isolates (25%) had the C-15T mutation alone.



Figure 4. Hybridized strips after laboratory manipulations.



* $p < 0.05$ — significant ** $p < 0.01$ — highly significant Values in red indicate statistically significant associations.

Figure 5. Percentage of resistance of mycobacterium tuberculosis complex strains.

Table 2. Distribution of mutation detected in resistant isolates.

Gene	Mutation	Number of isolates (n=8)	Percentage (%)	Associated resistance
rpoB	D516V	6	75.0	Rifampicin
katG	S315T	1	12.5	Isoniazid
inhA	C-15T + A-16G	1	12.5	Isoniazid
inhA	C-15T	2	25.0	Isoniazid

4. Discussion

Effective management of drug-resistant tuberculosis relies on several elements, including detection, treatment, prevention, surveillance, and ongoing program evaluation. The main aim of this research was to determine the prevalence of tuberculosis, resistance to anti-tuberculosis drugs and genotyping the isolates of MTBC among patients in Far-North region. we observed the predominance of males (73.8%) and a median age range of 30-45 years (33.0%), consistent with the established profile of TB in sub-Saharan Africa, where the disease disproportionately affects young adults in their prime productive years [2]. The majority of participants were urban residents (75.4%), employed in farming or livestock keeping (25.1%), in monogamous unions (53.4%), and had secondary-level education (50.3%), reflecting the socioeconomic fabric of the Diamar éDivision, where 75% of the population lives in absolute poverty [19].

The prevalence of bacteriologically confirmed tuberculosis by sputum smear microscopy was 76.4% (146/191). This high figure is primarily attributable to the facility-based recruitment in CDTs, where patients are referred because TB is already suspected or confirmed. Co- infection rate was 9.9% of the total sample (19/191) or 9.1% among confirmed TB cases. These figures are below the national PNLT estimate of 20.3%

HIV among TB patients in 2021 (down from 35.8% in 2015) [20], reflecting the structurally lower HIV prevalence in our study population. In neighboring Niger, [21] found 6.93% at the Niamey national anti-TB center. In Chad, which directly borders our study area, a national TB epidemiology study reports 7.4% TB-HIV co-infection, with strains predominantly of the 'Cameroon' genotype (43%) — confirming the molecular continuity of TB transmission across this transboundary region [22].

Three sociodemographic variables showed statistically significant associations with TB. Male sex was the strongest predictor ($p = 0.007$), with a male-to-female ratio of 2.8:1 among TB-positive cases. This finding is corroborated across the regional literature: Kuaban A. et al., (2021) [23] identified male sex as an independent predictor of unfavorable TB outcomes in Cameroon ($p < 0.001$), and Balkissou et al., (2021), [24] in a retrospective cohort covering the North and West regions of Cameroon, confirmed that male sex significantly increased the risk of death during TB treatment. These male-driven patterns align with WHO global data (54% of 2024 TB cases were men) [2] and are explained by greater occupational exposure, risky social behaviors, and well-documented barriers to care-seeking among men in the Far-North [19]. Urban residence also was significantly associated with TB ($p = 0.049$), with 75.4% of participants residing in urban areas. Occupation showed a

significant association with TB ($p = 0.021$). Farmers /hearer were the most represented group (25.7%), followed by housewife (19.4%), traders (15.7%), moto-taxi drivers (8.4%) and Prisoners (5.2%), all TB-positive, shaping the occupational profile of TB risk.

Concerning drug susceptibility testing, we noticed a rifampicin resistance of 1.9% in our study, suggesting a relatively low burden of drug-resistant tuberculosis, but however different from the higher rates reported in urban regions such as the Littoral, where rifampicin resistance reached 6.7%. this finding may reflect differences in treatment access, prior Tb treatment history, and diagnostic referral patterns between rural Far -North settings and more centralized urban regions of Cameroon. The Isoniazid resistance (up to 3.7%) aligns with previous studies in Cameroon showing that isoniazid mono-resistance is one of the most common resistance patterns, often associated with mutations in the *katG* and *inhA* genes [25, 26]. The concentration-dependent pattern observed here, with a higher resistance rate at INH1 than at INH0.2, is consistent with the presence of both high-level and low-level isoniazid resistance mechanisms within the study population, further revealing the clinical relevance of testing at multiple drug concentration to avoid underestimating resistance. these findings emphasize the clinical importance of highlighting significant geographical disparities within the country and detecting isoniazid and rifampicin resistance, as it may compromise the effectiveness of standard first-line treatment regimens.

The highest resistance rate observed for streptomycin (10.2%) is consistent with earlier reports from Cameroon and neighboring countries. Studies conducted in Nigeria have documented persistently high levels of streptomycin resistance, reflecting its historical overuse and widespread availability [27]. This suggests that streptomycin resistance in the region may largely reflect legacy treatment practices rather than ongoing programmatic failures.

Regarding multidrug resistance, we recorded 3 cases (2.7%). These results remain lower than the 4.8% obtained in the Littoral [28]. This could be explained by the lower proportion of previously treated or retreated TB cases within the study population. Indeed, retreatment cases are well known to have a significantly higher risk of developing MDR-TB due to prior exposure to anti-tuberculosis drugs and possible inadequate treatment adherence. This result could also be associated to the difference in access to diagnostics tools, particularly assays such as GeneXpert. Limited access to advanced diagnostics in the Far-North region could have led to under detection of resistance cases in our study, thereby contributing to a lower observed prevalence.

Regarding the *rpoB* gene, six (75%) of the eight (100%) resistant strains carried the D516V mutation at codon 516, of which three were associated with multidrug resistance. Although the common mutations associated with rifampicin resistance are amino acid alterations at codons 531, 526, and 516 [29]; This could be due to differences in strains and lineages. It is likely that among the strains included in this study, some

did not belong to the lineages which could be commonly encountered in this area, or that the strains typically found in this area may have undergone mutations that favored a greater predisposition toward mutation at codon 516.

For the *katG* gene, one strain (12.5%) carried the S315T mutation at codon 315, which was associated with multidrug resistance. The S315T mutation has been the most studied *katG* mutation worldwide and has been used in most tests as a molecular target to detect isoniazid [30]. Therefore, the low rate of *katG* mutations detected by this study may not reflect the true prevalence. Consequently, the use of new *katG* gene probes or further molecular analysis to detect new mutations that have been selected under therapeutic pressure or have evolved in different geographic areas would be needed to improve detection.

Regarding the *inhA* gene, only one (12.5%) simultaneously carried the mutations C-15T at position -15 and A-16G at position -16, associated with multidrug resistance, and 2 carried a C-15T mutation (25%). Conversely, a relatively low frequency (2.0%) of mutations in the *inhA* regulatory region has been observed in Zambia [30] and in Nigeria [16]. These results would probably be due to the fact that mutations in the *inhA* region confer low-level resistance to isoniazid, but when they occur in combination with mutations in the *katG* gene, an increase in the levels of resistance to isoniazid is observed; This would explain the low rate of isoniazid resistance observed in these results.

The apparent discordance between the MDR-TB prevalence estimated by phenotypic testing (2.7%, $n=108$) and molecular testing (7.5%, $n=40$) should not be interpreted as a direct contradiction, but rather as a consequence of differing sample scope and detection principles between the two methods. First, the two assays were performed on non-equivalent sample sizes. Beyond sampling considerations, phenotypic and genotypic testing interrogate resistance through fundamentally different mechanisms. Phenotypic DST measures observed bacterial growth in the presence of the drug and can be influenced by inoculum size, culture viability, and the presence of heteroresistant subpopulations, where a dominant susceptible population may mask a minority resistant clone. LPA, in contrast, detects specific mutations within defined hot-spot regions of the *rpoB*, *katG*, and *inhA* genes; while highly sensitive for common mutations such as *rpoB* D516V, it cannot detect resistance-conferring mutations located outside these targeted regions, nor resistance mechanisms unrelated to the genes covered by the assay, such as efflux-pump-mediated resistance. This asymmetry explains why molecular assays can, in some instances, detect more genetic resistance markers than are phenotypically expressed, and conversely why some phenotypically resistant strains may lack any mutation identifiable by LPA.

Such phenotype-genotype discordance has been widely documented in the literature, with concordance rates for rifampicin typically reported between 85% and 95%, and some-

what lower for isoniazid, reflecting the greater genetic heterogeneity underlying INH resistance mechanisms. Taken together, these observations support the complementary rather than interchangeable nature of phenotypic and molecular drug susceptibility testing in this setting, with LPA serving as a valuable rapid triage tool while phenotypic DST remains the reference standard for confirming and fully characterizing resistance.

5. Conclusion

This first regional assessment shows a high burden of TB and TB-HIV co-infection in the Far-North Region, a post-conflict, cross border setting where population movement likely worsens diagnostic delay. TB was associated with male sex, urban residence, and agricultural occupation. The higher MDR rate by LPA (7.5%) versus culture-based resistance (rifampicin 1.9%, isoniazid 3.7%) confirms the greater sensitivity of molecular methods, especially relevant given paucibacillary disease risk in HIV-positive patients. These findings support scaling up molecular diagnostics (Xpert MTB/RIF, LPA) and cross-border surveillance in this underserved region.

Abbreviations

TB	Tuberculosis
HIV	Human Immunodeficiency Virus
AIDS	Acquired Immunodeficiency Syndrome
UNAIDS	Joint United Nations Programme on HIV/AIDS
MDR (MDR-TB)	Multidrug-Resistant (Tuberculosis)
DR	Drug Resistance
DST	Drug Susceptibility Testing
CDT	Tuberculosis Diagnosis and Treatment Center
MTB	Mycobacterium Tuberculosis
MTBC	Mycobacterium Tuberculosis Complex
LJ	Löwenstein-Jensen
RIF	Rifampicin
INH	Isoniazid
EMB	Ethambutol
STM	Streptomycin
LPA	Line Probe Assay
DNA	Deoxyribonucleic Acid
SPSS	Statistical Package for the Social Sciences
BP	Base Pairs

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Assam Assam Jean Paul: Conceptualization, Data curation, Formal Analysis, Funding acquisition, Investigation, Methodology, Project administration, Resources, Supervision, Validation, Writing – review & editing

Youchaou Mobet: Data curation, Methodology, Writing – original draft

Yonga Tchoumi Loida Cindy: Writing – original draft

Beack Bayengue Sandrine Suzanne: Writing – original draft

Njike Ngamga Fabrice Herve: Writing – original draft

Ngono Ngane Rosalie Annie: Conceptualization, Funding acquisition, Investigation, Methodology, Project administration, Resources, Supervision, Validation

Penlap Beng Veronique: Conceptualization, Funding acquisition, Methodology, Project administration, Resources, Supervision, Validation

Conflicts of Interest

The authors declare no conflicts of interest.

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