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Research Article

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Characterization of Beijing Strains of Mycobacterium Tuberculosis and Analysis of Risk Factors Associated with Multidrug-Resistant Tuberculosis in the Republic of Congo

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ABSTRACT
In the Republic of Congo, the lack of national data on resistance to anti-tuberculosis drugs aggravates the difficulties of caring for patients with multidrug-resistant tuberculosis. The aim is to specifically detect Beijing strains of Mycobacterium tuberculosis, which are known for their increased drug resistance. We used samples from patients with confirmed tuberculosis, collected via Genexpert technology, to extract DNA. The extracted DNA was then used to perform multiplex PCR, allowing for further analysis. The results of the study show that 30 patients with tuberculosis, 53,33% were women and 80% were single. In terms of medical history, 80% of patients had received BCG vaccine, and 66.67% were not on TB treatment. Common clinical symptoms included cough (100%), asthenia (73.33%), and anorexia (76.67%). Among the risk factors, 73.33% of of patients consumed alcohol and 30% tobacco. Finally, the Beijing strain of Mycobacterium tuberculosis was detected in 4 patients (13.33%), and 4 (13.33%) were also HIV-positive.

Introduction

Tuberculosis remains a major public health challenge in the Republic of Congo, where the annual incidence in 2022 reached 378 cases per 100,000 inhabitants, and HIV-tuberculosis co-infection affected 112 people per 100,000 inhabitants [1]. These statistics reflect an ongoing battle against an infection which, in addition to being endemic, is becoming increasingly resistant to standard treatments. It is currently estimated that 2.4% of new cases of tuberculosis in the Congo are resistant to standard anti-tuberculosis treatments, a threat reinforced by the lack of national data on drug resistance in Mycobacterium tuberculosis. This lack of data is crucial because it limits the effectiveness of control measures and therapeutic adjustments. Multidrug-resistant TB (MDR-TB) and its even more formidable form, extensively drug-resistant TB (XDR-TB), impose complex challenges on clinicians, making diagnosis and treatment increasingly time-consuming and costly [2]. XDR-TB, resistant to rifampicin and isoniazid (like MDR-TB), but also to at least one second-line drug such as fluoroquinolones or injectable medicines, has proved particularly difficult to treat and represents an increased risk of spread within communities [3].

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Among the Mycobacterium tuberculosis lineages, the Beijing strain of lineage 2 stands out for its high transmission potential and superior virulence, leading to severe forms of the disease [4,5]. Its presence, combined with its ability to evade the GeneXpert test, the most commonly used rapid diagnostic test, often delays adequate management of patients, leaving the disease to progress dangerously [6]. Meanwhile, patients' health can deteriorate rapidly, with a high risk of death in some cases [7].

There is an urgent need to step up early detection, improve diagnosis and develop innovative treatment strategies. With this in mind, a previous study conducted in Brazzaville in 2017 identified Mycobacterium tuberculosis complex (MTBC) isolates, including strains of the Delhi/Central Asian lineage and the Beijing lineage, both known for their virulence and potential for rapid spread [8]. Effective management of MDR-TB and XDR-TB is therefore a major public health challenge, requiring ongoing efforts in screening, diagnosis, treatment and prevention [9].

Materials and Methods

The study was conducted in Brazzaville, between December 2022 and July 2023, at the Tuberculosis Centre, and involved Genexpert amplicon and blood samples. The study targeted adult patients with a positive GeneXpert test result and examined socio-demographic and biological variables, including Rifampicin resistance and TB-HIV co-infection.

Specimens

159 morning sputum samples were collected from patients with or without a history of pulmonary tuberculosis. Mycobacterium tuberculosis appeared in all Ziehl-Neelsen (ZN)-stained sputum smear samples. These 33 sputum samples were then treated with GeneXpert MTB / RIF (Xpert assay; Cepheid, Sunnyvale, CA, USA) to detect the presence of M. tuberculosis bacilli and rifampin resistance.

Detection of Beijing and Non-Beijing Strains by Multiplex PCR

An experimental PCR technique that does not require cultures or a biosafety infrastructure has been developed to detect Mycobacterium tuberculosis lineage types. This method uses the remaining sputum samples prepared for the Xpert test to identify the lineage of circulating Beijing and non-Beijing strains. This strategy was used, by Alame-Emane et al, to define the nature and extent of TB drug resistance in Libreville, Gabon [10]. Molecular detection of the Beijing strain of Mycobacterium tuberculosis by multiplex PCR is based on targeted amplification of a specific DNA sequence using Taq polymerase. Primers used include : for non-Beijing strains, nBjF (5′-AAGCATTCCCTTGACAGTCGAA-3′) and nBjR (5′-GGCGCATGACTCGAAAGAAG-3′), as well as the nBjTM probe (5′-6FAM-TCCAAGGTCTTTG-MGB-NFQ-3′), and for Beijing strains, BjF (5′-CTCGGCAGCTTCCTCGAT-3′), BjR (5′-CGAACTCGAGGCTGCCTACTAC-3′) and the BjTM probe (5′-YAK AACGCCAGAGACCAGCCGCCGGCT-DB-3′). Each primer was used at a final concentration of 0.32 µM in the reaction mixture. The PCR protocol, performed in a final volume of 25 µL, includes the addition of 1 µL of DNA, 1 µL of each primer, a master mix containing dNTPs and Taq polymerase, and distilled deionised water. The amplification programme included predenaturation at 95°C, denaturation at 95°C, hybridisation at 55°C and elongation at 72°C, repeated over 30 cycles, allowing accurate identification of Beijing and non-Beijing strains of Mycobacterium tuberculosis. Agarose gel electrophoresis is an essential method in molecular biology for separating and analysing DNA fragments amplified by PCR, enabling the size of amplicons to be assessed. To prepare a 3% gel, 3 g of agarose are mixed in 100 mL of TAE buffer, then heated and ethidium bromide added to visualise the DNA under UV light. The samples were then migrated at 100 Volts for 45 minutes. The expected fragments were 95 bp for non-Beijing strains and 129 bp for Beijing strains, allowing a clear assessment of their presence by comparison with a molecular weight marker.

Approval and Ethical Considerations

The Health Science Research Ethics Committee (CERSSA) of the Institut National de Recherche en Science de la Santé (IRSSA) approved the study (Decision 23022015-1). After a written or oral explanation, the patients signed an informed consent to authorise the use of their sputum and blood samples in the study and to provide socio-demographic data and information on previous anti-tuberculosis treatment.

Statistical Analyses

The data collected were entered and analysed using Epi Info software, version 7.2.6.0 and Microsoft Excel. The chi-square test or Fischer exact test was used to compare proportions, with a significance level of 5%.

Results

Epidemiology of MDR-TB Patients

Epidemiological data on MDR-TB patients are summarised in Figures 1, 2 and 3. Among the patients analysed, the distribution according to sociodemographic characteristics reveals equality between the sexes, with a total of 50% men and 50% women. The average age of the participants was 32 years, with a wide range from 18 to 54 years. In terms of medical history, Figure 2 shows that 70% of patients had a history of TB treatment, while 30% had never been treated before. Risk factors associated with MDR-TB are illustrated in Figure 3, showing that 40% of patients were co-infected with HIV, and 25% had a history of smoking. These data underline the importance of monitoring risk factors in the management of MDR-TB.

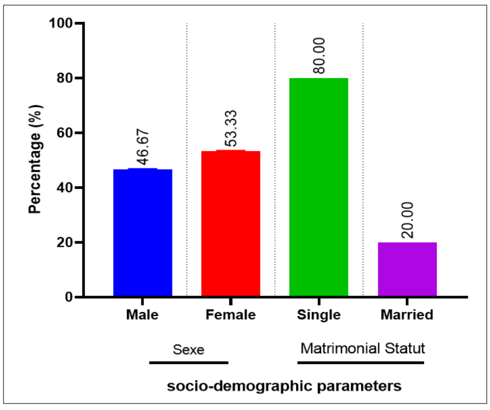

Figure 1 : Distribution of patients by socio-demographic characteristics

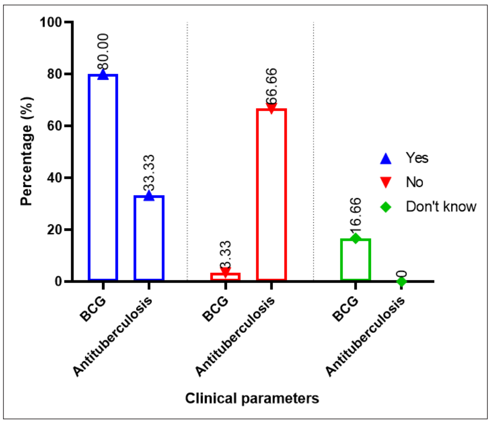

Figure 2: Distribution of individuals according to medical history

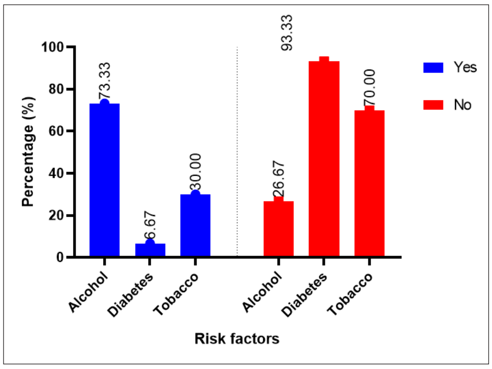

Figure 3 : Distribution of individuals according to risk factor characteristics

Identification of Mycobacterium Tuberculosis Strains in a Sample of Tuberculosis Patients

Of morning sputum analysed on the Xpert instrument, 30 were positive for M. tuberculosis and resistant to my rifampicin (17%). The remnants of the amplicons, which is Mycobacterium tuberculosis DNA used to identify the Beijing strain, a multiplex gradient PCR targeting the Rv2820 gene was performed. The results showed that samples 33, 28, 29 and 30 were positive for amplification of the targeted gene. The amplicons were obtained at the expected sizes as shown in Figure 4. Table 1 shows that 4 patients (13.33%) were due to the Beijing strain of Mycobacterium tuberculosis, 26 patients (86.67%) were not due to the Beijing strain, 4 patients (13.33%) were HIV positive, 26 patients (86.67%) were not HIV positive. Of the 30 cases of tuberculosis studied, only 4 (13.33%) were due to the Beijing strain of Mycobacterium tuberculosis. This low percentage indicates that, in this specific sample, the Beijing strain is not the most dominant. The majority of cases (26 cases, or 86.67%) were caused by other strains of Mycobacterium tuberculosis, suggesting significant genetic diversity in this sample. Of the 30 patients with tuberculosis, 4 (13.33%) were also HIV-positive. The majority of patients (26, 86.67%) were not infected with HIV. Of the 30 patients with tuberculosis, 10 (33.33%) were on anti-tuberculosis treatment. The majority of patients (20, or 86.67%) were not on treatment. Table 3 shows that 57.14% of patients on anti-tuberculosis treatment were men, whereas 12.50% of patients on treatment were women, with a significant difference (p = 0.01). These results suggest that there is a significant association between gender and tuberculosis drug history.

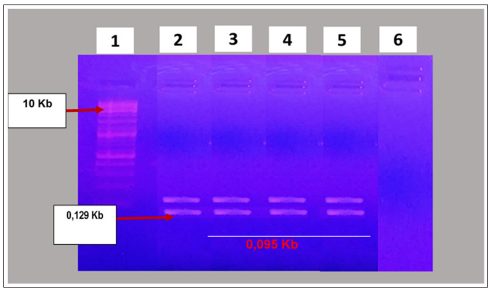

Figure 4 : Electrophoretic profil size of pcr products of Beijing strain on agarose gel 3%.
1: Molecular weight targett, 2: sample 1, 3: sample 2, 4: sample 3, 5: sample 4, 2=6: sample 5

Table 1: Distribution of Individuals According to Biological Characteristics

Biological variables	Numbers	N (%)	IC (95 %)
Beijing strain			
Yes No	4 26	13.33 86.67	3.76-30.72 69.28-96.24
HIV serology			
Yes No	4 26	13.33 86.67	3.76-30.72 69,28-96.24

Table 2: Breakdown of Patients by Anti-Tuberculosis Drug Resistance Status

On anti-tuberculosis treatment	N (%)	IC (95%)
No Yes	20 (66.67%) 10 (33.33%)	47.19-82.71 17.29-52.81
Total	30 (100%)	

Table 3: Breakdown of Patients by Sex and History of Anti-Tuberculosis Treatment

Gender	On anti-tuberculosis treatment		P-value (Fisher exact)
	Yes	No	
M	8 (57.14%)	6 (42.86%)	0,01
F	2 (12.50%)	14 (87.50%)	
Total	10 (33.33%)	20 (66.67%)	

Discussion

The data from our study reveal typical sociodemographic and clinical profiles of patients with tuberculosis. The slight predominance of males and the high rate of unmarried patients may reflect socioeconomic factors influencing susceptibility to the disease or access to care. Clinical features show a high prevalence of severe respiratory and systemic symptoms, which is consistent with the classic presentation of pulmonary TB. The high proportion of individuals with weight loss and anorexia indicates the significant impact of TB on patients' nutrition and general condition. The history of BCG vaccination in the majority of patients suggests high vaccination coverage, but the efficacy of this vaccination against severe or resistant forms of TB remains limited. The significant proportion of patients who had already received anti-tuberculosis treatment (33.33%) could indicate a prevalence of multidrug-resistant tuberculosis in this sample. The presence of the Beijing strain in 13.33% of patients, combined with the same percentage of HIV-positive patients, highlights the complexity of managing pulmonary tuberculosis in vulnerable populations. These risk factors increase the difficulty of treatment and the likelihood of transmission, necessitating targeted public health interventions and rigorous clinical management to reduce associated morbidity and mortality.

Prevalence of the Beijing Strain

In this sample of 30 pulmonary tuberculosis cases, the Beijing strain was not dominant, despite its concerning characteristics such as infection severity and potential treatment resistance. This indicates that in this specific population, non-Beijing strains are more common. This observation is consistent with several studies conducted in Africa. A study conducted in Nairobi, Kenya, found that, although present, the Beijing strain was not predominant among tuberculosis patients, but other studies have shown the significant presence of this strain [11,12]. Contrary to what is observed in many other regions, an analysis carried out in Malawi showed that non-Beijing strains were more prevalent than the Beijing strain of Mycobacterium tuberculosis [13]. These results highlight that the prevalence of the Beijing strain can vary significantly depending on the region and context. Previously, a study conducted in Brazzaville in 2017 detected 74 strains of the Mycobacterium tuberculosis complex (MTBC), including two strains of the Delhi/Central Asian lineage and one strain of the Beijing lineage. These strains, known for their virulence and rapid spread, can be attributed to migratory movements and international trade, facilitating the introduction and dissemination of exogenous strains in the region. Their presence in Brazzaville underscores the importance of strengthening surveillance and prevention measures to control their impact [8]. Analysis of our data shows that the diversity of pulmonary tuberculosis strains must be taken into account in disease control strategies. The presence of non-dominant strains such as the Beijing strain in some African populations may reflect specific local dynamics. Beijing strains are distributed worldwide and are associated with both treatment failure in some countries, leading to higher morbidity and mortality Zignol et al and an increased risk of transmission chains transmission [14,5]. The Beijing genotype has been shown to be more virulent than other MTB genotypes, showing higher pathogenicity as well as increased mortality in epidemiological studies [15]. This strain is also reported to be associated with a higher risk of developing multidrug-resistant tuberculosis (MDR-TB) and treatment failure thérapeutique [16]. Another particular characteristic of the Beijing genotype is its higher mutation rate, which facilitates the emergence of drug resistance [15]. The strong association between the Beijing genotype and drug-resistant tuberculosis is highlighted by the higher proportion of this lineage among MDR-TB and/or XDR-TB cases compared to drug-susceptible TB [9]. It is therefore crucial to develop effective tuberculosis control strategies that take into account local genetic diversity.

HIV Coinfection and Tuberculosis

HIV coinfection is a major risk factor for progression to active tuberculosis. In this sample, 13.33% of tuberculosis cases were associated with HIV infection. This rate, although relatively low compared to some regions with high HIV prevalence, is significant and deserves special attention in terms of treatment and prevention. The majority of pulmonary tuberculosis cases (86.67%) occur in HIV-uninfected individuals, indicating that tuberculosis remains a significant threat even in the absence of HIV coinfection in this population. A literature review on the impact of HIV on the prevalence and progression of tuberculosis in sub-Saharan Africa shows how HIV increases the risk of developing active tuberculosis. However, it also notes significant rates of pulmonary tuberculosis among HIV-uninfected individuals [17]. Another study examined the prevalence and factors associated with tuberculosis/HIV coinfection. This study found that although coinfection is a major concern, pulmonary tuberculosis is also prevalent among HIV-uninfected individuals [18,19]. These findings suggest that pulmonary tuberculosis treatment and prevention efforts should not focus solely on HIV-coinfected populations but should also include strategies targeting HIV-uninfected individuals.

Primary and Secondary Antituberculosis Drug Resistance

The majority of patients in this sample (66.67%) had not been previously treated for pulmonary tuberculosis, implying that drug resistance in this group will primarily be primary. This form of primary resistance found in our study is concerning because it reflects the transmission of resistant strains in the community. A high rate of primary resistance indicates the spread of resistant strains within the population, complicating disease management. Previous studies have addressed antibiotic resistance and its spread, particularly in the environment, which contributes to the emergence and dissemination of resistant bacterial [20,21]. This phenomenon complicates the treatment of infections, limiting the effectiveness of antibiotics and requiring more strategic approaches to control the spread of resistant pathogens in the population. One-third of patients (33.33%) have been previously treated for pulmonary tuberculosis, indicating that drug resistance in this group is primarily related to secondary resistance. Secondary resistance suggests challenges in the management of previously treated patients, potentially related to poor treatment adherence or problems with treatment protocols. Previous studies have addressed factors that influence treatment adherence, highlighting how poor adherence or difficulties in administering treatments can lead to secondary resistance [22,16]. Innovative drug delivery systems are being explored to improve adherence, addressing the barriers that hinder the effective management of patients requiring prolonged follow-up. Effective tuberculosis management must include strategies to prevent both the transmission of resistant strains (by reducing primary resistance) and the emergence of new resistance in previously treated patients, thereby reducing secondary resistance. This research highlights the importance of comprehensive strategies to combat multidrug-resistant tuberculosis, including the prevention of the transmission of resistant strains and rigorous treatment management in previously treated patients [23,24]. This helps limit the emergence of secondary resistance, which further complicates treatment, but also underscores the importance of rigorous patient screening and monitoring to effectively identify and treat cases of resistance.

Gender Disparities in Anti-TB Treatment

Data show that 80% of patients receiving anti-TB treatment are women, while 70% of patients with no prior treatment are men. This suggests that women in this sample are significantly more likely to have been receiving TB treatment compared to men. Several factors could explain this difference. First, there may be gender disparities in access to healthcare. Women may have better access to or adherence to TB treatment programs. Furthermore, they may be more frequently diagnosed and treated for pulmonary TB than men, which could reflect differences in clinical presentation or diagnostic and treatment practices. One study also showed that biological differences between the sexes may influence susceptibility to TB [25]. Moreover, according to a consensus statement on gender and TB, women and men face distinct challenges in managing this disease, which may affect their care pathways [26]. These findings highlight the need to adjust TB treatment and prevention strategies to address the specific needs of men, who appear to be less frequently treated or diagnosed with a history of TB treatment. Improving access and adherence to treatment among men to reduce observed disparities is becoming crucial.

Limitations of the Study

The main limitation of this study is the small sample size, with only 30 cases. A sample of this size may not be representative of the general population, limiting the generalisability of the results. In addition, with a small number of participants, statistical analyses may lack power, reducing the ability to detect significant differences between groups or to establish robust relationships between variables.

Conclusion

The results of this study reveal a marked genetic diversity of Mycobacterium tuberculosis strains in the Brazzaville population studied, with a preponderance of non-Beijing strains, and a limited but significant presence of the Beijing strain. This low level of the Beijing strain, although worrying because of its virulence and potential resistance, suggests that other Mycobacterium tuberculosis lineages play an important role in the dynamics of tuberculosis in the Congo. In addition, the proportion of cases of multi-drug-resistant tuberculosis, and the TB-HIV co-infection observed in some patients, highlight the challenges posed to clinical management and infection control.

These observations highlight the need to step up epidemiological surveillance, improve access to advanced diagnostic tests such as multiplex PCR for more accurate strain identification, and develop appropriate treatment strategies for resistant cases. It is also essential to step up public health interventions focusing on awareness, prevention and early detection, targeting vulnerable groups and HIV co-infected patients in particular. This type of integrated strategy could help to reduce the transmission, morbidity and mortality associated with tuberculosis in this region, thereby responding to an urgent public health need in the Republic of Congo.

References

1. WHO. Global Tuberculosis Report 2023. Geneva: WHO. 2023.
2. Dheda K, Gumbo T, Maartens G, Dooley KE, McNerney R, et al. The epidemiology, pathogenesis, transmission, diagnosis, and management of multidrug-resistant, extensively drug-resistant, and incurable tuberculosis. The lancet Respiratory medicine. 2017. 5: 291-360.
3. Falzon D, Schünemann HJ, Harausz E, González-Angulo L, Lienhardt C, et al. World Health Organization treatment guidelines for drug-resistant tuberculosis, 2016 update. European Respiratory Journal. 2017. 49.
4. Parwati I, van Crevel R, van Soolingen D. Possible underlying mechanisms for successful emergence of the Mycobacterium tuberculosis Beijing genotype strains. The Lancet infectious diseases. 2010. 10: 103-1 11.
5. Tao NN, He XC, Zhang XX, Liu Y, Yu CB, et al. Drug-resistant tuberculosis among children, China, 2006–2015. Emerging infectious diseases. 2017. 23: 1800.
6. Williamson DA, Roberts SA, Bower JE, Vaughan R, Newton S, et al. Clinical failures associated with rpoB mutations in phenotypically occult multidrug-resistant Mycobacterium tuberculosis. The international journal of tuberculosis and lung disease. 2012. 16: 216-220.
7. Fenner L, Egger M, Bodmer T, Altpeter E, Zwahlen M, et al. Effect of mutation and genetic background on drug resistance in Mycobacterium tuberculosis. Antimicrobial agents and chemotherapy. 2012. 56: 3047-3053.
8. Malm S, Linguissi LS, Tekwu EM, Vouvoungui JC, Kohl TA, et al. New Mycobacterium tuberculosis complex sublineage, Brazzaville, congo. Emerging infectious diseases. 2017. 23: 423.
9. Klotoe JB. Development of methods for the diagnosis, control, and surveillance of extensively drug-resistant tuberculosis and epidemic strains. Beijing (Doctoral dissertation, Université Paris Saclay (COmUE)). 2018.
10. Alame-Emane AK, Pierre-Audigier C, Aboumegone-Biyogo OC, Nzoghe-Mveang A, Cadet-Daniel V, et al. Use of GeneXpert remnants for drug resistance profiling and molecular epidemiology of tuberculosis in Libreville, Gabon. Journal of clinical microbiology. 2017. 55: 2105-2115.
11. Githui WA, Jordaan AM, Juma ES, Kinyanjui P, Karimi FG, et al. Identification of MDR-TB Beijing/W and other Mycobacterium tuberculosis genotypes in Nairobi, Kenya. The international journal of tuberculosis and lung disease. 2004. 8: 352-360.
12. Ogwang MO, Diero L, Ng'ong'a F, Magoma G, Mutharia L, et al. Strain structure analysis of Mycobacterium tuberculosis circulating among HIV negative, positive and drug resistant TB patients attending chest clinics in Western Kenya. BMC Pulmonary Medicine. 2023. 23: 497.
13. Glynn JR, Crampin AC, Traore H, Yates MD, Mwaungulu FD, et al. Mycobacterium tuberculosis Beijing genotype, northern Malawi. Emerging Infectious Diseases. 2005. 11: 150.
14. Zignol M, Dean AS, Falzon D, van Gemert W, Wright A, et al. Twenty years of global surveillance of antituberculosis-drug resistance. New England Journal of Medicine. 2016. 375: 1081-1089.
15. Keikha M, Majidzadeh M. Beijing genotype of Mycobacterium tuberculosis is associated with extensively drug-resistant tuberculosis: a global analysis. New Microbes and New Infections. 2021. 43: 100921.
16. Jin J, Sklar GE, Min Sen Oh V, Chuen Li S. Factors affecting therapeutic compliance: A review from the patient's perspective. Therapeutics and clinical risk management. 2008. 4: 269-286.
17. Gisso BT, Hordofa MW, Ormago MD. Prevalence of pulmonary tuberculosis and associated factors among

adults living with HIV/AIDS attending public hospitals in Shashamene Town, Oromia Region, South Ethiopia. SAGE open medicine. 2022. 10: 20503121221122437.

18. Zeru MA. Prevalence and associated factors of HIV-TB co-infection among HIV patients: a retrospective Study. African health sciences. 2021. 21:1003-1009.
19. Mitku AA, Dessie ZG, Muluneh EK, Workie DL. Prevalence and associated factors of TB/HIV co-infection among HIV Infected patients in Amhara region, Ethiopia. African health sciences. 2016. 16: 588-595.
20. Mancuso G, Midiri A, Gerace E, Biondo C. Bacterial antibiotic resistance: the most critical pathogens. Pathogens. 2021. 10: 1310.
21. Larsson DJ, Flach CF. Antibiotic resistance in the environment. Nature Reviews Microbiology. 2022. 20: 257-269.
22. Baryakova TH, Pogostin BH, Langer R, McHugh KJ. Overcoming barriers to patient adherence: the case for developing innovative drug delivery systems. Nature Reviews Drug Discovery. 2023. 22: 387-409.
23. Singh V, Chibale K. Strategies to combat multi-drug resistance in tuberculosis. Accounts of chemical research. 2021. 54: 2361-2376.
24. Liebenberg D, Gordhan BG, Kana BD. Drug resistant tuberculosis: Implications for transmission, diagnosis, and disease management. Frontiers in cellular and infection microbiology. 2022. 12: 943545.
25. Nhamoyebonde S, Leslie A. Biological differences between the sexes and susceptibility to tuberculosis. The Journal of infectious diseases. 2014. 15: S100-S106.
26. World Health Organization. Roadmap towards Ending TB in Children and Adolescents. 2nd ed. Geneva: World Health Organization. 2018.