STM JOURNALS

International Journal of
Antibiotics

ISSN:2584-2986
Volume 2, Issue 2, 2025
July -December
DOI (Journal): 10.37591/IJAB

https://journals.stmjournals.com/ijab

Review IJAB

Innovations in Tuberculosis Management: Advancements in Drug-Resistant TB Treatment and Rapid Diagnostics

Shireen Siddique[1], Priyanka Sharma[2,*]

Abstract

Tuberculosis (TB) remains one of the deadliest infectious diseases worldwide, exacerbated by the increasing prevalence of drug-resistant strains, such as multidrug-resistant (MDR-TB) and extensively drug-resistant TB (XDR-TB). Despite advancements in first-line and second-line treatments, resistance to conventional antibiotics has complicated therapeutic strategies, necessitating novel approaches. This mini review explores emerging advancements in TB treatment, including gene editing technologies, such as CRISPR, which offer potential for precise targeting of drug-resistant bacterial strains. Additionally, recent research has uncovered mechanisms underlying bedaquiline's enhanced efficacy in MDR-TB treatment, revealing metabolic vulnerabilities in resistant strains. Rapid diagnostic tools, including CRISPR-based platforms, have significantly improved TB detection and drug resistance profiling, enabling early and accurate interventions. Moreover, the development of shorter, all-oral regimens, such as the WHO-recommended BPaLM and BPaL regimens, has demonstrated high treatment success rates while reducing toxicity and improving patient adherence. These advancements signify a transformative shift in TB management, paving the way for more effective, patient-friendly, and sustainable treatment strategies.

Keywords: Tuberculosis, drug-resistant TB, CRISPR technology, bedaquiline, rapid diagnostics

INTRODUCTION

Tuberculosis (TB) is a highly contagious bacterial infection caused by *Mycobacterium tuberculosis*, primarily affecting the lungs but capable of spreading to other organs. The disease is transmitted through airborne particles when an infected individual coughs, sneezes, or speaks. Once inhaled, the bacteria multiply in the body, leading to symptoms, such as a persistent cough, fever, weight loss, and fatigue. Despite the availability of effective treatment, TB remains one of the world's deadliest infectious diseases and a leading cause of deaths related to antimicrobial resistance [1].

***Author for Correspondence**
Priyanka Sharma
E-mail: Priyanka30@yahoo.co.in

[1]Student, Department of Pharmacy, Barkatullah University, Bhopal, Madhya Pradesh, India.
[2]Faculty, Department of Pharmacy, Barkatullah University, Bhopal, Madhya Pradesh, India.

Received Date: February 21, 2025
Accepted Date: March 24, 2025
Published Date: March 28, 2025

Citation: Shireen Siddique, Priyanka Sharma. Innovations in Tuberculosis Management: Advancements in Drug-Resistant TB Treatment and Rapid Diagnostics. International Journal of Antibiotics. 2025; 2(2): 1–7p.

According to the World Health Organization (WHO) Global Tuberculosis Report 2024, TB once again became the leading cause of death from a single infectious agent worldwide in 2023, after being surpassed by COVID-19 for three years. The report, which includes data from 193 countries and territories – covering over 99% of the global population and TB cases – highlights the widespread impact of the disease. India carries a significant share of the global TB burden, accounting for 26% of cases – the highest among all countries – followed by Indonesia (10%) and China (6.8%). In 2024 alone, India reported over 2.55 million TB cases, making it the seventh leading cause of death in the country [1].

Despite advancements in antitubercular medications, the global TB burden remains a major public health crisis, exacerbated by the growing challenge of drug resistance. The standard treatment regimen for TB consists of a combination of antibiotics, categorized into first-line and second-line medications. The first-line drugs, commonly referred to as the "RIPE" regimen, include rifampicin, isoniazid, pyrazinamide, and ethambutol [2, 3]. Rifampicin, a potent bactericidal agent, inhibits bacterial RNA synthesis by targeting the RNA polymerase enzyme. However, resistance to Rifampicin, often due to mutations in the *rpoB* gene, is a defining feature of MDR-TB. Isoniazid functions as a prodrug that disrupts mycolic acid synthesis in the bacterial cell wall, with resistance typically associated with mutations in the *katG* and *inhA* genes Pyrazinamide, another key component, alters intracellular pH balance, leading to bacterial death, while resistance commonly arises from mutations in the *pncA* gene [4]. Ethambutol inhibits mycobacterial cell wall synthesis by targeting arabinogalactan biosynthesis, with resistance often linked to mutations in the *embB* gene [5]. When resistance to first-line drugs develops, second-line treatments become necessary. These include fluoroquinolones, aminoglycosides, and other less commonly used agents. Fluoroquinolones, such as Levofloxacin and Moxifloxacin, inhibit bacterial DNA gyrase and topoisomerase IV, essential enzymes for DNA replication. Resistance to these drugs is typically associated with mutations in the *gyrA* or *parC* genes [6]. Aminoglycosides, including Streptomycin, Amikacin, and Kanamycin, target bacterial protein synthesis by binding to the 30S ribosomal subunit, with resistance mechanisms involving ribosomal RNA mutations or enzymatic drug inactivation [7]. Other second-line drugs, such as Capreomycin, Linezolid, Clofazimine, and Cycloserine, act on different bacterial metabolic pathways but are often limited by their toxicity and severe side effects.

The growing prevalence of drug-resistant TB, particularly MDR-TB and extensively drug-resistant TB (XDR-TB), has significantly complicated treatment strategies. MDR-TB is characterized by resistance to at least Rifampicin and Isoniazid, whereas XDR-TB exhibits resistance to these drugs in addition to fluoroquinolones and at least one second-line injectable medication [8]. The treatment of MDR-TB and XDR-TB requires prolonged and more complex regimens involving second-line medications, which are not only less effective but also associated with higher toxicity and cost. Furthermore, the emergence of resistance makes it increasingly difficult to predict treatment outcomes, prolonging therapy duration and limiting therapeutic options.

Recognizing the urgency of TB eradication, the WHO launched the End TB Strategy as part of its post-2015 agenda. Adopted by the World Health Assembly in May 2014, the strategy aligns with the Sustainable Development Goals (SDGs) and aims to achieve an 80% reduction in TB incidence, a 90% reduction in TB deaths, and the elimination of catastrophic costs for TB-affected households by 2030 [9]. Unlike a one-size-fits-all approach, the strategy is designed to be adaptable, ensuring effective implementation across diverse country settings. Similarly, on World TB Day 2023, India's National TB Elimination Program (NTEP) set an ambitious goal of eliminating TB by 2025 by focusing on active case detection, improved diagnostics, and patient-centered care.

However, global progress remains significantly off-track. Between 2015 and 2023, the net reduction in TB incidence was only 8.3%, falling far short of the WHO End TB Strategy milestone of a 50% reduction by 2025. Likewise, the net reduction in global TB-related deaths during the same period was 23%, reaching merely one-third of the WHO's target of a 75% reduction by 2025. These shortfalls emphasize the urgent need for accelerated efforts, and innovative approaches to meet global TB elimination targets. This mini review paper presents the latest advancements in the field, highlighting innovative strategies and technological developments adopted both globally and nationally to accelerate diagnosis, treatment, and prevention efforts in pursuit of global TB elimination goals.

ADVANCEMENTS IN TREATMENT REGIMENS FOR DRUG-RESISTANT TUBERCULOSIS

To tackle the escalating issue of drug resistance, various innovative strategies and drug classes are currently under exploration:

RAPID DIAGNOSTIC TOOLS: TRANSFORMING TB DETECTION

The evolution of TB diagnostic methods has significantly improved detection speed, accuracy, and accessibility. Rapid diagnostic tools are crucial for identifying drug resistance and tailoring personalized treatment regimens. Table 1 provides an overview of some of the major rapid TB diagnostic methods that have evolved over time, highlighting their development, detection targets, time to results, advantages, and limitations.

Table 1. Some of the Major Rapid TB Diagnostic Methods.

Diagnostic Tool	Developed (Approx.)	Method	Detection Target	Time to Result	Key Advantages	Limitations	References
Fluorescent Microscopy with LED	2000s (LED adaptation)	Staining and microscopy	Acid-fast bacilli (AFB)	~1–2 hours	Cost-effective, widely used	Requires trained personnel	[10, 11]
LAMP (Loop-Mediated Isothermal Amplification)	Early 2000s	Isothermal DNA amplification	*M. tuberculosis* DNA	~1 hour	Low cost, simple setup	Lower specificity than PCR-based methods	[12, 13, 14]
GeneXpert MTB/RIF	2010	PCR-based molecular test	*M. tuberculosis* & rifampicin resistance	~2 hours	Rapid, automated, high sensitivity	Expensive, requires continuous power supply	[15]
Whole Genome Sequencing (WGS)	1998 (TB-specific applications later)	High-throughput sequencing	Comprehensive drug resistance profile	~1–2 days	Identifies all resistance mutations	Expensive, requires expertise	[16, 17]
Truenat MTB/RIF	2020	Chip-based real-time PCR	*M. tuberculosis* & rifampicin resistance	~1 hour	Portable, battery-operated	Expensive, limited availability	[18]
CRISPR-Based Diagnostics (SHERLOCK, DETECTR)	Late 2010s–2020s	CRISPR-Cas targeting specific DNA sequences	*M. tuberculosis* & drug resistance markers	~30 min	High specificity, rapid	Still in early development, not widely available for TB diagnosis	[19]

GENE EDITING AND CRISPR APPLICATIONS IN TB TREATMENT

The Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) system was first identified in *Mycobacterium tuberculosis* by Groenen et al. (1993) [20]. CRISPR technology encompasses various techniques with distinct mechanisms for gene editing and regulation [21–23]. CRISPR-Cas9 (Knockout, CRISPR-KO) introduces double-strand breaks in DNA, leading to gene disruption and loss of function. CRISPR Interference (CRISPRi) utilizes a catalytically inactive Cas9 (dCas9) to block gene expression without altering the DNA sequence [24]. Conversely, CRISPR Activation (CRISPRa) enhances gene expression by recruiting transcriptional activators [25]. CRISPR Knock-In (CRISPR-KI) facilitates the insertion of specific genetic sequences at targeted locations [26]. Additionally, CRISPR-Cas12 and CRISPR-Cas13 (originally known as C2c2) function in diagnostics, with Cas12 targeting single-stranded DNA [27] and Cas13 targeting RNA [28]. Notably, CRISPR-based diagnostic platforms, such as SHERLOCK and DETECTR employ CRISPR enzymes to enable rapid and precise bacterial DNA or RNA detection. These advancements highlight the versatility of CRISPR technology in both gene regulation and disease diagnostics.

Initially used for strain differentiation, CRISPR-based tools have evolved into powerful gene-editing systems with promising applications in TB research, drug resistance studies, and diagnostics [29]. Developed a novel endogenous CRISPR-Cas10 system in *Mycobacterium tuberculosis* for efficient gene editing and RNA interference (RNAi). This method, which requires only a single mini-CRISPR array plasmid, eliminates the need for exogenous proteins and minimizes proteotoxicity. The system enables targeted gene knock-in/out and facilitates genome-wide RNAi screening, allowing for the

identification of key genes involved in bacterial growth [30]. This method also explored the potential of CRISPR interference (CRISPRi) in intracellular *M. tuberculosis* infection models. Using human monocytic THP-1 cells, the study demonstrated that transcriptional repression of the mmpL3 and qcrB genes reduces bacterial viability within macrophages. The extent and duration of gene repression were directly correlated with the decline in bacterial survival. These findings highlight CRISPRi as a promising tool for studying gene function in intracellular *M. tuberculosis*, offering a novel approach for identifying drug targets relevant to host-pathogen interactions [31]. These findings assessed the antimicrobial potential of CRISPR-Cas9 in *Mycobacterium smegmatis*, demonstrating that while single-strand breaks were efficiently repaired, double-strand breaks (DSBs) were not, resulting in bacterial death. Moreover, selective targeting of hygromycin resistance genes in a mixed population rendered all cells sensitive to the antibiotic. Additionally, CRISPR-based targeting effectively eliminated plasmids from mycobacterial cells, highlighting its potential as an antimicrobial strategy.

A recent study by Sodani et al. (2023) [31] applied whole-genome CRISPR interference (WG-CRISPRi) screening to identify druggable vulnerabilities in isoniazid-resistant *M. tuberculosis* strains. This revealed specific biological pathways in resistant bacteria that are highly sensitive to inhibition, paving the way for novel targeted therapies.

MECHANISMS OF BEDAQUILINE'S ENHANCED EFFICACY

Recent research has provided insights into why bedaquiline is particularly effective against MDR-TB strains. Investigating MDR-TB susceptibility to bedaquiline, it was found that resistance to older antibiotics, particularly isoniazid, creates vulnerabilities that enhance bedaquiline efficacy. MDR-TB strains frequently exhibit deficiencies in the catalase-peroxidase enzyme *KatG*, leading to an accumulation of reactive oxygen species and increased DNA damage. These metabolic disruptions make MDR strains more susceptible to bedaquiline, offering new therapeutic opportunities. This aligns with the findings mentioned above, who identified physiological vulnerabilities in *katG*-mutant INH-resistant *M. tuberculosis* strains using CRISPRi, further reinforcing the potential for targeting metabolic weaknesses in drug-resistant TB.

SHORTER, ALL-ORAL REGIMENS

In response to the growing challenge of drug-resistant tuberculosis, the WHO updated its treatment guidelines in 2022, introducing shorter, more effective regimens. The introduction of these shorter regimens not only improves patient outcomes but also reduces treatment costs for both healthcare systems and individuals. The 6-month BPaLM regimen, comprising bedaquiline, pretomanid, linezolid, and moxifloxacin, was recommended for treating multidrug-resistant or rifampicin-resistant TB (MDR/RR-TB) and pre-XDR-TB. Additionally, a 9-month all-oral regimen was introduced for MDR/RR-TB cases without fluoroquinolone resistance, offering a viable alternative to traditional long-duration therapies. Following these recommendations, India adopted the shorter BPaLM regimen (with or without moxifloxacin) in 2024 for the treatment of MDR and XDR-TB [32]. Table 2 summarizes key clinical trials (Nix-TB, ZeNix, and TB-PRACTECAL) that contributed to the development and optimization of the BPaLM regimen for drug-resistant TB treatment [33].

Further supporting the shift toward shorter, all-oral therapies, a recent clinical trial [20] evaluated the efficacy and safety of five 9-month all-oral regimens compared to the standard WHO-recommended therapy in 754 participants with rifampin-resistant, fluoroquinolone-susceptible pulmonary tuberculosis, with or without HIV co-infection. The study investigated regimens incorporating various combinations of bedaquiline (B), delamanid (D), linezolid (L), levofloxacin (Lfx), moxifloxacin (M), clofazimine (C), and pyrazinamide (Z). The findings demonstrated that four of the experimental regimens were non-inferior to the standard treatment, with three achieving success rates above 85%. Although adverse events were reported across all groups, shorter regimens improved adherence and reduced toxicity, reinforcing their potential as a more effective and patient-friendly alternative to conventional long-term therapies.

Table 2. Key clinical trials supporting BPaLM regimen development.

Trial Name	Year of Study	Objective	Number of Participants	Geographical Area	Study Design	Key Findings	Significance
Nix-TB	2015–2017	Tested the BPaL regimen as a short, all-oral treatment for MDR-TB/XDR-TB	108	South Africa	Single-arm, uncontrolled trial	26-week BPaL regimen showed high efficacy in patients with few treatment options	Provided first evidence that an all-oral, 6-month regimen could effectively treat highly resistant TB
ZeNix	2017–2022	Optimized the BPaL regimen by adjusting linezolid dose and duration to improve tolerability	181	Georgia, Moldova, Russia, South Africa	Randomized controlled trial (RCT) testing four groups with different linezolid dosages	Lower linezolid doses (600 mg) reduced toxicity while maintaining high cure rates	Helped refine the BPaL regimen, making it safer and more tolerable for broader use
TB-PRACTECAL	2017–2022	Compared multiple 24-week regimens using BPaL as a backbone against standard of care (SoC) for MDR-TB	419	Belarus, South Africa, Uzbekistan	Phase 2–3 open-label RCT testing: – BPaL (600 mg linezolid for 16 weeks, 300 mg for 8 weeks) – BpaLM (BPaL + moxifloxacin) – BpaLC (BPaL + clofazimine)	BPaLM had the highest success rate (89%), outperforming standard MDR-TB treatment (52%)	Confirmed BPaLM as the most effective regimen, leading to WHO's 2022 recommendation

These results highlight the potential of shorter, all-oral regimens in enhancing treatment success rates while minimizing the burden of prolonged medication use. The development of such regimens marks a major breakthrough in improving treatment outcomes and reducing side effects, addressing critical challenges in global TB management.

CONCLUSIONS

The fight against tuberculosis, particularly drug-resistant TB, is at a critical juncture. While traditional treatment regimens have been instrumental in controlling the disease, rising antibiotic resistance necessitates a paradigm shift in therapeutic strategies. Advances in gene editing technologies, such as CRISPR, offer unprecedented opportunities for targeted TB treatments and diagnostics, while new insights into bedaquiline's efficacy have revealed metabolic weaknesses in resistant bacterial strains. The introduction of rapid diagnostic tools has significantly improved early detection and drug resistance identification, enabling timely and effective interventions. Furthermore, the transition to shorter, all-oral regimens marks a significant milestone in TB treatment, improving patient adherence, reducing side effects, and increasing cure rates. As global health organizations, governments, and researchers continue to refine TB control strategies, integrating these innovations into national programs will be essential in achieving TB elimination goals. The convergence of molecular biology, advanced diagnostics, and optimized pharmacotherapy offers renewed hope in the global effort to eradicate tuberculosis.

REFERENCES

1. World Health Organization. Global tuberculosis report 2024. Geneva: World Health Organization; 2024.

2. Padda IS, Muralidhara Reddy K. Antitubercular medications. In: StatPearls [Internet]. Treasure Island (FL): StatPearls Publishing; 2023 [cited 2025 Jul 17]. Available from: https://www.ncbi.nlm.nih.gov/books/NBK557666/.
3. World Health Organization. Treatment of tuberculosis: guidelines. 4th ed. Geneva: WHO; 2010.
4. Shi J, Su R, Zheng D, Zhu Y, Ma X, Wang S, et al. Pyrazinamide resistance and mutation patterns among multidrug-resistant Mycobacterium tuberculosis from Henan Province. Infect Drug Resist. 2020;13:2929–41.
5. Ofori-Anyinam B, Hamblin M, Coldren ML, Li B, Mereddy G, Shaikh M, et al. Catalase activity deficiency sensitizes multidrug-resistant Mycobacterium tuberculosis to the ATP synthase inhibitor bedaquiline. Nat Commun. 2024;15(1):9792.
6. Hooper DC, Jacoby GA. Topoisomerase inhibitors: fluoroquinolone mechanisms of action and resistance. Cold Spring Harb Perspect Med. 2016;6(9):a025320.
7. Krause KM, Serio AW, Kane TR, Connolly LE. Aminoglycosides: an overview. Cold Spring Harb Perspect Med. 2016;6(6):a027029.
8. Dheda K, Chang KC, Guglielmetti L, Furin J, Schaaf HS, Chesov D, et al. Clinical management of adults and children with multidrug-resistant and extensively drug-resistant tuberculosis. Clin Microbiol Infect. 2017;23(3):131–40.
9. World Health Organization. The End TB Strategy. Geneva: WHO; 2015 [cited 2025 Jul 17]. Available from: https://www.who.int/publications/i/item/WHO-HTM-TB-2015.19.
10. Steingart KR, Henry M, Ng V, Hopewell PC, Ramsay A, Cunningham J, et al. Fluorescence versus conventional sputum smear microscopy for tuberculosis: a systematic review. Lancet Infect Dis. 2006;6(9):570–81.
11. Marais BJ, Brittle W, Painczyk K, Hesseling AC, Beyers N, Wasserman E, et al. Use of light-emitting diode fluorescence microscopy to detect acid-fast bacilli in sputum. Clin Infect Dis. 2008;47(2):203–7.
12. Notomi T. Loop-mediated isothermal amplification of DNA. Nucleic Acids Res. 2000;28(12):E63.
13. World Health Organization. The use of loop-mediated isothermal amplification for the diagnosis of TB: policy guidance. Geneva: WHO; 2016 [cited 2025 Jul 17]. Available from: http://www.who.int/tb/features_archive/TB_LAMP/en/.
14. Global Laboratory Initiative. Practical considerations for implementation of TB-LAMP. Geneva: Stop TB Partnership; 2016 [cited 2025 Jul 17]. Available from: http://www.stoptb.org/wg/gli/assets/documents/.
15. Helb D, Jones M, Story E, Boehme C, Wallace E, Ho K, et al. Rapid detection of Mycobacterium tuberculosis and rifampin resistance by use of on-demand, near-patient technology. J Clin Microbiol. 2010;48(1):229–37.
16. Cole ST, Brosch R, Parkhill J, Garnier T, Churcher C, Harris D, et al. Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence. Nature. 1998;393(6685):537–44.
17. Wang L, Yang J, Chen L, Wang W, Yu F, Xiong H. Whole-genome sequencing of Mycobacterium tuberculosis for prediction of drug resistance. Epidemiol Infect. 2022;150:e22.
18. Molbio Diagnostic Product Limited. Truenat™ MTB Plus package insert. 2020 [cited 2025 Jul 17]. Available from: http://www.molbiodiagnostics.com/uploads/product_download/20190927.152146~Truenat-MTB-Plus-packinsert.pdf.
19. Kaminski MM, Abudayyeh OO, Gootenberg JS, Zhang F, Collins JJ. CRISPR-based diagnostics. Nat Biomed Eng. 2021;5(7):643–56.
20. Groenen PMA, Bunschoten AE, van Soolingen D, van Embden JD. Nature of DNA polymorphism in the direct repeat cluster of Mycobacterium tuberculosis; application for strain differentiation by a novel typing method. Mol Microbiol. 1993;10(5):1057–65.
21. Gootenberg JS, Abudayyeh OO, Kellner MJ, Joung J, Collins JJ, Zhang F. Multiplexed and portable nucleic acid detection platform with Cas13, Cas12a, and Csm6. Science. 2018;360(6387):439–44.

22. Wang X, Jowsey WJ, Cheung C-Y, Smart CJ, Klaus HR, Seeto NE, et al. Whole genome CRISPRi screening identifies druggable vulnerabilities in an isoniazid resistant strain of Mycobacterium tuberculosis. Nat Commun. 2024;15(1):9791.
23. Ofori-Anyinam B, Hamblin M, Coldren ML, Li B, Mereddy G, Shaikh M, et al. Catalase activity deficiency sensitizes multidrug-resistant Mycobacterium tuberculosis to the ATP synthase inhibitor bedaquiline. Nat Commun. 2024;15(1):9792.
24. Qi LS, Larson MH, Gilbert LA, Doudna JA, Weissman JS, Arkin AP, et al. Repurposing CRISPR as an RNA-guided platform for sequence-specific control of gene expression. Cell. 2013;152(5):1173–83.
25. Chavez A, Scheiman J, Vora S, Pruitt BW, Tuttle M, Patter L, et al. Highly efficient Cas9-mediated transcriptional programming. Nat Methods. 2015;12(4):326–8.
26. Cong L, Ran FA, Cox D, Lin S, Barretto R, Habib N, et al. Multiplex genome engineering using CRISPR/Cas systems. Science. 2013;339(6121):819–23.
27. Chen JS, Ma E, Harrington LB, Da Costa M, Tian X, Palefsky JM, et al. CRISPR-Cas12a target binding unleashes indiscriminate single-stranded DNase activity. Science. 2018;360(6387):436–9.
28. Abudayyeh OO, Gootenberg JS, Konermann S, Joung J, Slaymaker IM, Cox DB, et al. C2c2 is a single-component programmable RNA-guided RNA-targeting CRISPR effector. Science. 2016;353(6299):aaf5573.
29. Zein-Eddine R, Refrégier G, Cervantes J, Yokobori NK. The future of CRISPR in Mycobacterium tuberculosis infection. J Biomed Sci. 2023;30(1):34.
30. Cheung C-Y, McNeil MB, Cook GM. Utilization of CRISPR interference to investigate the contribution of genes to pathogenesis in a macrophage model of Mycobacterium tuberculosis infection. J Antimicrob Chemother. 2022;77(3):615–9.
31. Sodani M, Misra CS, Rath D, Kulkarni S. Harnessing CRISPR-Cas9 as an anti-mycobacterial system. Microbiol Res. 2023;270:127319.
32. Press Information Bureau, Government of India. Union Health Ministry approves introduction of new shorter and more efficacious treatment regimen for drug-resistant TB in India [Internet]. 2024 Sep 6 [cited 2025 Jul 17]. Available from: https://pib.gov.in.
33. World Health Organization. Module 4: Drug-resistant tuberculosis treatment, 2022 update – The 6-month bedaquiline, pretomanid, linezolid and moxifloxacin (BPaLM) regimen. WHO TB Knowledge Sharing Platform; 2022 [cited 2025 Jul 17]. Available from: https://tbksp.who.int/en/node/576.

