

Understanding the Molecular Epidemiology of Multi-drug Resistant Tuberculosis in High-burden Regions

Torres Ruiz*

Department of Infectious Diseases, University of Seville, Seville, Spain

Abstract

Tuberculosis (TB) remains a significant global health challenge, particularly in high-burden regions. The emergence of Multi-Drug Resistant Tuberculosis (MDR-TB) complicates treatment strategies and exacerbates public health concerns. Molecular epidemiology provides critical insights into the transmission dynamics, genetic diversity and resistance mechanisms of MDR-TB, enabling more targeted and effective interventions. Tuberculosis is an infectious disease caused by the bacterium *Mycobacterium tuberculosis*. Despite significant advances in medicine and public health, TB remains a major global health concern, particularly in low- and middle-income countries. Understanding the epidemiology, diagnosis, treatment and prevention of TB is crucial for effective control and eventual eradication of this disease. TB is one of the top 10 causes of death worldwide and the leading cause of death from a single infectious agent, ranking above HIV/AIDS.

Keywords: Multi-drug resistant tuberculosis • Molecular epidemiology • *Mycobacterium tuberculosis*

Introduction

The World Health Organization (WHO), an estimated 10 million people fell ill with TB in 2020, with 1.5 million succumbing to the disease. While TB is present in all regions of the world, the burden is disproportionately high in certain areas, including sub-Saharan Africa, Southeast Asia and the Western Pacific region. TB is primarily spread through the air when an infected individual coughs, sneezes, or talks, releasing droplets containing the bacteria. Factors contributing to TB transmission include overcrowded living conditions, poor ventilation and limited access to healthcare. Individuals with weakened immune systems, such as those living with HIV/AIDS, malnutrition, or diabetes, are at higher risk of developing active TB disease upon exposure. TB can manifest in various forms, with pulmonary TB being the most common presentation. Symptoms may include prolonged cough (often with sputum), chest pain, fatigue, weight loss, fever and night sweats.

Treatment of TB involves a combination of antibiotics administered over several months. Standard treatment regimens for drug-susceptible TB typically consist of a combination of isoniazid, rifampicin, pyrazinamide and ethambutol. Drug-resistant TB, including multidrug-resistant TB and extensively drug-resistant TB, requires more prolonged and complex treatment regimens, often with second-line drugs that are more costly and may have more adverse effects. Extrapulmonary TB can affect other organs such as the lymph nodes, bones, kidneys and brain, presenting with symptoms specific to the affected area. Tuberculosis remains a formidable global health challenge, affecting millions of people each year and causing significant morbidity and mortality [1,2]. Efforts to combat TB require a multifaceted approach, including improved diagnostics, access to quality treatment, preventive measures and investment in research and innovation. By prioritizing TB control and addressing social determinants of health, we can work towards the ambitious goal of eliminating TB as a public health threat worldwide.

Literature Review

*Address for Correspondence: Torres Ruiz, Department of Infectious Diseases, University of Seville, Seville, Spain, E-mail: torresruiztoz@gmail.com

Copyright: © 2024 Ruiz T. This is an open-access article distributed under the terms of the creative commons attribution license which permits unrestricted use, distribution and reproduction in any medium, provided the original author and source are credited.

Received: 28 May, 2024, Manuscript No. jid-24-141957; **Editor Assigned:** 30 May, 2024, Pre QC No. P-141957; **Reviewed:** 12 June, 2024, QC No. Q-141957; **Revised:** 17 June, 2024, Manuscript No. R-141957; **Published:** 24 June, 2024, DOI: 10.37421/2684-4559.2024.8.273

The development of MDR-TB is often due to improper treatment regimens, patient non-compliance and transmission of resistant strains. High-burden regions, including parts of India, China, Russia and sub-Saharan Africa, face significant challenges in controlling MDR-TB due to resource limitations and high transmission rates. Multi-drug resistant tuberculosis is a form of tuberculosis caused by strains of *Mycobacterium tuberculosis* resistant to at least isoniazid and rifampicin, the two most powerful first-line anti-TB drugs. MDR-TB is defined as tuberculosis caused by *Mycobacterium tuberculosis* strains resistant to at least isoniazid and rifampicin, the two most potent TB drugs. This resistance significantly complicates treatment and control efforts, leading to higher morbidity and mortality rates.

The integration of molecular diagnostics, personalized treatment plans and robust public health strategies can help mitigate the impact of this formidable public health challenge. By investing in research, improving healthcare infrastructure and fostering international collaboration, the fight against MDR-TB can be more effective, ultimately moving towards the goal of eliminating TB as a global health threat. The epidemiology of MDR-TB varies significantly across high-burden regions, influenced by socio-economic factors, healthcare infrastructure and population mobility. Strain diversity and transmission networks in high-burden areas, a limited number of dominant MDR-TB strains often drive the epidemic. For example, Understanding and addressing MDR-TB is crucial for global TB control efforts, the Beijing genotype is prevalent in East Asia and is associated with high transmission rates and drug resistance. WGS and spoligotyping help identify TB clusters and track transmission pathways. Studies in South Africa, for instance, have shown that MDR-TB outbreaks are frequently linked to healthcare settings and densely populated urban areas. Migration and travel contribute to the spread of MDR-TB across borders. Molecular data indicate that strains from high-burden countries often appear in neighboring regions, necessitating international collaboration in TB control efforts [3,4].

Discussion

The emergence and spread of drug-resistant strains of *Mycobacterium tuberculosis*, the bacterium that causes tuberculosis, pose significant challenges to TB control efforts worldwide. Understanding the molecular mechanisms underlying drug resistance is crucial for developing effective diagnostic methods and treatment strategies. Isoniazid is a cornerstone drug in the treatment of TB, targeting the mycobacterial enzyme enoyl-acyl carrier protein reductase, which is essential for cell wall biosynthesis. The majority of isoniazid resistance is attributed to mutations in the *katG* gene, which encodes catalase-peroxidase. These mutations disrupt the activation of isoniazid, preventing the conversion of the prodrug to its active form, which subsequently inhibits cell wall synthesis. Mutations in the promoter region of

the *inhA* gene, which codes for the NADH-dependent enoyl-ACP reductase, can lead to overexpression of this enzyme. This overexpression compensates for the loss of KatG activity, providing an alternative mechanism of resistance to isoniazid.

Rifampicin is another crucial first-line drug used in the treatment of TB. It inhibits bacterial RNA synthesis by targeting the β -subunit of RNA polymerase. Resistance to rifampicin is primarily conferred by mutations in the *rpoB* gene, which codes for the β -subunit of RNA polymerase. These mutations occur within a specific region known as the Rifampicin Resistance-Determining Region (RRDR) and can lead to a reduced affinity of RNA polymerase for rifampicin, thereby rendering the drug ineffective. Resistance to pyrazinamide, an important drug in short-course chemotherapy, can result from mutations in the *pncA* gene, which encodes pyrazinamidase, the enzyme required for pyrazinamide activation [5,6]. Mutations in this gene lead to reduce or loss of enzyme activity, limiting the conversion of pyrazinamide to its active form. Resistance to pyrazinamide, an important drug in short-course chemotherapy, can result from mutations in the *pncA* gene, which encodes pyrazinamidase, the enzyme required for pyrazinamide activation.

Conclusion

Understanding these mechanisms is essential for the development of rapid and accurate diagnostic tests for drug-resistant TB and for the design of effective treatment regimens tailored to individual patients. Moreover, ongoing research into novel drug targets and alternative treatment strategies is critical for addressing the global challenge of drug-resistant TB and improving outcomes for patients. Resistance to fluoroquinolones and second-line injectable drugs such as kanamycin, amikacin and capreomycin can arise from mutations in genes associated with DNA gyrase (*gyrA* and *gyrB*) and the ribosomal protein S12 (*rrs*), respectively. The molecular mechanisms of drug resistance in TB are multifaceted and involve mutations in specific genes associated with drug targets or metabolic pathways.

Acknowledgement

None.

Conflict of Interest

None.

References

1. Klopper, Marisa, Robin Mark Warren, Cindy Hayes and Nicolaas Claudius Gey van Pittius, et al. "Emergence and spread of extensively and totally drug-resistant tuberculosis, South Africa." *Emerg Infect Dis* 19 (2013): 449.
2. Caulfield, Adam J. and Nancy L. Wengenack. "Diagnosis of active tuberculosis disease: From microscopy to molecular techniques." *J Clin Tuberc Other Mycobact Dis* 4 (2016): 33-43.
3. Gholoobi, Aida, Ali Masoudi-Kazemabad, Mojtaba Meshkat and Zahra Meshkat. "Comparison of culture and PCR methods for diagnosis of *Mycobacterium tuberculosis* in different clinical specimens." *Jundishapur J Microbiol* 7 (2014).
4. Pasechnik, Oksana, Anna Vyazovaya, Stanislav Vitriv and Marina Tatarintseva, et al. "Major genotype families and epidemic clones of *Mycobacterium tuberculosis* in Omsk region, Western Siberia, Russia, marked by a high burden of tuberculosis-HIV coinfection." *Tuberculosis* 108 (2018): 163-168.
5. Migliori, Giovanni Battista, Johannes Ortmann, Enrico Girardi and Giorgio Besozzi, et al. "Extensively drug-resistant tuberculosis, Italy and Germany." *Emerg Infect Dis* 13 (2007): 780.
6. Velayati, Ali Akbar, Mohammad Reza Masjedi, Parissa Farnia and Payam Tabarsi, et al. "Emergence of new forms of totally drug-resistant tuberculosis bacilli: Super extensively drug-resistant tuberculosis or totally drug-resistant strains in Iran." *Chest* 136 (2009): 420-425.

How to cite this article: Ruiz, Torres. "Understanding the Molecular Epidemiology of Multi-drug Resistant Tuberculosis in High-burden Regions." *Clin Infect Dis* 8 (2024): 273.