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DIAGNOSIS OF TUBERCULOSIS BY ADVANCE GENEXPERT METHOD IN DISTRICT BANNU, KHYBER PAKHTUNKHWA (KP) PAKISTAN

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Abstract

Background: Mycobacterium tuberculosis (MTB) remains a major global health challenge. Accurate and rapid diagnosis is essential for effective treatment and control of tuberculosis (TB). **Methods**: This study involved testing 1477 suspected cases of MTB using the GeneXpert diagnostic method. The cases were categorized into MTB positive, MTB negative, relapse, and follow-up (FUP) cases. MTB positive cases were further classified based on bacterial load into low, medium, and high levels. **Results**: Out of 1477 suspected cases, 313 (21.2%) were confirmed as MTB positive, while 1037 (70.2%) were MTB negative. Additionally, 11 cases (0.7%) were identified as relapse, and 16 cases (1.1%) as follow-up. Among the 313 MTB positive cases, 121 (38.7%) had a low bacterial load, 117 (37.4%) had a medium bacterial load, and 70 (22.4%) had a high bacterial load. **Conclusion**: The GeneXpert method effectively diagnoses MTB and categorizes bacterial load, which is crucial for guiding treatment strategies. The significant proportion of MTB positive cases underscores the importance of rapid and accurate diagnostics in TB management. Understanding bacterial load distribution aids in tailoring patient-specific treatment plans, while the identification of relapse and follow-up cases highlights the need for continuous patient monitoring. This study emphasizes the necessity of advanced diagnostic tools and personalized treatment approaches to effectively manage and reduce the burden of tuberculosis.

INTRODUCTION:

Tuberculosis is one of the known global diseases first diagnosed by the scientist Robert Koch who diagnosed. Mycobacterium tuberculosis the causative agent of TB. In March 24, 1882 [Al-Alwani et al., 2022]. Tuberculosis is an infectious disease that is caused by the tubercle bacillus, Mycobacterium tuberculosis. In most forms of the disease, the bacillus spreads slowly and widely in the lungs, causing the formation of hard nodules (tubercles) or large cheese like masses that break down the respiratory tissues and form cavities in the lungs [Mendelson, 2018].

The probability of developing TB disease is much higher among people infected with HIV, and also higher among people affected by risk factors such as mal -nutrition, diabetes, smoking and alcohol consumption [suryanarayan VK, 1998; Aljanabi et at 2020]. Drug-resistant Mycobacterium tuberculosis (Mtb) remains a significant challenge to global tuberculosis (TB) care and control efforts. According to the Global TB Report 2021, approximately 10 million people fell ill with TB, including ~50,000 incident cases of

drug-resistant TB (DR-TB). Over 1.4 million people died from TB in 2020, with more than 95% of these deaths occurring in low- and middle-income countries [Bagcchi, 2023]. Despite a 20% decrease in TB mortality from 2015 to 2020, the prevalence rates of multidrug-resistant TB (MDR-TB) and extensively drug-resistant TB (XDR-TB) continue to rise among both new and previously treated TB cases [Steingart, 2021].

Tuberculosis (TB) is a persistent health issue in Pakistan, with its impact significantly felt in District Bannu. The region grapples with a substantial burden of this disease, which has strained healthcare resources and affected the lives of many residents. The prevalence of TB in Bannu is exacerbated by various factors, including poverty, overcrowding, limited access to healthcare, and high rates of migration [Demelash et al., 2023]. Traditionally, diagnosing TB in resource-limited settings like District Bannu has been challenging. Conventional methods like smear microscopy, while widely used, often lack accuracy, particularly in detecting drug-resistant strains and in cases where patients have HIV/AIDS or other conditions that compromise their immune systems. These limitations have led to delayed diagnoses, contributing to the spread of TB within communities [soni et al., 2023].

The introduction of advanced diagnostic tools, like the GeneXpert machine, has marked a turning point in the approach to TB diagnosis in District Bannu. Unlike smear microscopy, the GeneXpert technology utilizes molecular techniques to rapidly detect the presence of Mycobacterium tuberculosis bacteria and identify resistance to Rifampicin, a key anti-TB drug. Its ability to provide results within a few hours, compared to the days or weeks required for traditional methods, has significantly enhanced the speed and accuracy of TB diagnosis [Getahun et al 2023]. District Bannu, located in the Khyber Pakhtunkhwa province of Pakistan, has faced persistent challenges in combating tuberculosis due to limited resources, high population density, and inadequate healthcare infrastructure. Traditional TB diagnostic methods, such as smear microscopy, have limitations in terms of sensitivity and specificity, leading to delayed or inaccurate diagnoses [Demelash et al., 2023]

In untreated patients, the death rate due to active tuberculosis is more than 66 %. Active tuberculosis may become latent TB in most patients infected that lead to producing fibrosis or caseous necrosis in upper or lower part of lung lobes [Crowley, 2013]. In latent TB the MTB utilized the granuloma formation to prevent antigen presentation and prevent the destruction of MTB by host immune system [Al-Alwani et al., 2022]. When Mycobacterium tuberculosis penetrates the blood circulation, Military tuberculosis leading to TB lesions will be emerging in another organ of the body such as (bone, lymph node, kidney and brain [Crowley, 2013; vilayati et al 2011].

When Mycobacterium tuberculosis spreads outside the lungs producing different type of TB, the most common types of extra-pulmonary tuberculosis are pleural TB, tuberculous meningitis, lymphatic system (especially around the neck), Urogenital tuberculosis and the bones or joints [Al-Alwani, 2022; Crowley et al 2013]. There is an increasing rate of the drug-resistant tuberculosis strains toward the drugs for curing of tuberculosis in large sector of risk groups, the problems of emergency multi-drug resistant TB (MDR) is major conflict in the world. AccD3 gene is a good drug target in MDR M. tuberculosis strains [Asra'a et al., 2018]

The GeneXpert machine, a molecular diagnostic tool, has emerged as a game-changer in TB diagnosis [Derese et al., 2023]. Utilizing nucleic acid amplification techniques, this technology detects Mycobacterium tuberculosis and rifampicin resistance within a few hours. Its speed, accuracy, and ability to diagnose drug-resistant TB make it an invaluable asset in high-burden settings like District Bannu. The impact of GeneXpert technology on TB diagnosis has been significant [Zhao et al., 2023]. The rapid and accurate detection of TB cases has facilitated timely initiation of treatment, reducing transmission rates and preventing further complications.

Moreover, the identification of drug-resistant cases has enabled tailored treatment regimens, improving patient outcomes [Boehme et al., 2010]. Tuberculosis is a major public health problem in the developing world. It is estimated that 10 million people in the world get TB infection annually with 1.7 million deaths. [Bruchfeld et al., 2015]. Pakistan ranks 5th in the estimated global TB burden list. [Grobusch and Kapata et al 2018; Chakaya et al., 2020]. Multi-drug-resistant tuberculosis (MDR-TB) is a major public health issue, particularly in developing countries [Ormerod, 2005; Taniguchi et al., 1996]. World Health Organization (WHO) has reported 600,000 individuals with rifampicin resistant tuberculosis (RR-TB) and 490,000 of these RR cases develop MDR-TB. Among those RR-TB cases, 47% of these patients belong to India, China, Russian Federation and Pakistan.[Harding, 2020; Munir et al., 2018].According to WHO 2018 report, Pakistan is one of the 27 high MDR-TB burden countries with an MDR-TB rate of 4.2 % in new (category-I) cases and 16% among the previously treated (category-II) TB cases.8,9 The increase in MDR-TB cases is correlated to treatment failure & relapse, which exhibits extra difficulties in TB control.10 RR has a precise epidemiological variety and is a valuable marker for MDR-TB strains since 90% or above of those strains resistant to rifampicin (RIF) are also resistant to isoniazid which are said to be MDR-TB. RIF is the key first-line anti-TB drug that works by inhibiting the synthesis of ribonucleic acid (RNA) directed by the deoxyribonucleic acid (DNA) of mycobacterium tuberculosis (MTB) proteins by binding to the β subunit of the bacterial DNA-dependent RNA

polymerase enzyme protein (rpo-β) [Goldstein, 2014]. Mutations in the rpo-β gene are reported as 95 to 97% of RRMTB strains throughout the world which is usually situated in a region at the 507-533 amino acid residues (81bp) within the rpo-β genetic feature known as RR determining region (RRDR)[Taniguchi et al., 1996; Adékambi et al., 2009].

Laboratory diagnosis of tuberculosis (TB) is primarily done by a simple method of smear microscopy using Zeil Nelson (ZN) staining method [Singhal, 2015]. Other methods of diagnosis are also available like fluorescent microscopy (FM), culturing of bacteria on artificial media and an advanced molecular technique called Xpert MTB/RIF assay [Robledo et al., 2006]. PCR-based methods developed over the last decades have significantly improved and accelerated diagnosis of drug-resistant tuberculosis (DR-TB); however, such methods require a specific molecular diagnostic laboratory setup. The need for simpler PCR systems has been solved with the real-time PCR-based system Xpert MTB/RIF assay. It can simultaneously detect MTB and RR in less than two hours. Since 2013, the GeneXpert test is being recommended by WHO as an initial diagnostic test for patients with suspected pulmonary TB, including new, retreatment cases, suspected/ contact multidrug resistant (MDR) TB and HIV-infected patients with chest complications because of its high sensitivity and specificity associated with a tremendously short turnaround time. Detection of rpo-β gene mutations is considered a surrogate marker for MDR-TB detection and can be used as a tool in MDR-TB diagnostics. The patterns and frequency of mutations in the RRDR region of the rpo-β gene in the MTB clinical isolates vary significantly according to the geographical location. Limited data is available regarding the pattern of rpo-β mutation in the MDR-TB patients in Pakistan [Steingart et al.,2014; Opota et al., 2016]

1.1 Epidemiology of Tuberculosis:

Tuberculosis is the seventh leading cause of death worldwide, second only to human immunodeficiency virus (HIV) acquired immunodeficiency syndrome (AIDS) among infectious diseases (Keeler et al., 2006). There are 2 billion people today infected with Mycobacterium tuberculosis (MTB) and 1.7 million deaths worldwide are attributed to TB (WHO, Acute Respiratory Infections, 2009). In 1990 there were 6.6 million TB cases, while in 2007 there were an estimated 9.27 million cases per year (WHO report, 2009). Most of the estimated TB cases (92%) in 2007 were in developing countries (WHO report, 2009). Also, 98% of TB-related deaths occur in the developing world (Charles et al., 2006). TB is generally referred to as a poverty-related disease. The TB epidemic has been contained in developed countries by introducing health measures such as screening, surveillance and follow-up and a general improvement in living conditions (Modi et al.,

2009). However, international travel and countries caught in war and conflict have contributed to a TB increase worldwide [Frothingham et al., 2005; Modi et al., 2009).

1.2 Mycobacterium tuberculosis structure and morphology:

Mycobacterium tuberculosis complex (MTBC) is a group of closely related species and subspecies that include MTB, namely Mycobacterium africanum, Mycobacterium bovis, Mycobacterium caprae, Mycobacterium microti, and Mycobacterium pinnipedii (Gordon et al., 2009). MTBC is clustered with Gram-positive bacteria, since it has a peptidoglycan layer. However, MTB peptidoglycan has some distinctive characteristics as its outer layer consists of glycolipids – major cell wall component, lipoarabinomannan (LAM), polysaccharides and unique lipids with a hallmark molecule of Mycobacteria, mycolic acid (Cole et al., 1998, Chatterjee, 1997). In addition, such membranes form dye complexes that are not decolourised following exposure to acidic ethanol or mineral acids. This property is recognised as acid fastness (Barksdale et al., 1977).

Almost 60% of the bacteria"s dry weight consists of lipids, which makes it highly hydrophobic and as a consequence, impermeable for drugs (Cole et al., 1998). In vivo fatty acids are a major nutrient source and besides their role as nutrients, fatty acids, primarily in the form of mycolic acids, are a source of pathogenicity (Ehrt et al., 2007). Some differences in the host"s immune response to different strains are related to the lipid composition in MTB"s cell envelope (Ehrt et al., 2007). Mycobacteria are obligate aerobes, non-spore forming and non-motile (Dinnes et al., 2007, Barksdale et al., 1977). Microscopically, mycobacteria appear as spherical cells although, in cultures, mycobacteria show an inhibition of post-divisional cell separation forming short filaments, which can be branched (Barksdale et al., 1977). Tubercle bacilli from clinical specimens are usually rod-like cells. Individual bacilli are 0.5 to 1.0 μm in diameter and 1.5 and 10 μm long (Friedman, 2000).

1.3 Pathogenesis of Tuberculosis

Pathogenesis of tuberculosis is divided into various steps from the entry of pathogen to the causing fulminant disease.

1.3.1 Invasion of Tubercle Bacilli into the Body

Mycobacterium tuberculosis is an obligate aerobic, intracellular organism that has an affinity for the lung tissue. Bacilli enter the human body through respiratory route. Once it reaches the lungs which is the primary site of infection, it spreads to the different organs through lymphatics and hematogenous route. The apex of the lungs and regional LN's are the most favorable sites. Since the organism affects different organs, disease manifests with different clinical signs with respect to the organ affected.

1.3.2 Journey of Bacilli in Causing Tuberculosis:

i) Tubercle Bacilli and Macrophage Interaction:

With the help of complement receptors (CR1, CR3 and CR4), CD14, mannose receptors(MR) and other cell surface receptors the process of phagocytosis begins in which the organism is engulfed into macrophage by endocytosis in the alveoli of the lung. Mannose receptors binds to glycolipid of bacterial cell and complement receptors binds to the opsonized bacteria [Alamelu Raja., 2004]

ii) Survival of Bacilli within the Macrophage:

Tubercle bacilli prevent the formation of phagolysosome by inhibiting the gathering of the proteins and blocking the calcium signals. Once the fusion is inhibited, bacteria will start replicating unchecked within the vesicle. [Robbins et al., 2015]

In non-sensitised individuals, during the early stage of the disease, bacteria replicates and proliferates within the pulmonary alveolar macrophages causing bacteraemia and seeding it into multiple sites of the body. This results in theextra pulmonary spread of tuberculosis. [Robbins et al., 2015]

iii) Immune Response to the Tubercle Bacteria:

Once the mycobacterial antigen enters regional LN's, they are presented to the T-cells through antigen-presenting cells (APC's). This interaction leads to the differentiation of T-cell to form Helper-T-cell in the presence of IL-12 produced by APC's.These Helper-T-cells produce interferon-gamma (IFN-γ) which are critical mediators for macrophages containing M. tuberculosis bacteria. Thereby IFN-γ carry on three functionsa)

A) It stimulates phagolysosome maturation and allows the bacteria to face bactericidal actions of lysosomes.

b) It also stimulates the formation of nitric oxide, which combines with other oxidants to form nitrogen intermediates which in-turn again has a killing effect on the bacterium.

c)IFN-γ produces antimicrobial peptides which again has a lethal effect on the bacteria.

iv) Granuloma Formation: The hallmark feature of tuberculosis infection is the formation of granuloma or tuberculoma. IFN-γ transforms activated macrophages to epithelioid histiocytic which aggregate to form granulomas. Once these epithelioid cells start disintegrating from the center, it gives the appearance of central granular caseous necrosis. The periphery of the necrotic zone is surrounded by activated epithelioid cells and lymphocytes. Few of these epithelioid cells combine and form multinucleated giant cells (Langhan's giant cells [Robbins et al., 2015; Raviglione., 2010]

v) Cavitary Tuberculosis:

When the formation of caseous necrosis predominates, it gets transformed into a pus-filled cavity. This abscess cavity without the features of inflammation is called as cold

abscess. The tubercle bacilli multiply to the highest number within this cavity. If the cavity expands and erodes blood vessels, bacilli spread to the whole body. Whereas if the cavity gets ruptured into the airway, it becomes the mode of transmission. [Raviglione., 2010]

vi) Secondary TB Infection:

Secondary TB infection or reactivation of TB is seen when the dormant tubercle bacilli reactivate after the primary infection. It can present as a pulmonary or EPTB infection. Several risk factors are responsible for development of secondary TB namely immunosuppressed state due to HIV
infection, renal failure, sepsis, diabetes mellitus, malnutrition and long term use of corticosteroids. The lifetime risk of developing secondary TB is 10% in immunocompromised individuals [Grosset and Chaisson, 2017].

1.4 Clinical Manifestations of Tuberculosis

Tuberculosis presents with varied clinical signs and symptoms depending upon the Site and duration of infection.

Primary infection is always seen in the lungs. Clinically these patients present with Low-grade fever lasting for 3 weeks with other non- specific symptoms like productive cough, Pharyngitis and fatigue. [Davies et al., 2014].] Common Symptoms of pulmonary tuberculosis which includes chest pain, cough, bloody sputum, night sweating and fever are highly observed in such cases. And about 10 % of all (PTB) seem asymptomatic [Crowley, 2013; Al-Alwani et al 2022] .

1.5 Advancements in Tuberculosis Diagnostic Methods: The Role of GeneXpert Technology:

GeneXpert is considered more advanced than other methods for tuberculosis diagnosis for several reasons:

Molecular Detection: GeneXpert utilizes molecular techniques, specifically polymerase chain reaction (PCR), to detect the DNA of Mycobacterium tuberculosis complex. This method offers higher sensitivity and specificity compared to traditional techniques like Ziehl-Neelsen staining and fluorescent microscopy, which rely on visual identification of bacterial morphology.

Automation: GeneXpert is an automated system that performs sample processing, amplification, and detection in a closed cartridge system. This automation reduces the need for manual handling of samples, minimizes the risk of contamination, and standardizes the testing process, leading to more consistent and reliable results [Steingart et al.,2014; Opota et al., 2016].

Rapid Turnaround Time: GeneXpert provides rapid results, typically within 2 hours, compared to several days required for culture-based methods like Ziehl-Neelsen staining and fluorescent microscopy. This quick turnaround time enables healthcare providers to promptly initiate treatment and infection control measures, improving patient outcomes and reducing the risk of transmission.

Simultaneous Detection of Rifampicin Resistance: GeneXpert assays include detection of rifampicin resistance-associated mutations in the rpoB gene, allowing for simultaneous identification of multidrug-resistant tuberculosis (MDR-TB). This capability is crucial for guiding appropriate treatment decisions and preventing the spread of drug-resistant strains.

Ease of Use: GeneXpert systems are user-friendly and require minimal training to operate, making them suitable for use in a variety of healthcare settings, including resource-limited settings and point-of-care facilities. This accessibility facilitates widespread adoption and implementation of molecular diagnostic testing for tuberculosis (Barksdale et al., 1977).

MATERIALS AND METHODS

The Study Design and Study Area:

This cross-sectional study was conducted at the TB center DHQ Hospital Bannu, Pakistan. Study duration:I collect data of four months from December 2023 to march 2024 in twelve
(12) days duration of my research work at DHQ hospital Bannu.

Materials:

- GeneXpert machine
- GeneXpert MTB Cartridges
- Sputum collection cups
- Sample reagent buffer
- Pipettes
- Biosafety cabinet
- Computer with GeneXpert software
- Personal Protective Equipment (PPE) (gloves, lab coat, mask, goggles)

Diagnosis of the Patients:

Those patients Complaining of cough for more than two weeks, Moderate pyrexia in the evening time, chest pain, Sputum containing blood, low body mass/ height Ratio was advised early morning sputum specimen For the sputum microscopy and Xpert MTB/RIF Assay to detect MTB level. Study was based on Factors associate frequency of deformities in road traffic accident presented to

Samplecollection:

Mucoussamplewascollectedfrompatientsina collectioncups.

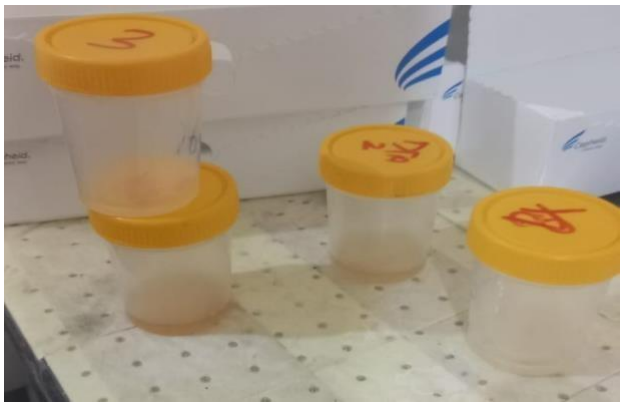

Figure 1: Sample

Data Collection:

The Data was collected from TB GeneXpert register in TB center at DHQ hospital BannuKpkPakistan.

XpertMTB/RIFassay:

The specimens for Xpert MTB/RIF assay were processed using the Standard N-Acetyl-L-cysteine–NaOH technique. N-Acetyl-L-cysteine–NaOH was added to the Specimen in a closed sterilecontainer ina2:1ratio forde-contamination andliquefactionof themucus Sample.Using a fresh transfer pipette, 2 ml of the Prepared specimen was transferred to an Xpert MTB/Rif assay cartridge. The cartridge was then Loaded into the specified module of the GeneXpert Machine. The interpretation Is software-based. The result was recorded as MTB detected (high, medium, low, and very low)/MTB not detected and rifampicin-resistance (RR) Detected/ not detected/ in determinant.

Figure 2: Cartridge

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Figure 3: GeneXpert Machine

RESULTS:

In this study, we analyzed a total of 1477 suspected cases of Mycobacterium tuberculosis (MTB) using the GeneXpert diagnostic method. The results are detailed as follows:

MTB Positive Cases: Out of 1477 suspected cases, 313 (21.2%) were confirmed to be MTB positive.

Low Level: Among these positive cases, 121 (38.7%) had a low level of bacterial load.

Medium Level: 117 (37.4%) of the positive cases had a medium level of bacterial load.

High Level: 70 (22.4%) of the positive cases had a high level of bacterial load.

MTB Negative Cases: A significant majority, 1037 (70.2%) of the cases, were found to be MTB negative.

Relapse Cases: We identified 11 (0.7%) cases as relapse, indicating patients who had previously been treated for TB and are now experiencing a return of the disease.

Follow up cases (FUP): Additionally, 16 (1.1%) cases were categorized as follow-up, referring to patients who were under ongoing observation or treatment.

Distribution of patients by months:

Months	Susceptible cases	MTB positive (+ve)cases	MTB(-ve) cases	Relapse	FUP	Percentageof detected(+ve) patients
December	457	100	344	05	08	21%
January	398	70	314	06	08	17%
February	358	85	273	0	0	23%
March	264	58	206	0	0	21%
Total	1477	313	1037	11	16	82%

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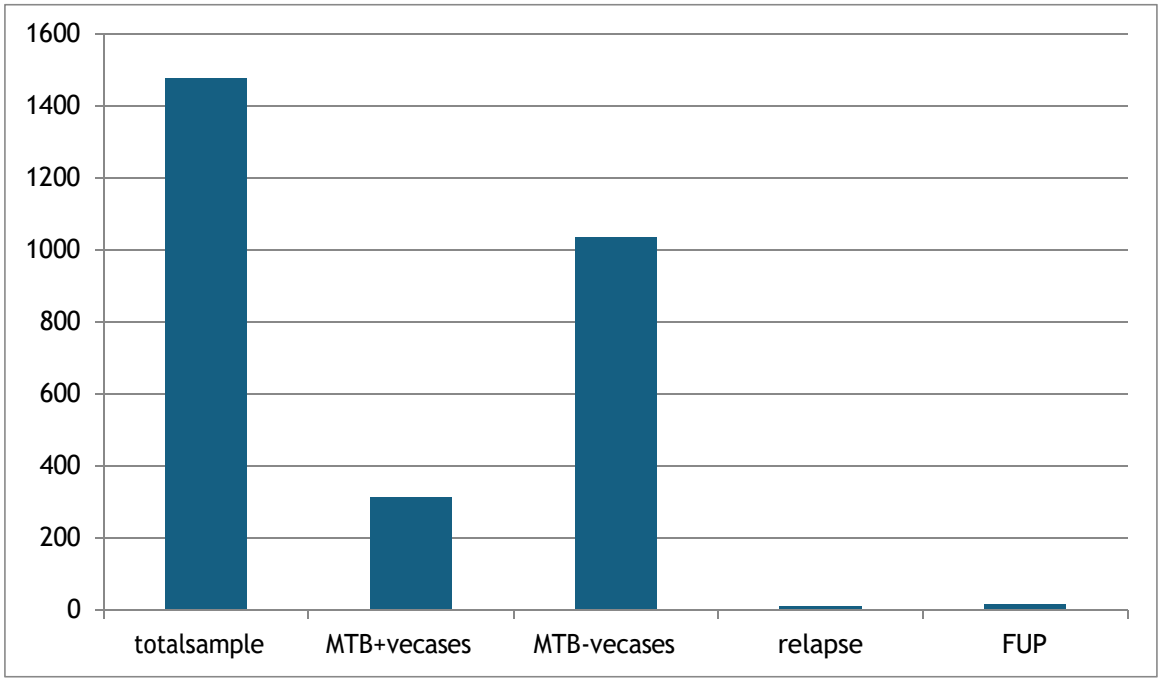
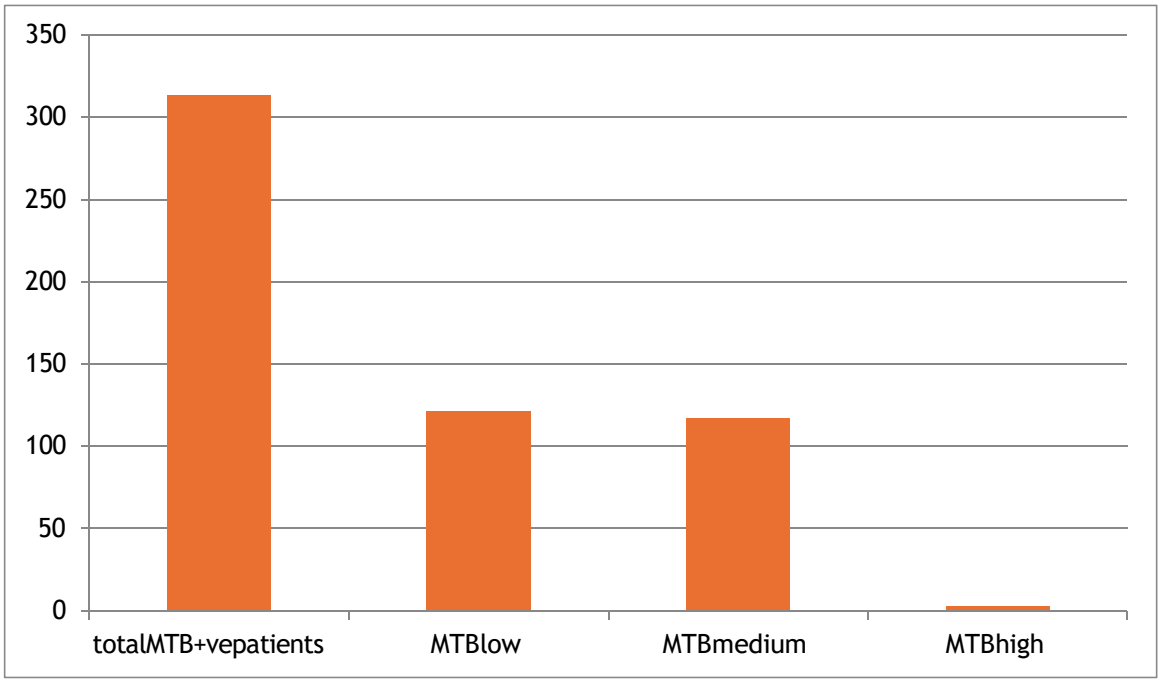
Distribution of MTB detected patients with low/medium/high Levels:

Months	Patients with positive result	MTB Low	MTB Medium	MTB High
December	100	55	20	25
January	70	29	35	06
February	85	20	33	27
March	58	17	29	12
Total	313	121	117	70

Graph 1



Graph 2



DISSCUSSION:

In this study, we utilized the GeneXpert method to diagnose Mycobacterium tuberculosis (MTB) in a large sample of 1477 suspected cases. The results provide important insights into the prevalence and severity of MTB in the studied population.

Prevalence of MTB:

Out of 1477 suspected cases, 313 (21.2%) were confirmed to be MTB positive. This indicates that more than one-fifth of the tested individuals were infected with MTB, highlighting a significant public health concern. This prevalence rate emphasizes the need for effective diagnostic methods and prompt treatment to control the spread of tuberculosis (TB).

Bacterial Load Distribution:

The MTB positive cases were further categorized based on bacterial load:

Low Level: 121 cases (38.7%) had a low bacterial load.

Medium Level: 117 cases (37.4%) had a medium bacterial load.

High Level: 70 cases (22.4%) had a high bacterial load.

The distribution of bacterial loads is crucial for understanding the potential infectiousness and disease severity. Patients with a high bacterial load are likely to be more infectious and may require more intensive treatment and isolation measures. On

the other hand, those with a low bacterial load might be in the early stages of infection or may have a less severe form of the disease.

MTB Negative Cases:

A significant portion of the cases, 1037 (70.2%), were MTB negative. This suggests that while these individuals showed symptoms or signs that warranted testing, they did not have active TB. This high percentage of negative results could be due to other respiratory conditions presenting with similar symptoms to TB, underscoring the importance of differential diagnosis in respiratory diseases.

Relapse and Follow-Up Cases:

The study also identified 11 relapse cases (0.7%) and 16 follow-up (FUP) cases (1.1%). Relapse cases represent individuals who have previously been treated for TB but have experienced a recurrence of the disease. Follow-up cases include patients who are being monitored after initial diagnosis and treatment. The identification of these cases is important for understanding the challenges in TB treatment and the necessity for continuous monitoring to prevent relapse and ensure successful treatment outcomes.

Implications for TB Management:

The use of the GeneXpert method provided rapid and accurate diagnosis, which is essential for effective TB management. By categorizing MTB positive cases into low, medium, and high bacterial loads, healthcare providers can tailor treatment strategies to the severity of the infection. Patients with higher bacterial loads may need more aggressive treatment and closer monitoring, while those with lower loads may benefit from standard treatment protocols.

Public Health Significance:

The data from this study underscore the importance of widespread and accessible TB diagnostic services. Early detection and appropriate categorization of MTB cases can significantly impact the management and control of TB. Public health efforts should focus on increasing the availability of diagnostic tools like GeneXpert, enhancing follow-up care for patients, and implementing targeted interventions for those with high bacterial loads.

CONCLUSION

This study used the GeneXpert method to test 1477 individuals for Mycobacterium tuberculosis (MTB). We found that 313 (21.2%) were MTB positive, and 1037 (70.2%) were MTB negative. Among the positive cases, 121 had a low bacterial load, 117 had a medium bacterial load, and 70 had a high bacterial load. Additionally, we identified 11 relapse cases and 16 follow-up cases. The GeneXpert method was highly effective in diagnosing MTB and determining the severity of the infection based on bacterial load.

This is important because it helps doctors provide the right level of treatment for each patient. Patients with higher bacterial loads might need more aggressive treatment. The large number of MTB negative cases indicates that many people with TB-like symptoms do not actually have TB, highlighting the need for precise diagnosis. Continuous monitoring of relapse and follow-up cases is essential to prevent the recurrence of TB and to ensure that treatments are successful.

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