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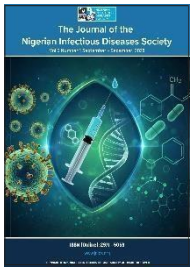

Original Article

Prevalence of Pulmonary Tuberculosis among Hausa-Fulani Patients attending National Tuberculosis, Leprosy and Buruli Ulcer Training Centre and Referral Hospital Saye Zaria, Kaduna State Nigeria

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ABSTRACT

Tuberculosis (TB), a disease caused by Mycobacterium tuberculosis (MTB), is the main cause of death due to an infectious disease.) A total of 1.25 million people died from tuberculosis (TB) in 2023 (including 161 000 people with HIV). The Hausa-Fulani identity came into being as a direct result of the migration of Fulani people to Hausa land around the 14th century and their cultural assimilation "into the Hausa society" Consumption of “Nono” (fermented milk) by Hausa-Fulani in Nigeria is a well-known accepted tradition. Depending on its preservation and process-line, microorganisms other than lactic acid bacteria including MTB could be found in the nono. Bacterial load of TB patients determines their level of infectiousness. This research was aimed at determining the Prevalence of Pulmonary Tuberculosis among Hausa- Fulani Patients attending National Tuberculosis, Leprosy and Buruli ulcer Training Centre Saye Zaria, Kaduna state Nigeria. In total, 557 patients with presumptive TB were screened using Xpert MTB/RIF ultra and 51 (9.2%) turn out to be positive for PTB. From 51 positive TB patients, majority (27) have high bacterial load. This study reveals high prevalence of PTB among the study population and have greater chances of spreading infection.

Background

Tuberculosis (TB), a disease caused by Mycobacterium tuberculosis (MTB), is the main cause of death due to an infectious disease (1). TB is a global health threat with its detrimental effects mostly occurring in developing countries (2). A total of 1.25 million people died from tuberculosis (TB) in 2023 (including 161 000 people with HIV). Worldwide, TB has probably returned to being the world’s leading cause of death from a single infectious agent, following three years in which it was replaced by coronavirus disease (COVID-19).

Keywords: Tuberculosis, Hausa-Fulani, Prevalence

It was also the leading killer of people with HIV and a major cause of deaths related to antimicrobial resistance [1]. About a quarter of the global population is estimated to have been infected with TB bacteria. About 5-10% of people infected with TB will eventually get symptoms and develop TB disease. MTB is distinct from other microorganisms not only due to its slow growth and difficulties to study in the laboratory, but also due to its inherent physiology such as its complex cell envelope and its metabolic pathways [3]. Most of the people who develop TB disease each year are in 30 high TB burden countries, which accounted for 87% of the global total in 2023 [1].

TB is predominantly a disease of the lung, with pulmonary TB accounting for 70% of cases, although MTB can disseminate to other organs, including lymph nodes, bone, and meninges, and cause extrapulmonary disease [4]. Infectious airborne droplets are responsible for TB transmission and are directly related to duration of exposure to airborne infectious particles [5]. Five minutes of talking, or 1 cough, produce equivalent numbers of infectious particles, which can remain airborne for 30 minutes [6]. Airborne transmission requires multiple steps to occur. The first is aerosol generation by an infectious source, which must then be transported through the air to a susceptible host with successful deposition in an anatomical location that facilitates infection. Throughout this journey, the pathogen must retain viability, despite considerable environmental stressors, such as desiccation and ultraviolet light exposure [7]. Crowded living conditions in the ghettos and concentration camps, poor sanitation, and near starvation diets contributed to the spread of TB [8].

WHO recommends the use of rapid molecular diagnostic tests as the initial diagnostic test in all persons with signs and symptoms of TB. Rapid diagnostic tests recommended by WHO include the Xpert MTB/RIF Ultra and Truenat assays. These tests have high diagnostic accuracy and will lead to major improvements in the early detection of TB and drug-resistant TB [1].

The Hausa-Fulani identity came into being as a direct result of the migration of Fulani people to Hausa land around the 14th century and their cultural assimilation into the Hausa society [9]. As a result of this assimilation, Hausa-Fulani form the core and vast majority of the populations of Daura, Zamfara, Kano, Katsina, Zazzau, and Sokoto [10].

Consumption of “Nono” (fermented milk) by Hausa-Fulani in Nigeria is a well-known accepted tradition [11]. Depending on its preservation and process-line, microorganisms other than lactic acid bacteria could be found in the *nono*. Milk’s nutritional composition makes it not only suitable for human nutrition but also ideal for microbial life. Different categories of microorganisms including fungi, bacteria, rickettsia and viruses could be found in milk since the udder of the animal could harbour organisms while others come as contaminants due to poor handling [11].

This research was aimed at determining the Prevalence of Pulmonary Tuberculosis among Hausa-Fulani Patients attending National Tuberculosis, Leprosy and Buruli ulcer Training Centre Saye Zaria, Kaduna state Nigeria

METHODOLOGY

Study design

This was a cross-sectional study

Study area

The study was conducted in Kaduna State located in the Northwest Geopolitical Zone of Nigeria. The State lies between latitudes 60 and 110 North and longitude 70 and 440 East and 608 meters above sea level. It has distinct wet and dry seasons and is within the Northern Guinea Savannah zone and part of Sahel Savannah zone of Nigeria. The State shares geographical boundaries with Katsina and Zamfara States to the North, Plateau and Bauchi States to the East, Nasarawa State and the Federal Capital Territory to the South, Niger State to the West, and Kano State to the Northeast. Kaduna State occupies about 48,473.25 sq km, with a human population of over 6,066,562 people according to the census figures of 2006 [12].

Figure 1: Map of Nigeria showing study area (Source- premium times Nigeria)

Study population

Hausa-Fulani presumptive PTB patients were enrolled in the study after they consented

Ethical consideration

The study was carried out in accordance with The Code of Ethics of the World Medical Association (Declaration of Helsinki) for experiments on humans. The Ethical approval for the research was sought from Health and Research Ethical Committee of NTBLTC Saye, Zaria (NTBLTCZ/HREC/E18/2022). Written informed consent was also sought from all participants.

Laboratory analysis

Xpert MTB/RIF Assay

The GeneXpert system is a fully automated semi quantitative nested real-time PCR system, which detects MTB complex DNA in sputum and other extra pulmonary samples.

It simultaneously identifies mutations in the *rpoB* gene, which are associated with rifampicin resistance.

The primers in the Xpert MTB/RIF assay amplify a portion of the *rpoB* gene containing the 81base pair "core" region. The probes are able to differentiate between the conserved wild-type sequence and mutations in the core region that are associated with Rifampicin resistance. Furthermore, the assay includes a sample processing control (SPC) to control for adequate processing of the target bacteria and to monitor the presence of inhibitor(s) in the PCR reaction. A Probe Check Control (PCC) verifies reagent rehydration, PCR tube filling in the cartridge, probe integrity, and dye stability [13].

Data analysis

The data was edited and summarized using Microsoft excel, missing values and outliers were identified and recorded appropriately. Normality test and tests of significance was conducted using Graph Pad Prism version 8. For ethical reasons, participants' initials were de-identified and coded. Results obtained was presented in charts and table

Results

In total, 557 patients with presumptive TB were screened and a total of 51 (9.2%) turn out to be positive for PTB. This is depicted in figure 2.

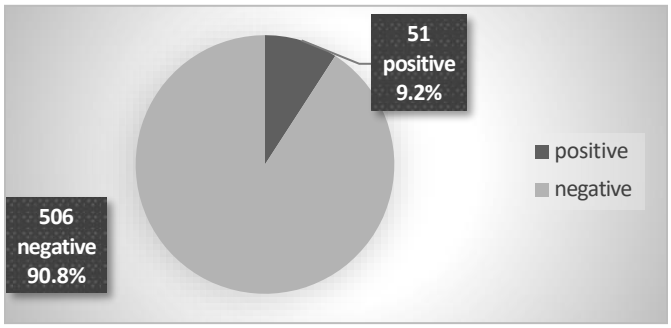

Figure 2: Prevalence of PTB among study participants

The results are interpreted by the GeneXpert DX System from measured fluorescent signals and embedded calculation algorithms and will be automatically displayed. Lower Ct values represent a higher starting concentration of DNA template; higher Ct values represent a lower concentration of DNA template [14].

TB Results	RIF Results
MTB DETECTED HIGH	RIF Resistance DETECTED
MTB DETECTED HIGH	RIF Resistance NOT DETECTED
MTB DETECTED HIGH	RIF Resistance INDETERMINATE
MTB DETECTED MEDIUM	RIF Resistance DETECTED
MTB DETECTED MEDIUM	RIF Resistance NOT DETECTED
MTB DETECTED MEDIUM	RIF Resistance INDETERMINATE
MTB DETECTED LOW	RIF Resistance DETECTED
MTB DETECTED LOW	RIF Resistance NOT DETECTED
MTB DETECTED LOW	RIF Resistance INDETERMINATE
MTB DETECTED VERY LOW	RIF Resistance DETECTED
MTB DETECTED VERY LOW	RIF Resistance NOT DETECTED
MTB DETECTED VERY LOW	RIF Resistance INDETERMINATE
MTB Trace[a] DETECTED	RIF Resistance INDETERMINATE
MTB NOT DETECTED	
INVALID	
ERROR	
NO RESULT	

Ct range: High <16, Medium 16-22, Low 22-28, Very low >28

Figure 3: Possible GeneXpert result (Cepheid, 2021)

Table 1 shows bacterial load of MTB among study participants. Majority (52.9%) of the participants had a high bacterial load of MTB with a frequency of 27. Participants with medium bacterial load had a frequency of 10 (19.6%), those with low and very low had a frequency of 8 and 6 (15.7 and 11.8%) respectively.

Table 1: Bacterial load of MTB among study participants

Level	Frequency	% (95% CI)
High	27	52.9 (38.5 – 67.1)
Medium	10	19.6 (9.8 – 33.1)
Low	8	15.7 (7.0 – 28.6)
Very low	6	11.8 (4.4 – 23.9)

Univariate analysis; CI: confidence interval

Discussion

This study showed a high prevalence of 9.2(%) Pulmonary Tuberculosis (PTB) among the study participants which could be as a result of recovery from COVID related disruption since the study was conducted after the pandemic. It may also be associated with lifestyle of the study participant which are culturally known to consume mostly unpasteurised milk; a major source of zoonotic TB [15]. Nigeria has also been known to have high TB burden [16].

Also, may be due to the fact that the study was a hospital based one, conducted in one of the National TB Reference Centre as such most of the people visiting the hospital are presumptive of the disease. This is similar to that reported by Ogbudebe et al. [17] who shows a prevalence of 10.1(%) among his study participants. High prevalence 12.2(%) and 13.6(%) were reported by Agabi et al. [18] and Ajide et al. [19] in Jos and Nasarawa respectively. A Higher prevalence than that found in this study was also reported by Tukur et al. [20] in Kano state (22.8%), Obadire et al. [21] in Jigawa state (19.1%), Amala and Goodluck [22] in Bayelsa state (40%), Babajide et al. [23] in Ogun state (16.7%), Edem et al. [24] in Akwaibom state (22.9%), Oyodeji et al. [25] in Osun state, Nigeria. Similarly, higher prevalence was also identified by Audu et al., [26] in Nasarawa North Central and Abdulkadir and Ibrahim [27] in Kebbi who reported 18.8% and 17.3% respectively. The differences observed between this study and that of other previous researchers may be due to differences in sample size, study design, socio-economic factors and participants used.

Genexpert machine is an indispensable tool in early TB diagnosis especially in low- and middle-income countries [28]. It has the ability to detect DNA of all Mycobacterium Tuberculosis Complex (MTBC) including M. bovis [29]. Even though in clinical practice, the interest relies usually on the result being positive or negative, the description of semi quantitative values also details sensitivity of the tool. However, it was not possible to find a study that focused on the bacterial load upon which the technique classified the results (high, medium, low, very low or trace) for comparison with the findings from this study.

The findings of this study shows that; majority of study participants 27(52.9%) had high MTB detection result while only 6(11.8%) had Very low result. The findings of the research, in addition to giving insight of the technique's sensitivity, also tells that majority of the participants produced a good quality sputum specimen. This can be attributed to proper patient education on how to produce a qualitative specimen, which will in turn lead to adequate bacterial yield in the specimen. The quality of specimen has been associated with MTB positivity in Xpert MTB/RIF result [29]. Also, the study was conducted in National TB Reference Laboratory which is an accredited Laboratory and possesses expertise in TB diagnosis as such patients are expected to be properly educated on how to produce a good quality specimen. The bacterial load in tuberculosis (TB) patients is a key factor in determining their level of infectiousness.

It has also been established that the more tubercle bacilli a patient expels into the air, the more infectious they are. Hence, patients with a higher bacterial load, are more likely to spread the infection [30].

Conclusion: This study reveals high prevalence of PTB among the study population and have greater chances of spreading infection

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