Trends and Risk Factors for Drug-Resistant Tuberculosis in Nairobi County, Kenya: A Comparative Analysis Before, During and After COVID-19

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Abstract

Background: Drug-resistant tuberculosis (DR-TB) is associated with a significant health burden and poses a major impediment to TB eradication. In Kenya, the COVID-19 pandemic disrupted healthcare services between March 2020 and February 2022. Consequently, the burden of DR-TB was projected to worsen. Despite these concerns, the impact of the pandemic on its trends remains unexplored. We conducted a quasi-experimental study to compare epidemiological trends of DR-TB before, during, and after the COVID-19 pandemic, and to identify associated risk factors in Nairobi County.

Methodology: A quasi-experimental design utilising single-group interrupted time series (ITSA) was employed to assess the impact of COVID-19–related health system disruptions on DR-TB trends in Nairobi County. Laboratory-confirmed DR-TB data were retrieved from the TIBULIMS database and stratified by diagnosis period: pre-pandemic (March 2018–February 2020), intra-pandemic (March 2020–February 2022), and post-pandemic (March 2022–February 2024). Analyses were performed in STATA version 15.

Results: A total of 616 DR-TB patient records were analysed. Overall, DR-TB cases rose slightly by 2.82%, from 213 pre-COVID-19 to 219 intra-COVID-19, and then declined significantly by 15.98% to 184 post-COVID-19 ($p < 0.001$). Cases were over twice as common among males. HIV infection was significantly associated with RR-TB (43.55%; $n = 248$, $p < 0.0001$) and monoresistant TB (21.02%; $n = 214$, $p < 0.0001$). ITSA showed significant COVID-19-related level changes in RR-TB, with an upsurge trend at the onset of the pandemic (+5.96 cases per quarter, $p = 0.006$), followed by a non-significant decline intra-pandemic, and a subsequent moderate increase post-pandemic (+2.56 cases per quarter, $p = 0.022$). Level changes observed in MDR-TB and MR-TB trends were not attributable to the pandemic ($p = 0.094$ and $p = 0.0799$, respectively).

Conclusion: The study revealed fluctuations in MDR-TB, RR-TB, and MR-TB trends during the period. COVID-19-related health disruptions caused significant level changes in RR-TB trends. These findings highlight the importance of sustaining DR-TB diagnostic and treatment services to safeguard progress in TB control even during future public health crises.

***Keywords**: Drug-resistant, Nairobi, Tuberculosis, COVID-19*

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Introduction

Drug-resistant tuberculosis (DR-TB) is a clinically significant and severe form of tuberculosis (TB) characterised by infection with Mycobacterium tuberculosis (M. tuberculosis) strains resistant to one or more of the standard anti-TB drugs, typically due to inadequate treatment, suboptimal regimens, or poor adherence to therapy(1, 2).

Different subtypes of DR-TB exist based on resistance patterns—including; mono-resistant TB (MR-TB), polydrug-resistant TB (PDR-TB), rifampicin-resistant TB (RR-TB), multidrug-resistant TB (MDR-TB), pre-extensively drug-resistant TB (Pre-XDR-TB), and extensively drug-resistant TB (XDR-TB)(3, 4). All these subtypes are associated with substantial treatment challenges, marked by narrowed therapeutic options and increased drug-related toxicity, often resulting in adverse clinical outcome(5, 6).

According to the Global Tuberculosis Report 2022, the emergence of the COVID-19 pandemic in 2019 severely disrupted access to TB care, resulting in a major setback to global TB control efforts. For instance, in most countries, health resources were extensively redirected toward pandemic response, shifting focus away from TB control efforts(7, 8). Government-imposed restrictions, stigma, and hesitancy among healthcare providers driven by fear of COVID-19 infection further limited access to TB diagnostic and treatment services, leaving many presumptive TB and DR-TB cases undiagnosed(9-11).

Consequently, the WHO 2022 report documented a 3.1% increase in DR-TB incidence, with cases rising from 437,000 to 450,000 between 2020 and 2021(12). In contrast, Kenya's National Tuberculosis, Leprosy and Lung Disease Program (NTLD-P) reported a 48% decline in overall TB case detection rates, with a notable 16% reduction in DR-TB notification rates, falling from 961 to 804 cases over the same period. This decline suggested increased community transmission resulting from disrupted diagnosis and treatment services(13).

At the subnational level, a pre-COVID-19 survey conducted in Nairobi County reported a 1.5% prevalence of resistance to both first- and second-line TB drugs(14). While these trends were expected to change following the COVID-19-related healthcare disruptions, there have been no recent studies into the burden of the disease in the Nairobi—the county worst hit by the pandemic(15, 16). We hypothesised that trends of major DR-TB subtypes were significantly altered in the aftermath of the pandemic in the county.

This study compared temporal trends of major DR-TB subtypes before, during, and after the pandemic, and identified the associated risk factors, including HIV co-infection. Understanding these trends and risk factors is critical for guiding targeted interventions, optimising resource allocation, and strengthening TB control policies in high-burden urban settings, particularly during public health crises.

Methodology

Research design

The study adopted a quasi-experimental design. A single-group interrupted time series analysis with a segmented regression model was fitted to assess the impact of the COVID-19 pandemic on the trends of DR-TB across Nairobi County. This approach was chosen for its robustness in capturing temporal changes in outcomes following a clearly defined intervention or disruption(17). The model was formulated as:

$$Yt=\beta0+ \beta1Tt + \beta2\ Xt + \beta3Tt + \beta4Xt + \beta5Tt +\epsilon t$$

Where: β_0: baseline level; $\beta_1 T_t$: pre-pandemic trend; $\beta_2 X_t$: immediate impact of COVID-19 emergence on trend; $\beta_3 T_t$: trend during pandemic; $\beta_4 X_t$: immediate impact on trend post-pandemic; $\beta_5 T_t$: post-pandemic trend; ϵ_t: error term.

Study setting

This study was conducted in Nairobi, the county worst affected by the COVID-19 pandemic. As of March 31, 2022, the county accounted for nearly 40% of all reported COVID-19 cases countrywide. Consequently, stringent containment policies were implemented to control the outbreak, significantly disrupting the utilisation of TB services in the county(18).

Study population

Patients with confirmed pulmonary DR-TB diagnosed at public health facilities in Nairobi County were included, and data were abstracted from their medical records for secondary analysis.

Inclusion and exclusion criteria

Patients with confirmed pulmonary DR-TB attending public health facilities in Nairobi County between March 2018 and February 2024 were included, while those with extra-pulmonary DR-TB were excluded.

Sample size determination

Sample size was determined using a formula for comparing proportions(19), with p_1 = 1.5% based on a 2019 DR-TB prevalence study in Nairobi (pre-COVID-19), and p_2 = 4.5%, assuming a three-fold increase post-COVID-19(12, 14). Using $Z\alpha/2 = 1.96$ (5% significance) and $Z\beta = 0.84$ (80% power).

$$n = \frac{p_1(1-p_1) + p_2(1-p_2)}{(p_2-p_1)^2} * (Z_\beta + Z_\alpha)^2$$

Thus, sample size (n):

n= [(0.015(1-0.015) +0.045(1-0.045))/(0.045-0.015)] *(1.96+0.84)2

n= [(0.014775+0.042975)/0.032] *7.84

n= 504

Considering a 20% attrition rate. Therefore, 504 represents 80% of the intended sample size.

n=504/0.8

n=630

A minimum of 504 patient records was required. To account for potential data attrition, a 20% adjustment was applied, as adopted by similar studies(20). This yielded a target of approximately 630 cases. However, due to minor data losses during abstraction, 616 patient files were ultimately included, which still satisfied the desired buffer and ensured adequate power and data completeness.

Sampling procedure

Proportional stratified sampling was employed, with three strata defined by the period of diagnosis: pre–COVID-19 (March 2018–February 2020), during COVID-19 (March 2020–February 2022), and post–COVID-19 (March 2022–February 2024), comprising a total of 24 quarters.

Within each quarter, all eligible cases were assigned unique random numbers generated in Microsoft Excel using the RAND() function. The dataset for each quarter was then sorted in ascending order of these random numbers to randomise the records. From each randomised list, a proportional number of cases, corresponding to that quarter's share of the overall caseload, was selected to ensure representative sampling across all strata.

Data source

Secondary data covering March 2018 to February 2024 were extracted from the Tuberculosis Information Basic Unit Laboratory Information Management System (TIBULIMS), Kenya's national TB surveillance database.

Data collection

The dataset, containing relevant variables such as date of case registration, age, residence, gender, height, weight, history of previous TB infection, drug susceptibility results, and comorbidities, was exported in Excel format, which is TIBULIMS's default standardised export format developed and predefined by the NTLD-P.

To minimise bias, duplicate records were removed after cross-checking patient identifiers and demographic variables. The demographic profiles of excluded extra-pulmonary DR-TB cases were also compared with those of included pulmonary cases to ensure data accuracy.

Data analysis

Extracted data were cleaned, coded and analysed using STATA ver. 15. Descriptive statistics, including frequency tabulations and summary measures, were used to describe the characteristics of the patient population. Multivariate Poisson regression analysis was used to assess risk factors, while trends were assessed using a segmented regression model designed for a single-group interrupted time series analysis. Outputs with p-values < 0.05 and those within a significant 95% confidence interval were reported.

Ethical considerations

Ethical approval was sought from the Scientific and Ethics Review Unit (No: KEMRI/SERU/CRDR/107/5012) and the research license from the National Commission for Science, Technology and Innovation (License No: NACOSTI/P/24/39931). In compliance with data protection requirements, patient identifiers were excluded during data extraction. Further, the data were anonymised and access to the dataset was restricted to the study team. As this study utilised secondary de-identified data from routine TB surveillance, a waiver of informed consent was granted.

Results

Characteristics of the DR-TB Patients

A total of 616 DR-TB patients' records were retrieved from the TIBULIMS database and reviewed for analysis. Of these, 69.16% were males while 30.84% were females (n=616). The average age of the cases at registration was 35.11 years, with a range of 4 months to 75 years.

Trends of DR-TB cases pre-, during-, and post-COVID-19 pandemic

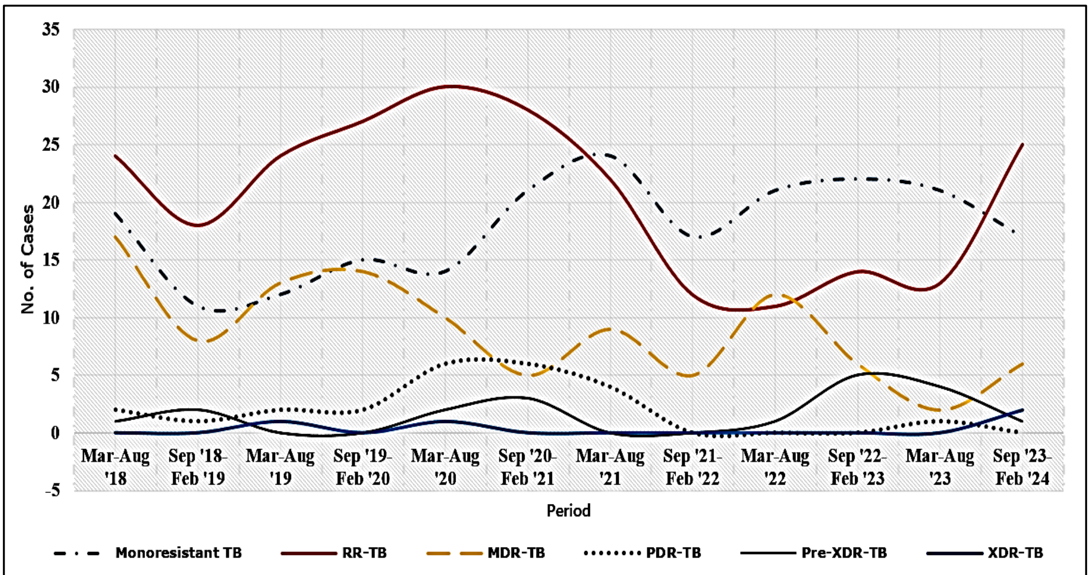
Overall, DR-TB cases showed a slight increase of 2.82%, rising from 213 pre-COVID-19 to 219 during the pandemic, followed by a significant decline of 15.98% to 184 in the post-pandemic period ($p < 0.001$). In terms of subtype patterns, MDR-TB declined from 24.4% (n=213) pre-COVID-19 to 13.2% (n=219) during COVID-19, and 14.1% (n=184) post-COVID-19. RR-TB dropped from 43.7% (n=213) to 42.0% (n=219) during COVID, and further to 34.2% (n=184) post-COVID-19. Conversely, MR-TB trends were on the upward trajectory, with numbers rising from 26.76% (n=213) pre-COVID-19 to 44.02% (n=184) post-COVID-19, as shown in Figure 1.

The distribution patterns of DR-TB subtypes

Young adults were disproportionately affected, with this group constituting more than half of all the RR-TB cases (56.9%, n = 248), as illustrated in Figure 2. With respect to prior TB history, newly diagnosed cases represented the majority of DR-TB cases (59.1%, n = 616), as shown in Figure 3.

The influence of socio-demographic and clinical factors on the incidence of DR-TB in Nairobi County

Candidate variables for the multivariate Poisson regression model were selected based on statistically significant chi-square tests and supporting evidence from prior literature. The chi-square tests showed significant associations between MR-TB and age, RR-TB and TB history, MR-TB and TB history, and both RR-TB and MR-TB with HIV co-infection. The findings are tabulated in Table 1.

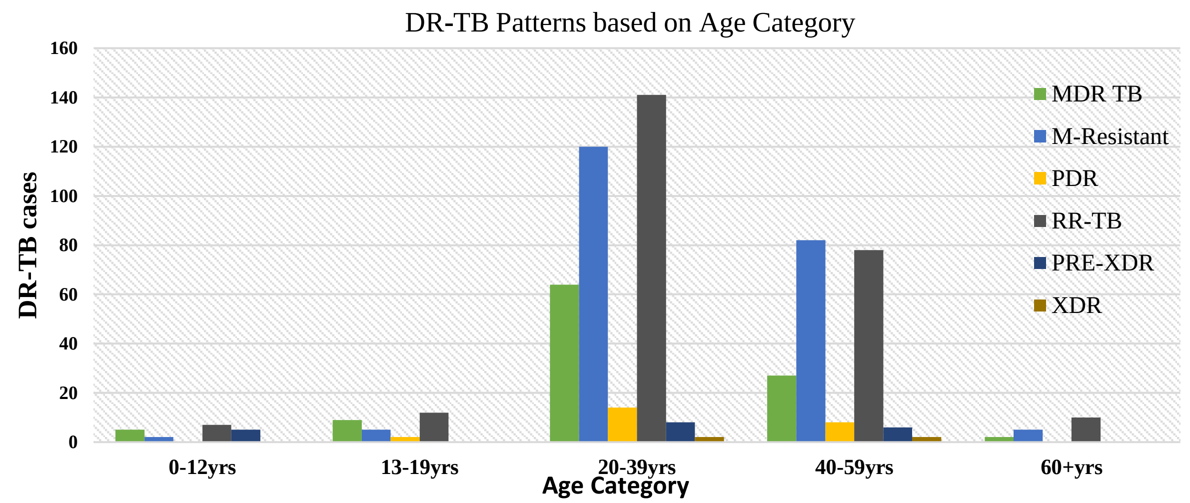


Legend: TB: Tuberculosis, MDR-TB: Multidrug-resistant TB, RR-TB: Rifampicin-resistant TB, PDR-TB: Polydrug-resistant TB; Pre-XDR-TB: Pre-extensively drug-resistant TB, XDR-TB: Extensively drug-resistant TB

Figure 1:
Trends in DR-TB subtypes across three periods: pre-COVID-19 (March 2018–February 2020), during COVID-19 (March 2020–February 2022), and post-COVID-19 (March 2022–February 2024) in Nairobi County.

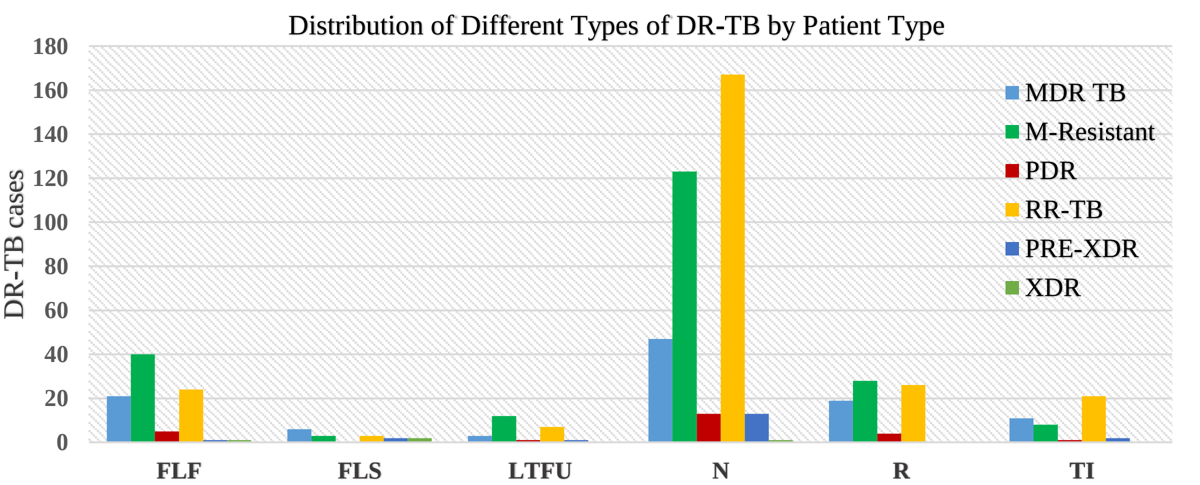
The regression model findings indicated that MDR-TB incidence declined by 44.91% intra-COVID-19, compared to the pre-COVID-19, controlling for other factors (irr= 0.55, p = 0.012). Additionally, MDR-TB incidence was significantly higher among the first-line treatment failures (1.7 times, p = 0.046), first-line treatment success group (2.69 times, p = 0.025), relapse group (1.97 times, p = 0.014), and transfer-in group (2.25 times, p = 0.019), compared to newly diagnosed individuals. Further, the incidence of MR-TB increased by 59.5% in the post-pandemic period compared to the pre-pandemic period, after adjusting for other factors (irr = 1.5945, p = 0.008).

HIV status was a significant predictor of RR-TB incidence, with HIV-positive individuals having a 66.4% higher RR-TB infection compared to their HIV-negative counterparts (irr = 1.6636, p < 0.001).



Legend: DR-TB - drug-resistant Tuberculosis; MDR-TB - Multidrug-resistant TB; M-Resistant - Monoresistant TB; RR-TB - Rifampicin-resistant TB; PDR-TB - Polydrug-resistant TB; Pre-XDR- Pre-extensively drug-resistant TB; XDR- Exte

Figure 2:
Distribution of various DR-TB subtypes by age category in Nairobi County



Legend: FLF: First-line treatment failures, FLS: First-line treatment success, R: Relapse, N: New, TI: Transfer-ins, LTFU: Lost-to-follow-up, TB: Tuberculosis; M-Resistant: Monoresistant TB; MDR-TB: Multidrug-resistant TB; RR-TB: Rifampicin-resistant TB;

Figure 3:
Distribution of DR-TB subtypes by patient type (history of previous TB infection) in Nairobi County.

PDR-TB, pre-XDR-TB, and XDR-TB cases were excluded from the Poisson regression analysis due to their low sample sizes, which would have led to unreliable estimates. Age was an effect modifier, affecting the relationship between history of previous TB infection and DR-TB risk.

Impact of the COVID-19 pandemic on DR-TB trends

Trends of RR-TB

The model significantly predicted RR-TB trends ($p < 0.0001$). Baseline cases were eight ($\beta 0$), with a non-significant rising trend pre-COVID ($\beta 1$ =+0.7 cases/quarter, $p = 0.418$).

Table 1:

A Characterisation of DR-TB Cases by Sociodemographic and Clinical Factors

Risk Factor Analysis							
Outcome	Significant variable	irr	Std. Err.	z	P>z	[95% CI]	
MDR-TB	COVID-19 Period	Reference					
	Intra-COVID-19	0.5509	0.1309	-2.5100	0.0120	0.3458	0.8776
	Post-COVID-19	0.6424	0.15876	-1.7900	0.0730	0.3958	1.0428
	HIV Status						
	Negative	Reference					
	Not done	0.0000	0.00116	-0.0200	0.9840	0.0000	.
	Positive	1.0249	0.21672	0.1200	0.9070	0.6771	1.5512
	Patient type						
	Newly diagnosed	Reference					
	First-line failure	1.6978	0.4509	1.9900	0.0460	1.0089	2.8573
	First-line success	2.6926	1.1920	2.2400	0.0250	1.1308	6.4117
	Relapse	1.9693	0.5433	2.4600	0.0140	1.1468	3.3818
	Transfer-ins	2.2463	0.7731	2.3500	0.0190	1.1443	4.4098
Monoresistant TB	COVID-19 Period						
	Pre-COVID-19	Reference					
	Intra-COVID-19	1.3170	0.2331	1.5600	0.1200	0.9310	1.8631
	Post-COVID-19	1.5945	0.2806	2.6500	0.0080	1.1293	2.2512
	Patient type						
	Newly diagnosed	Reference					
	First-line failure	1.3365	0.2454	1.5800	0.1140	0.9325	1.9153
	First-line success	0.5878	0.3448	-0.9100	0.3650	0.1862	1.8560
	Lost-to-follow-up	1.4391	0.4378	1.2000	0.2310	0.7928	2.6122
	Relapse	1.1013	0.2336	0.4600	0.6490	0.7268	1.6689
	Transfer-ins	0.5930	0.2179	-1.4200	0.1550	0.2886	1.2186
RR-TB	HIV Status						
	Negative	Reference					
	Not done	1.3580	0.6985	0.6000	0.5520	0.4956	3.7213
	Positive	1.6636	0.2205	3.8400	0.0000	1.2830	2.1572
	Patient type						
	Newly diagnosed	Reference					
	First-line failure	0.5368	0.1180	-2.8300	0.0580	0.3489	0.8258
	First-line success	0.3878	0.2272	-1.6200	0.1060	0.1230	1.2228
	Lost-To-follow-up	0.6410	0.2479	-1.1500	0.2500	0.3003	1.3681
	Relapse	0.6881	0.1468	-1.7500	0.0800	0.4530	1.0452
	Transfer-ins	0.9394	0.2226	-0.2600	0.7920	0.5905	1.4946
	COVID-19 Period						
	Pre-COVID-19	Reference					
	Intra-COVID-19	0.8994	0.1343	-0.7100	0.4780	0.6711	1.2053
	Post-COVID-19	0.7510	0.1264	-1.7000	0.0890	0.5400	1.0446

Legend: TB – Tuberculosis; MDR-TB: Multidrug-resistant TB, RR-TB: Rifampicin-resistant TB; HIV – Human immunodeficient virus; irr – incidence rate ratio; COVID-19 – Coronavirus Disease 2019.

A significant surge (β_2 =+5.96 cases/quarter, p = 0.006) at the onset of the COVID-19 pandemic was observed. This was followed by a non-significant decline trend during the pandemic (β_3= -2.55, p = 0.142). Trends started rising in the post-pandemic era (β_5 =+2.56 cases/quarter, p = 0.022). Overall, cases were declining throughout the period, as illustrated in Figure 4.

Trends of MR-TB

With regard to MR-TB trends, there was a lack of statistically significant evidence to attribute the observed level changes to the healthcare disruptions caused by COVID-19 pandemic (p = 0.0799).

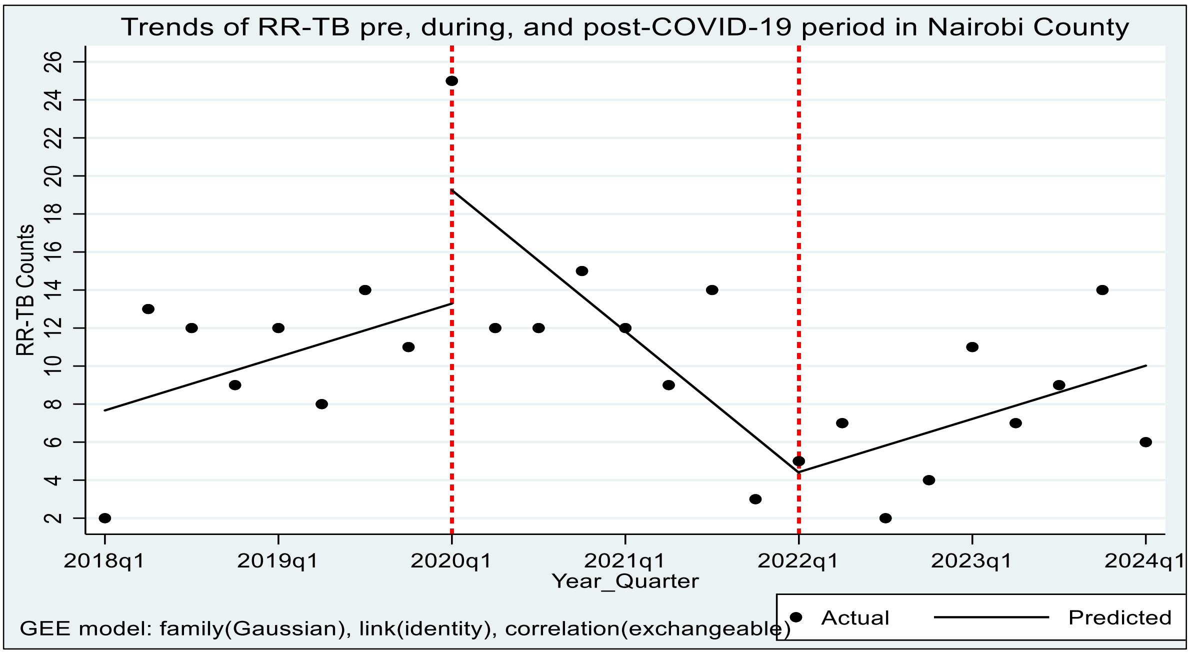


Figure 4:

Trends of RR-TB pre, during and post-COVID-19 in Nairobi County. Legend: TB: Tuberculosis, RR-TB: Rifampicin-resistant TB, COVID-19: Coronavirus Disease 2019, q: quarter

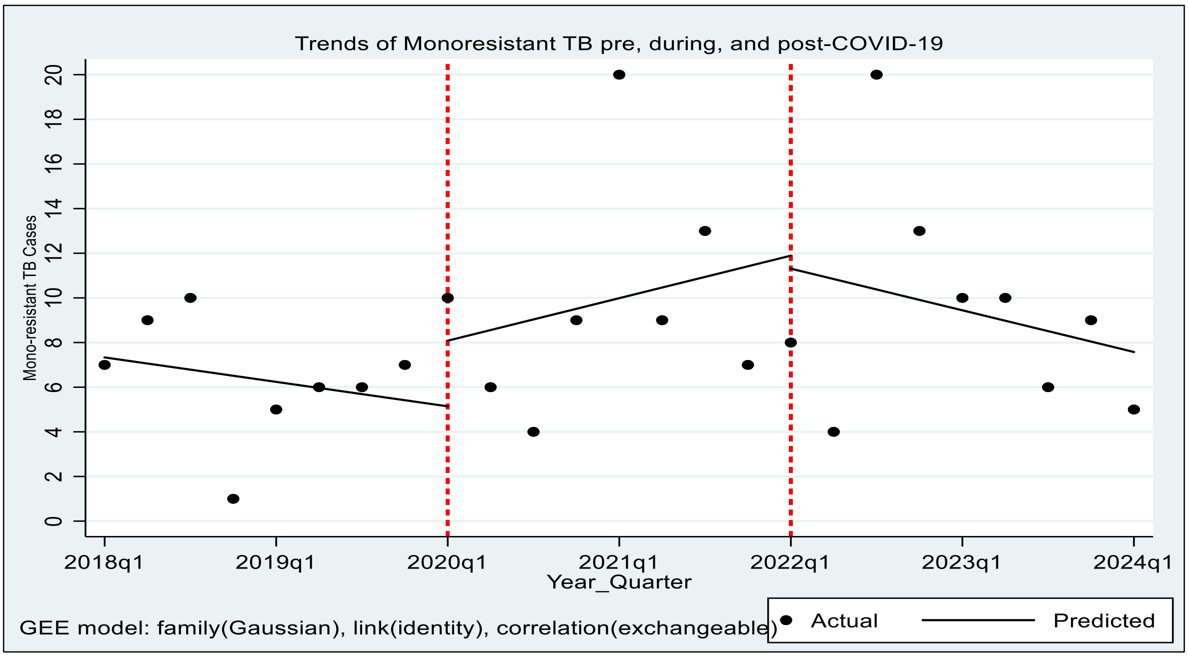


Figure 5

Trends of Mono-resistant TB before, during and after COVID-19 in Nairobi County. Legend: TB – Tuberculosis; COVID-19 – Coronavirus Disease 2019; q – quarter.

Trends of MDR-TB

There was a lack of statistically significant evidence to suggest that the pandemic affected MDR-TB trends (overall model p = 0.094).

Trends of PDR-TB, Pre-XDR-TB, and XDR-TB

The small sample sizes for PDR-TB (N=24), pre-XDR-TB (n = 19), and XDR-TB (n = 4) invalidated the granularity and reliability of trend analyses for these subtypes.

Discussion

RR-TB emerged as the most prevalent form of DR-TB, contributing over 40% of all cases. A study in Kajiado County found that RR-TB prevalence was, in fact, higher than the official notifications. Notably, rifampicin is one of the most effective first-line anti-TB drugs and is often a proxy marker for MDR-TB. A high rate of resistance to rifampicin may indicate treatment failures, high rates of M. tuberculosis mutations due to selective pressure, or ongoing active transmission(21). However, some studies have suggested that the apparent rise observed in many studies may partly reflect routine screening for RR-TB, as it is a critical molecular marker for detecting MDR-TB, rather than a true increase in incidence(22). These findings suggest that existing screening algorithms may need to better detect major DR-TB subtypes—particularly MR-TB, MDR-TB, and RR-TB—to enhance early detection within similar settings.

Additionally, the number of male cases was twice that of females, consistent with findings from Nigeria, where 66.9% of DR-TB patients were male(23). Male gender may be at greater risk of developing DR-TB, possibly due to factors including higher exposures, differences in health-seeking behaviours, occupational risks, or social determinants like smoking and alcohol use(24). This pattern suggests that gender dynamics influence DR-TB transmission and detection, contributing to disparities in disease burden and access to care.

In terms of comorbidities, HIV infection was associated with the occurrence of the disease, with 32.4% of all cases being HIV-positive ($p < 0.0001$). Abdul et al reported comparable findings, with a third of all DR-TB cases having HIV coinfections in Gabon(25). Additionally, comparable findings have been reported in multiple studies conducted in sub-Saharan Africa and Asia(4, 26, 27). This is possibly due to adverse effects arising from drug–drug interactions and the resulting poor adherence(28, 29). The strong association between TB and HIV observed indicates that treatment outcomes may be shaped by drug-drug interactions compromising adherence, and increasing the complexity of managing co-infection.

In terms of patient TB history, more than half of the DR-TB cases were newly diagnosed, suggesting a high transmission rate of primary drug-resistant strains. Similar findings were reported in Makkah, where 78.3% of all DR-TB cases were newly diagnosed cases, which was three times higher than those with a previous TB history(30). This suggests active transmission of resistant M. tuberculosis strains to individuals without prior history of tuberculosis, rather than solely developing due to poor or inadequate therapy in previously treated patients(31). Nguyen et al., in their study, emphasised the need to intensify active surveillance and strengthen infection control to interrupt transmission(32).

Some studies have reported an association between diabetes mellitus and the development of drug-resistant M. tuberculosis strains, especially among the older age groups(33, 34). However, this study found no evidence of such a relationship, consistent with a study conducted in India that reported no significant differences in incidences of various DR-TB subtypes between patients with and without diabetes mellitus(35). This discrepancy may be explained by differences in population characteristics and the adopted study design. Still, the relationship often observed appears complex and requires further exploration.

In terms of trends, a local surge of DR-TB incidence was observed during the COVID-19 pandemic, with a 2.82% intra-COVID-19 was observed, findings that mirrored the global trends, as highlighted in the WHO 2022 Global TB Report, which documented a 3.1% increase in reported DR-TB cases between 2020 and 2021(12). More specifically, RR-TB cases showed a statistically significant jump immediately after the onset of COVID-19 was declared a pandemic, the first quarter of 2020 ($p = 0.006$). This may reflect heightened case detection preceding the implementation of COVID-19 response measures. However, overall incidence was on a declining trend, with its proportion relative to the period-specific caseload decreasing from 43.7%(n=213) to 34.24% (n=184). A similar study in Nigeria reported a reduction in RR-TB incidence, with notifications dropping from 9.5% pre-COVID-19 to 2.5% during the COVID-19 pandemic ($p < 0.001$)(36).

Additionally, a study conducted in South Africa documented a 23% decline in RR-TB cases during COVID-19. This study attributed these observations to the reorientation of primary healthcare services towards COVID-19 response strategies, ultimately leading to reduced notification rates(37). Evidence from similar research has shown that health system shocks can disrupt TB diagnostic and treatment services, emphasizing the vulnerability of intervention programs during such situations(38-40).

The study also revealed stable MDR-TB trends throughout the study period. This aligns with a study in Uganda, which reported that its case notifications remained largely unaffected by COVID-19 restrictions, with a lack of significant difference in mean monthly notifications before and during the pandemic (p-value = 0.661). Apio et al ascribed these observations to a high baseline in areas with the persistent presence of resistant strain, resulting in steady case notifications, even in the face of the pandemic(41). This pattern suggests that variabilities in reported cases may reflect difference in detection efficiency rather than true epidemiological surges.

Limitations

This study relied on secondary data from TIBULIMS, which may have excluded undiagnosed cases, such as those lacking access to diagnostic services or who were misdiagnosed, potentially leading to an underestimation of the actual DR-TB burden.

Conclusions

This study demonstrated that COVID-19-related disruptions negatively impacted DR-TB detection and reporting, as reflected by fluctuations in MDR-TB, RR-TB, and MR-TB trends. These disruptions likely slowed progress toward achieving TB control targets.

Recommendations

Continued monitoring of DR-TB patterns in the post-pandemic era is crucial to inform preparedness and strengthen the health system's capacity to manage potential future outbreaks.

Definition of key terms:

- **Mycobacterium tuberculosis (M. tuberculosis).** A bacterium that causes Tuberculosis TB in humans.
- **Drug-Resistant Tuberculosis (DR-TB).** Tuberculosis caused by M. tuberculosis strains resistant to one or more anti-TB drugs
- **Monoresistant Tuberculosis (MR-TB).** Infection with M. tuberculosis strains resistant to only one first-line anti-TB drug.
- **Polydrug-Resistant Tuberculosis (PDR-TB).** Resistance to more than one first-line anti-TB drug, excluding concurrent resistance to both isoniazid and rifampicin.
- **Rifampicin-Resistant Tuberculosis (RR-TB).** Characterised by resistance to rifampicin alone or in combination with other first-line drugs, except isoniazid.
- **Multidrug-Resistant Tuberculosis (MDR-TB).** Defined by concurrent resistance to at least isoniazid and rifampicin, the two most potent first-line anti-TB drugs.
- **Pre-Extensively Drug-Resistant Tuberculosis (Pre-XDR-TB).** An MDR-TB strain that shows additional resistance to any fluoroquinolone.
- **Extensively Drug-Resistant Tuberculosis (XDR-TB).** Characterised by resistance to isoniazid, rifampicin, a fluoroquinolone, and at least one of the key second-line injectable drugs

- **Treatment Information from Basic Unit Laboratory Information Management (TIBULIMS).** A national digital database used to record, store, and manage patient-level TB diagnostic and treatment data from healthcare facilities.
- **Coronavirus Disease 2019 (COVID-19**). An infectious disease caused by the Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) that mainly affects the human respiratory system and spreads through respiratory droplets.

Author contributions

- S.K. Naphtali conceptualized the study, curated the data, conducted the formal analysis, and drafted the original manuscript.
- V.O. Were contributed to the methodology, supervision, and manuscript review.
- J.R. Ong'ang'o and G.A. Makalliwa provided additional supervision and critical review.
- Funding was secured by S.K. Naphtali.
- All authors read and approved the final version of the manuscript.

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Conflict of interest. All authors declare that they have no competing interests to disclose.

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