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Evolving landscape of respiratory infections and AMR in the UAE: A 12-year nationwide study of regional burden, epidemiologic trends and policy implications

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ABSTRACT

Objectives: This study characterizes the epidemiological trends and resistance profiles of respiratory tract infections (RTIs) in the United Arab Emirates (UAE) from 2010 to 2022, aiming to inform national control strategies.

Method: We conducted a retrospective observational study of RTI cases across 345 UAE healthcare settings using data from the national surveillance network. Pathogen identification and resistance profiling were performed using advanced diagnostics and standardized antimicrobial susceptibility testing, in accordance with Clinical and Laboratory Standards Institute (CLSI) guidelines.

Results: Lower respiratory tract infections (LRI) comprised most cases (73.1%; n = 100,856), including 6416 due to *Mycobacterium tuberculosis*, while upper respiratory infections made up 26.9%. LRI incidence was stable until 2014 but rose significantly from 2015 to 2022 (AAPC = 1.58; 95% CI: 1.58-3.87), especially in the Northern Emirates. Carbapenem resistance among Enterobacterales was 22.5% (14.4% in *K. pneumoniae*), and third-generation cephalosporin resistance 30.1% (62.3% in *E. coli*). Resistance was highest in *A. baumannii* (61%) and *P. aeruginosa* (27.4%). Macrolide and MRSA resistance increased significantly. The majority (85%) of tuberculosis cases were identified among individuals from South Asian and East African regions, with a post-COVID surge, while drug resistance remained below 15%.

Conclusion: These findings underscore the urgent need for regionally tailored infection control strategies, enhanced antimicrobial stewardship, and expanded pathogen surveillance to prevent further escalation of AMR.

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Introduction

Respiratory tract infections remain the leading global health threats, accounting for more deaths each year than any other infectious disease worldwide [1]. Despite global efforts to reduce incidence, an estimated 344 million episodes of lower respiratory tract infections (LRI) and 2.18 million deaths occurred in 2021 alone [2,3]. In 2019, LRI ranked as the primary driver of AMR–related mortality, with an estimated 1.5 million associated deaths [4]. Compounding this threat, the extensive use of antibiotics during COVID-19 is believed to have accelerated the emergence and spread of antimicrobial resistance (AMR) [5,6]. The rise in antimicrobial resistance has emerged as a critical public health threat, complicating treatment regimens and escalating mortality rates [7]. Although these landmark papers quantify the overall mortality burden of AMR, they do not delineate pathogen-specific contributions within individual clinical syndromes. Our analysis addresses this gap by establishing the pathogen-attributable burden of RTIs and the corresponding prevalence of WHO priority antimicrobials.

The Middle East and North Africa (MENA) region faces unique challenges in mitigating respiratory infections, exacerbated by diverse socio-demographic factors, high population mobility, and increasing regional instability [8,9]. In the Middle East, research on respiratory infections has focused mainly on viral respiratory pathogens, and the bacterial causes of respiratory infections are less well-characterised due to a lack of surveillance data. Similarly, fungal pathogens are generally overlooked as opportunistic respiratory pathogens. However, an increasing number of individuals are at risk of fungal respiratory infections due to factors such as age, immunocompromised status, and other predisposing risk factors [10].

Over the past decade, the UAE has seen a marked increase in carbapenem-resistant Enterobacterales, largely driven by *Escherichia coli* and *Klebsiella pneumoniae* [11], alongside a rising prevalence of methicillin-resistant *Staphylococcus aureus* (MRSA) [12]. Although *S. aureus* and *K. pneumoniae* are among the leading contributors to LRI-related mortality globally, their epidemiology in respiratory infections within the Middle East remains insufficiently explored, hindering the development of regionally tailored specific intervention strategies [3,13]. Furthermore, the unprecedented rise in drug-resistant fungal pathogens, particularly *Candida* species [14], presents additional challenges to managing respiratory infections in the UAE. Similarly, although the incidence of tuberculosis in the UAE remains low [15], a large proportion of the UAE population is from high-TB burden regions, raising concerns around importation of TB and latent TB reactivation.

In this study, we analyze from the UAE National AMR surveillance data from 2010 to 2022 [16] to characterize the epidemiology of respiratory tract infections. We assess pathogen-specific patterns of AMR, evaluate clinical outcomes, and present annual trends in incidence. This work offers critical insights for shaping public health policies and clinical strategies in a region where precision-guided interventions are urgently needed.

Material and methods

Study setting and population

We conducted a retrospective observational surveillance study design spanning a 13-year period from 2010 to 2022. The study was built on the existing AMR surveillance framework established by the Ministry of Health and Prevention (MOHAP), which was initiated in Abu Dhabi in 2010 and was extended to include all seven Emirates by 2022, forming a network of 317 surveillance sites and 45 laboratories [17]. Adult and pediatric patients exhibiting symptoms of RTI had respiratory secretions collected under sterile conditions, depending on the severity and clinical signs of infection, such as fever, coughing, and difficulty in breathing. Specimens classified as URI included nasal, nasopharyngeal, throat, maxillary sinus samples, and samples designated as upper respiratory tract specimens. LRI specimens comprised bronchoalveolar lavage, bronchial samples, sputum, lung aspirates, and other specimens designated as lower respiratory tract specimens in the records. A census sampling approach was adopted whereby all patients presenting with symptoms suggestive of a respiratory tract infection who had microbiologically confirmed infection were included, with no demographic restrictions.

Data collection and data variables

Data were aggregated from laboratory information systems and national surveillance databases maintained by the Ministry of Health and Prevention (MOHAP) using the WHONET software. Patient demographic data, including age, gender, nationality, and geographical location, were recorded. Where available, clinical outcomes, including ward of admission or patient encounter, length of hospital stay, and death, were recorded. However, clinical variables such as underlying medical conditions, comorbidities, previous exposure to antimicrobials, involvement in invasive procedures, and hospitalization history were not documented, precluding a detailed assessment of the clinical context surrounding each RTI case. Duplicate isolates (i.e., multiple positive cultures for the same pathogen during a single episode) were excluded to avoid overestimation.

Sample collection and laboratory analysis

Respiratory tract specimens were collected and analyzed through standard microbiological methods that were compliant with Clinical and Laboratory Standards Institute (CLSI) guidelines [18]. Specimens were analyzed using a combination of automated systems (e.g., BacT/ALERT for aerobic cultures) and manual techniques, depending on the pathogen type. Blood agar, Chocolate agar, and MacConkey agar were used for isolating common bacterial pathogens. For suspected fungal RTIs, Sabouraud dextrose agar was used. Incubation was performed at 35-37°C, in 5% CO_2 for fastidious organisms such as *Streptococcus pneumoniae*, or ambient air for others [19].

Identification methods included MALDI-TOF MS for rapid bacterial identification and Vitek ID cards for Gram-negative bacilli. Tube coagulase testing was used to differentiate coagulase-positive *S. aureus* from coagulase-negative Staphylococci. β-hemolytic Streptococci were typed using Lancefield antigen testing, essential for distinguishing clinically relevant strains.

Clinical and antimicrobial susceptibility data for *M. tuberculosis* were obtained from three reference laboratories serving all seven Emirates. Identification and processing of MTB-complex isolates followed standard diagnostic protocols, including smear microscopy (Ziehl–Neelsen or auramine-O stains) and culture on solid Lowenstein–Jensen medium and liquid MGIT™ 960 (Becton Dickinson). Full laboratory procedures are described in the original article [16].

RTI classification and population data

RTI cases were classified based on the anatomical site of infection and implicated pathogens. Upper respiratory tract infections (URTI), including conditions like pharyngitis and sinusitis, were differentiated from LRI, such as pneumonia and bronchitis. The pathogens responsible for RTI were categorized into bacteria or fungi. Bacteria were further divided into Gram-positive and Gram-negative organisms and *Mycobacterium tuberculosis* complex. Fun-

gal species, including *Candida* spp., were also identified, which are less commonly involved in RTI but are critical in certain immunocompromised populations. Hospital-associated pathogens were defined as positive culture samples 72 hours after admission.

Antimicrobial susceptibility testing and interpretation

Antimicrobial susceptibility testing (AST) was conducted using disk diffusion and automated platforms, including VITEK® 2 (BioMérieux, France) and BD Phoenix™ (Becton Dickinson, USA). Interpretations followed CLSI guidelines, with supplementary reference to EUCAST and BSAC standards.

Isolates were classified as susceptible (S), intermediate (I), or resistant (R) based on CLSI breakpoints. Multidrug resistance (MDR) was defined as non-susceptibility to at least three antimicrobial classes, following the Magiorakos *et al.* [20] criteria. Resistance patterns were analyzed using WHONET, in accordance with CDC/ECDC recommendations.

Quality control

All participating laboratories adhered to internal and external quality assurance protocols, aligned with CLSI and ISO 15189 standards. Proficiency testing was conducted through external sample panels, allowing independent verification of pathogen identification and AST accuracy. The laboratories were accredited by the College of American Pathologists (CAP) and ISO 15189, ensuring rigorous performance monitoring.

Data analysis

The incidence of LRI per 100,000 population was estimated using the number of reporting hospitals and their average infection burden as a proxy for healthcare system coverage. Each hospital's contribution was normalized to its average annual number of bacterial/fungal RTI diagnoses. Abu Dhabi estimates were further adjusted for the 9% compound annual growth rate in hospital infrastructure reported by the Abu Dhabi Department of Statistics (https://www.doh.gov.ae/resources/opendata), reflecting its longer 13-year surveillance period and the substantial expansion in healthcare capacity that could otherwise skew temporal trends.

A Poisson logistic regression model was applied to annual case counts to estimate incidence trends. From 2010 to 2014, data were restricted to Abu Dhabi; from 2015 to 2022, nationwide data were incorporated. Because the underlying catchment population changed substantially between these periods, trends were analyzed in two distinct phases to minimize bias and ensure comparability.

All statistical analyses were conducted in RStudio (version 2022.12.0+353) using a two-sided significance level of 0.05. The JoinPoint Regression Program (v5.3.0, November 12, 2024), developed by the National Cancer Institute, was used to calculate average annual percentage change (AAPC) and assess statistical significance of temporal trends. Fisher's Exact Test was used to calculate odds ratios for associations between pathogens and clinical outcomes, and Wilcoxon rank-sum tests were applied for associations with hospital length of stay.

Results

Demographic details of the study isolates

We analysed data from 137,975 isolates obtained from respiratory tract specimens of patients presenting at hospitals in Abu Dhabi (n = 76,884, 55.7%), Dubai (n = 30,381, 22.0%), and the Northern Emirates (30,710, 22.3%) between 2010 and 2022 (Supplementary Table 1, Supplementary 1). These were isolates from the lower respiratory tract (n = 94,440, 68.4%), including 6416 (4.7%) belonging to the *Mycobacterium tuberculosis* complex, and the upper respiratory tract (n = 37,119, 26.9%). Patients were a mix of Emiratis (n = 33,291 (36.6%)) and expatriates (57,646 (63.4%)) representing 175 different nationalities. The age distribution of patients differed by region: in Abu Dhabi, the median age was 38 years (IQR 20-65), which was higher than Dubai 33 years (IQR 7-53), and lower than the Northern Emirates 56 years (IQR 37-72). Overall, 25,355 (21.8%) patients were admitted to the intensive care unit, and 8220 (16.3%) had a fatal outcome, primarily among patients with LRI, which accounted for 95.8% of total ICU admissions and 99.2% of total deaths.

Temporal trends and aetiology of lower respiratory tract infections in the UAE

We tracked the temporal trends in the burden of disease by estimating the population-level incidence of lower respiratory tract infections. Due to a small sample size, the estimate from 2010 was not included in the temporal analysis. Overall, there was no significant change in the incidence of LRI in the UAE between 2011 and 2014, but between 2015 and 2022, a steady significant increase in LRI incidence was observed (AAPC = 1.58; 95% CI: 1.58-3.87) (Supplementary Figure 2 and Supplementary Table 2). Both Abu Dhabi and Dubai had a decline in the incidence of LRI, which was not statistically significant. However, a significant increase in LRI incidence was observed in the Northern Emirates between 2015 and 2022 (AAPC = 11.03; 95% CI: 5.29-17.04) (Supplementary Figure 3).

Nine pathogens accounted for 75% of LRI cases: *P. aeruginosa* (17,490, 18.6%), *K. pneumoniae* (15,791, 16.8%), *S. aureus* (11,940, 12.7%), *E. coli* (5324, 5.6%), *Stenotrophomonas maltophilia* (4471, 4.7%), *S. pneumoniae* (4411, 4.7%), *Acinetobacter baumanii* (4344, 4.6%), *H. influenzae* (3851, 4.1%), and *C. albicans* (3315, 3.5%). The trends in incidence for each of the leading pathogens was evaluated in order to assess their contribution to the burden of LRI in the UAE. The results showed that the incidence of pathogens remained largely stable throughout the study period (Figure 1A). Notably, there was a statistically significant increase in the incidence of *C. albicans*, alongside a significant decline in the incidences of *A. baumannii, E. coli*, and *H. influenzae* (Figure 1B).

Antimicrobial resistance patterns for the leading causes of respiratory infection in the UAE

The prevalence of resistance to antimicrobial classes that are listed under the WHO priority list for AMR surveillance was estimated (Table 1). For each of the leading bacteria causing respiratory infection in the UAE, the annual prevalence of resistance to carbapenems, 3rd-generation cephalosporins, and fluoroquinolones was presented. Additionally, for Gram-positive bacteria and *H. influenzae,* the annual prevalence of resistance to penicillin, macrolides, vancomycin, and methicillin (only *S. aureus)* was also reported. Additionally, temporal trends in antimicrobial resistance were assessed to identify significant shifts in resistance patterns across key pathogen groups and antibiotics (Figure 2).

Among Enterobacterales, carbapenem resistance was 22.5% overall, with species-specific rates ranging from 4.2% in *Serratia marcescens* to 14.4% in *K. pneumoniae*. Notably, carbapenem resistance increased significantly in *E. coli* and *S. aureus*, whereas it declined in *S. maltophilia* and *Enterobacter cloacae* (Figure 2). Resistance to third-generation cephalosporins was also high, particularly in *E. coli* (62.3%) (Table 2). A. baumannii exhibited 61.0% resistance to carbapenems, although resistance to carbapenems, cephalosporins, and fluoroquinolones declined significantly over time (Figure 2).

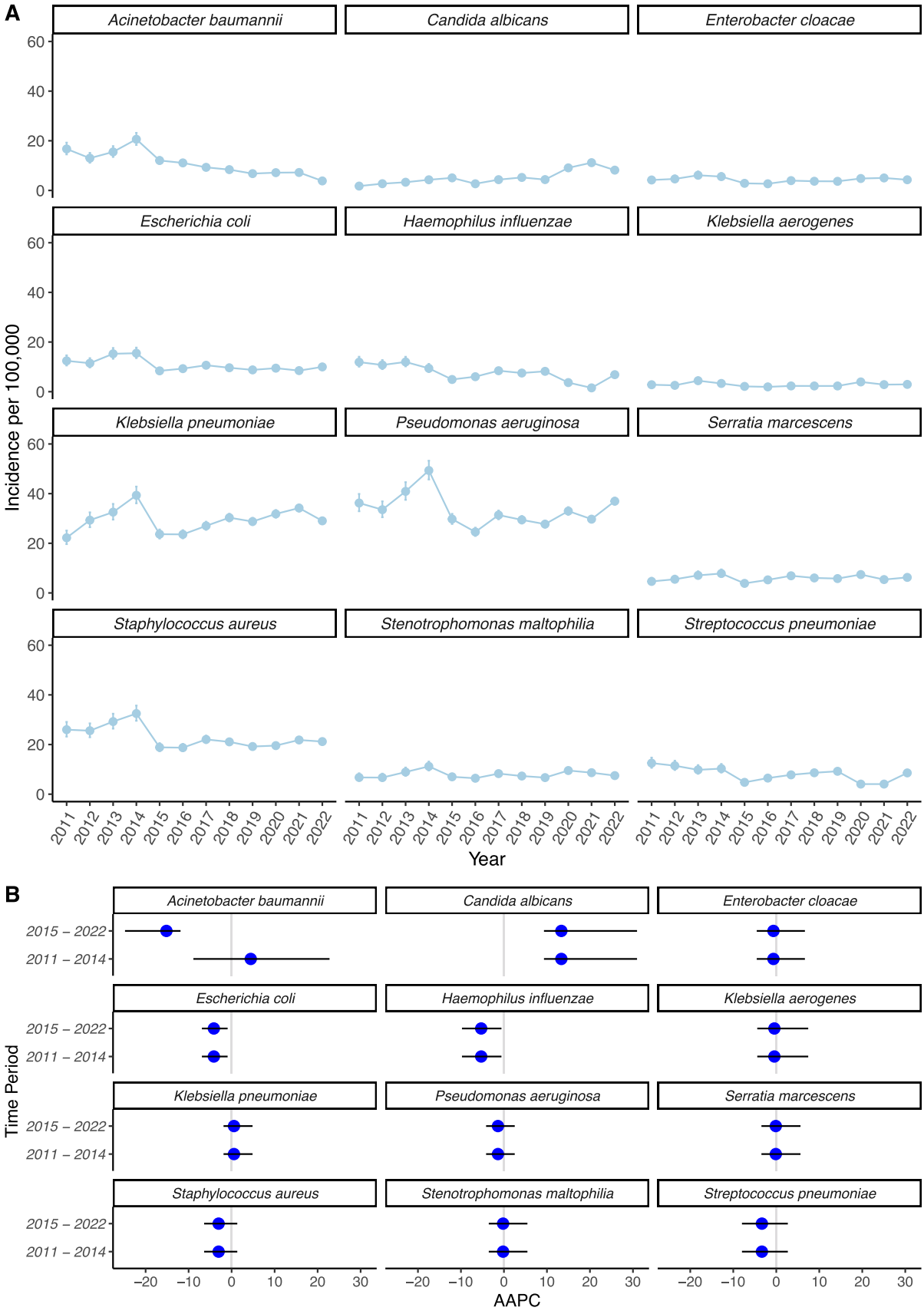

Figure 1. Incidence of invasive respiratory infections associated with leading pathogens in the UAE (2011-2022). (A) The figure displays annual incidence rates of invasive respiratory infections, stratified by pathogen. Error bars represent the 95% confidence intervals, providing an estimate of the uncertainty around the incidence measurements. (B) Average Annual Percentage Change in Incidence of Leading Lower Respiratory Infection Causes in the UAE (2011-2022). The figure presents pathogen-specific estimates of the average annual percentage change in incidence rates, with 95% confidence intervals reflecting the precision of these estimates. Statistically significant trends are identified when the confidence intervals do not cross zero, indicating a consistent increase or decrease in resistance over time.

Table 1
Rates of resistance among UAE priority pathogens for AMR surveillance.

Label	Antibiotic	Number of isolates tested	Resistance (%)	95% CI
Priority 1: Critical				
Enterobacterales (all)	Carbapenems	59,892	22.5	22.2-22.8
Klebsiella aerogenes	Carbapenems	1432	7.0	5.7-8.3
Enterobacter cloacae	Carbapenems	2241	6.6	5.6-7.6
Escherichia coli	Carbapenems	5044	4.6	4-5.2
Klebsiella pneumoniae	Carbapenems	14,834	14.4	13.8-15
Serratia marcescens	Carbapenems	3030	4.2	3.5-4.9
Enterobacterales (all)	Third-generation cephalosporin	66,194	30.1	29.8-30.4
Klebsiella aerogenes	Third-generation cephalosporin	1458	32.6	30.2-35
Enterobacter cloacae	Third-generation cephalosporin	2262	27.0	25.2-28.8
Escherichia coli	Third-generation cephalosporin	5068	62.3	61-63.6
Klebsiella pneumoniae	Third-generation cephalosporin	15,094	31.4	30.7-32.1
Serratia marcescens	Third-generation cephalosporin	3102	10.0	8.9-11.1
Acinetobacter baumannii	Carbapenems	4132	61.0	59.5-62.5
Priority 2: High				
Enterococcus faecium	Vancomycin	87	10.3	3.9-16.7
Pseudomonas aeruginosa	Carbapenems	16,443	27.4	26.7-28.1
Priority 3: Medium				
Streptococcus pyogenes (Group A)	Macrolide	781	55.2	51.7-58.7
Streptococcus pneumoniae	Macrolide	4062	56.9	55.4-58.4
Haemophilus influenzae	Ampicillin	3287	30.6	29-32.2
Streptococcus agalactiae (Group B)	Penicillin	193	0.5	−0.5 to 1.5

Table 2
Multidrug resistance among leading pathogens for invasive and non-invasive isolates.

Lower respiratory tract – Invasive isolates

Pathogen_Name	Non-MDR	MDR	PDR	XDR	Total
Acinetobacter baumannii	2173 (54.2%)	81 (2.0%)	840 (21.0%)	915 (22.8%)	4009 (100.0%)
Escherichia coli	3187 (79.8%)	501 (12.5%)	42 (1.1%)	264 (6.6%)	3994 (100.0%)
Enterobacter cloacae	1720 (78.0%)	429 (19.5%)	16 (0.7%)	40 (1.8%)	2205 (100.0%)
Enterococcus cecorum	317 (73.9%)	108 (25.2%)	0 (0.0%)	4 (0.9%)	429 (100.0%)
Enterococcus faecium	34 (43.6%)	41 (52.6%)	0 (0.0%)	3 (3.8%)	78 (100.0%)
Enterococcus faecalis	270 (80.4%)	66 (19.6%)	0 (0.0%)	0 (0.0%)	336 (100.0%)
Klebsiella pneumoniae	11,379 (83.7%)	766 (5.6%)	889 (6.5%)	556 (4.1%)	13,590 (100.0%)
Pseudomonas aeruginosa	12,786 (85.7%)	1179 (7.9%)	338 (2.3%)	614 (4.1%)	14,917 (100.0%)
Staphylococcus aureus	9771 (88.4%)	1283 (11.6%)	1 (0.0%)	1 (0.0%)	11,056 (100.0%)
Streptococcus pneumoniae	1575 (83.2%)	206 (10.9%)	8 (0.4%)	103 (5.4%)	1892 (100.0%)

Upper Respiratory tract – non-invasive isolates

Pathogen_Name	Non-MDR	MDR	PDR	XDR	Total
Acinetobacter baumannii	156 (86.2%)	6 (3.3%)	3 (1.7%)	16 (8.8%)	181 (100.0%)
Escherichia coli	220 (84.6%)	36 (13.8%)	0 (0.0%)	4 (1.5%)	260 (100.0%)
Enterobacter cloacae	147 (86.5%)	22 (12.9%)	0 (0.0%)	1 (0.6%)	170 (100.0%)
Enterococcus cecorum	35 (92.1%)	3 (7.9%)	0 (0.0%)	0 (0.0%)	38 (100.0%)
Enterococcus faecium	4 (80.0%)	1 (20.0%)	0 (0.0%)	0 (0.0%)	5 (100.0%)
Enterococcus faecalis	28 (93.3%)	2 (6.7%)	0 (0.0%)	0 (0.0%)	30 (100.0%)
Klebsiella pneumoniae	1321 (95.4%)	53 (3.8%)	4 (0.3%)	7 (0.5%)	1385 (100.0%)
Pseudomonas aeruginosa	642 (93.4%)	28 (4.1%)	7 (1.0%)	10 (1.5%)	687 (100.0%)
Staphylococcus aureus	7765 (89.0%)	961 (11.0%)	0 (0.0%)	0 (0.0%)	8726 (100.0%)
Streptococcus pneumoniae	1230 (89.1%)	112 (8.1%)	5 (0.4%)	33 (2.4%)	1380 (100.0%)

P. aeruginosa showed 27.4% carbapenem resistance, while *E. faecium* has a relatively lower vancomycin resistance rate of 10.3%. Vancomycin resistance remained low across all Gram-positive isolates. Macrolide resistance was notably high: *S. pyogenes* at 55.2%, *S. pneumoniae* at 56.9%, and ampicillin resistance was highly prevalent in *H. influenzae* at 30.6%, in stark contrast to the minimal penicillin resistance of 0.5% seen in *S. agalactiae*. Macrolide resistance increased significantly for both *S. aureus* and *S. pneumoniae*, and the prevalence of methicillin-resistant *S. aureus* infections also rose markedly (Figure 2).

Multidrug resistance classification

Pathogens were classified as multidrug-resistant (MDR), extensively drug-resistant (XDR), or pandrug-resistant (PDR) to determine the extent of combinations of resistance to multiple antibiotic classes. Among invasive lower respiratory tract isolates, *A. baumannii* exhibited a particularly high resistance burden, with only 54% classified as non-MDR and nearly 44% as PDR or XDR. This was in contrast to other pathogens such as *E. coli, K. pneumoniae*, and *P. aeruginosa* with non-MDR rates above 80%. Notably, non-invasive upper respiratory isolates showed lower resistance overall, with most pathogens exceeding 85% of non-MDR classifications (Table 2).

Clinical outcomes by pathogen

Clinical outcomes varied significantly among the major LRI pathogens. Odds ratios for LRT involvement ranged widely, with some organisms displaying odds ratios >25, reflecting strong LRT tropism (Supplementary Figure 6). *C. albicans, S. maltophilia, A. baumannii*, and *P. aeruginosa* exhibited the strongest associations with LRT infection. These same pathogens also showed strong correlations (Pearson $r > 0.80$) with ICU admission and hospital-associated

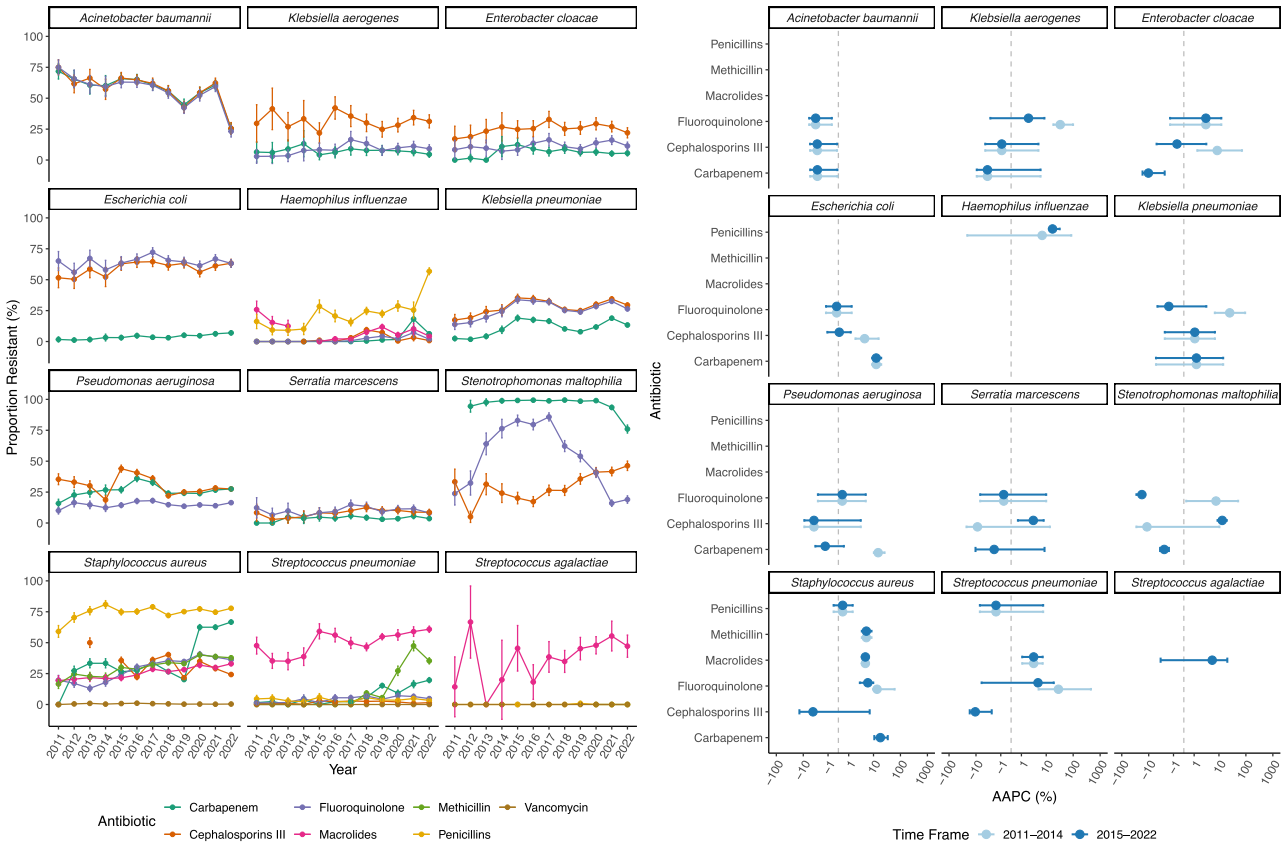

Figure 2. Annual prevalence of antibiotic resistance among major respiratory pathogens in the UAE (2011-2022). (A) This panel displays the yearly resistance prevalence estimates—with corresponding 95% confidence intervals—for major antibiotic classes among the most common pathogens causing respiratory tract infections. Data are stratified by pathogen to facilitate comparison of resistance trends over time. (B) Average Annual Percentage Change in Prevalence of Resistance Among Major Respiratory Pathogens in the UAE (2011-2022). This figure presents the estimated annual average percentage change in antibiotic resistance prevalence among the leading pathogens causing respiratory tract infections in the UAE. For each pathogen, the point estimate is shown with corresponding 95% confidence intervals. Statistically significant trends are identified when the confidence intervals do not cross zero, indicating a consistent increase or decrease in resistance over time.

infection. Conversely, *S. pneumoniae, H. influenzae*, and *S. aureus* were not significantly associated with ICU admission or prolonged hospital stay, suggesting less severe clinical outcomes.

Assessing the burden of tuberculosis in the UAE

Given its unique clinical and microbiological profile, tuberculosis (TB) was assessed separately.

Over 85% of TB cases occurred in foreign nationals, primarily from South Asia and East Africa (Figure 3A). Based on data from Abu Dhabi (the only Emirate with consistent reporting), TB incidence increased significantly between 2011 and 2022 (AAPC = 3.38; 95% CI: 1.13-6.19). A sharper rise was observed during the post-pandemic period (2020-2022) (AAPC = 18.91; 95% CI: 4.05-30.91) (Figure 3B). Resistance to isoniazid and rifampicin remained low (<15%), and multidrug resistance was detected in fewer than 5% of cases (Figure 3C).

Discussion

This nationwide surveillance study provides the first comprehensive analysis of the epidemiology and antimicrobial resistance trends of respiratory tract infections in the United Arab Emirates over a 13-year period. Against the backdrop of rapid healthcare development and global interconnectedness, the UAE presents a distinctive respiratory disease profile shaped by high population mobility, medical globalization, and demographic diversity. Our findings reveal a notable increase in LRI incidence from 2015 to 2022, particularly in the Northern Emirates, suggesting either true epidemiological expansion or improved detection linked to population growth, post-COVID healthcare shifts, and improved diagnostics. This regional heterogeneity underscores the urgent need for geographically tailored surveillance, with a focus on high-burden subpopulations and healthcare settings.

Three-quarters of LRI cases were attributable to nine pathogens, led by *P. aeruginosa, K. pneumoniae*, and *S. aureus*, which mirrors global trends in hospital-associated respiratory infections, but also highlights the hybrid nature of transmission in the UAE, where nosocomial and community-acquired strains converge [2,3,11,21]. Of note, *S. aureus*, often considered hospital-acquired, demonstrated strong community linkage, possibly due to spillover from community-associated MRSA lineages [22]. The decline in *A. baumannii, E. coli*, and *H. influenzae* may reflect successful infection control measures and vaccine coverage, particularly the Hib vaccine in childhood immunization programs. However, this decline is counterbalanced by the alarming rise in *Candida albicans* infections, especially among vulnerable ICU patients. This fungal surge, coupled with the increasing threat of *Candida auris*, positions multidrug-resistant fungi as an emerging frontier in respiratory infection control [14,23–25].

Our resistance data paint a sobering picture: carbapenem and third-generation cephalosporin resistance remain stubbornly high in key pathogens, including *K. pneumoniae, E. coli*, and *A. baumannii*. These findings emphasize the limited efficacy of current empiric treatment regimens, many of which rely on these critically important antibiotics [26,27]. *A. baumannii*, despite its decline in

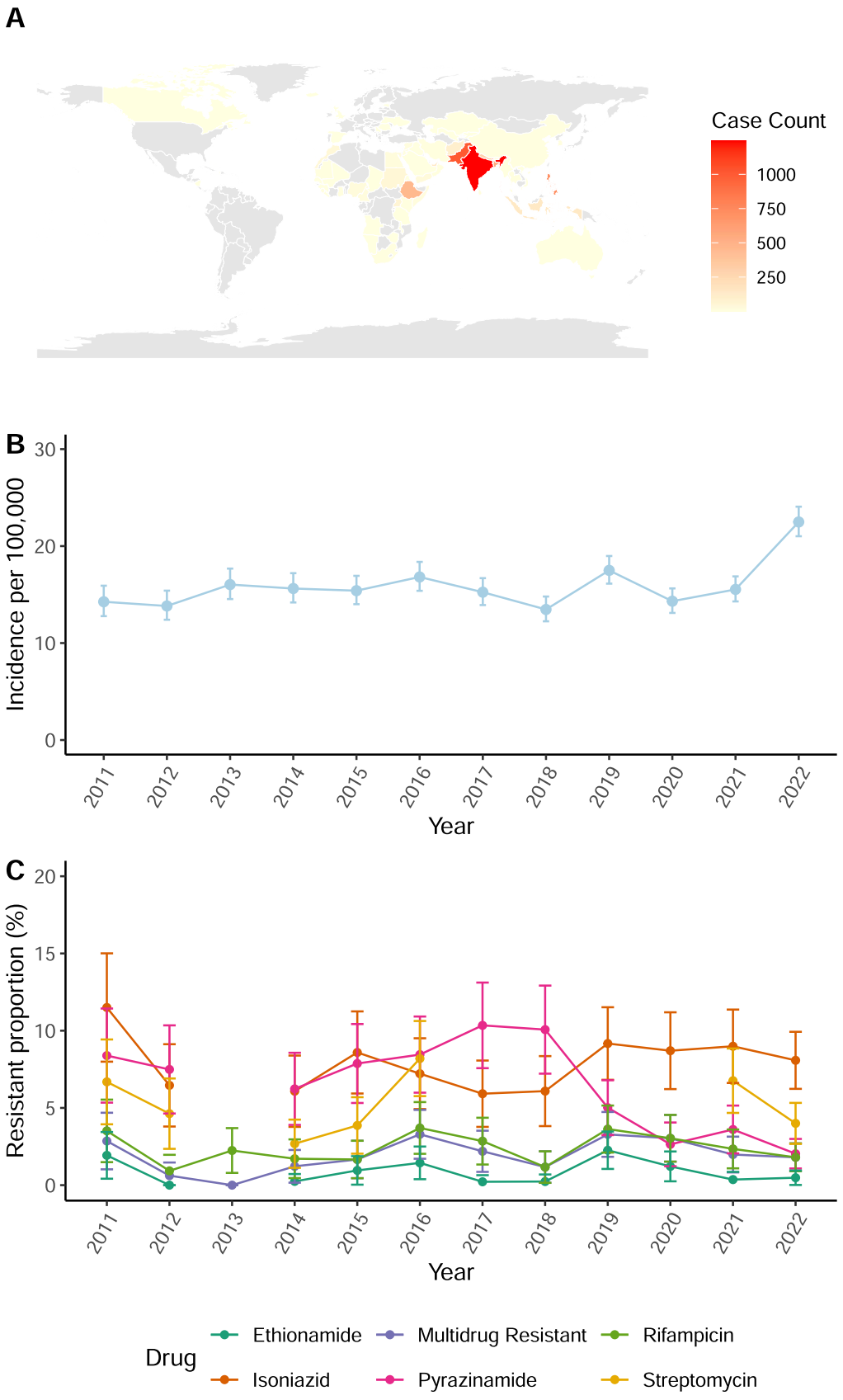

Figure 3. Tuberculosis burden in the United Arab Emirates (UAE): patient nationality, incidence trends, and drug resistance. (A) presents a global map with a heatmap overlay illustrating the number of TB cases by patients' nationality, with the highest case counts observed among individuals from South Asia. (B) depicts the annual incidence of TB in the UAE from 2011 to 2022, demonstrating a consistent trend over time; error bars represent 95% confidence intervals. (C) shows temporal trends in resistance to major TB drugs, including isoniazid, rifampicin, pyrazinamide, streptomycin, and ethionamide, with corresponding 95% confidence intervals.

incidence [28], remains a formidable challenge due to its XDR/PDR profiles and strong ICU association. The continued empirical use of broad-spectrum antibiotics, often in the absence of susceptibility data, likely fuels this resistance loop [29].

The rise in MDR fungal pathogens and the emergence of carbapenem-resistant Enterobacterales (CRE) present a dual microbial threat in the UAE's respiratory wards. These pathogens drive longer hospital stays, higher ICU admission rates, and elevated healthcare costs, reinforcing the call for strengthened antimicrobial stewardship and fungal diagnostics capacity [30]. Though tuberculosis incidence remained relatively low, the post-COVID resurgence, especially among foreign-born residents from TB-endemic countries, underscores the vulnerability of migrant communities to delayed diagnosis and disrupted care pathways. The pandemic's disruption of TB control programs serves as a cautionary tale on the fragility of parallel surveillance systems [31].

To transition from data to action, we recommend strengthening region-specific surveillance and scaling up real-time pathogen and resistance tracking, especially in the Northern Emirates. This includes expanding genomic surveillance to monitor high-risk clones, including XDR *K. pneumoniae* and *A. baumannii*. Furthermore, empiric guidelines need to be revised to incorporate local AMR data into clinical algorithms, especially for ICU protocols, and new or combination therapies need to be evaluated where carbapenem resistance is prevalent. The emerging fungal threat requires investment in fungal diagnostic capacity, including fungal screening in ICUs, and *Candida*-specific stewardship frameworks, especially in institutions with rising *C. auris* cases. Finally, the UAE needs to bolster the Tuberculosis Control Programs by resuming active TB screening among high-risk expatriate communities and reinforcing cross-border notification systems and digital tools for case tracking.

Conclusions

This study highlights critical trends in the epidemiology and resistance landscape of respiratory infections in the UAE, with wide-ranging implications for policy, practice, and pandemic preparedness. The increasing burden of drug-resistant bacterial and fungal pathogens, particularly in ICU settings, mandates enhanced surveillance, rigorous stewardship, and tailored treatment protocols. As the UAE continues to evolve as a global health hub, targeted public health responses rooted in robust local data will be key to safeguarding respiratory health and preserving the effectiveness of life-saving antimicrobials.

Limitations

This study provides important insights into the burden and etiology of respiratory infections in the UAE; however, several limitations should be noted. Clinical variables such as underlying conditions, co-morbidities, prior antimicrobial exposure, treatment regimens, and hospitalization history were not collected as part of the surveillance, limiting our ability to fully assess the clinical context or severity of individual cases. The number of participating hospitals and clinics increased over time; although adjustments were made, changes in site participation may introduce uncertainty into incidence estimates. In addition, surveillance relied on laboratory-confirmed cases, which captures only those who sought care and were tested, thereby missing individuals with milder or untested illness. Finally, we could not assess the burden of clinically suspected but test-negative respiratory infections, nor the broader community burden given the inherent under-ascertainment of upper respiratory infections.

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Authors contribution

JT, FJ, SW, and NMA were involved in designing and implementing the surveillance. DE, NMA, JT, GM, CA, and AS conceptualized the study. JT, NMA, and Consortium members contributed to the collection, cleaning, and management of the data. SW, FJ, and Consortium members handled specimens and laboratory protocols. MS, DE, and JT conceptualized the analysis for the study. MS and WC carried out the statistical analysis and data visualization. MS, DE, and EK produced the initial draft of the manuscript. All authors contributed to the curation of drafts and approved the final draft.

Ethics statement

Ethical approval for this study was provided by the Ministry of Health and Prevention Research Ethics Committee (MOHAP/DXB-REC/J.J.J./No. 86/2023), Dubai Scientific Research Ethics Committee (DSREC-GL17-2023), and Abu Dhabi Health Research and Technology Ethics Committee (DOH/ZHCD/2023/1316). The studies were conducted following the local legislation and institutional requirements. Written informed consent for participation was not required from the participants or the participants' legal guardians/next of kin following the national legislation and institutional requirements.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Supplementary materials

Supplementary material associated with this article can be found, in the online version, at doi:10.1016/j.ijid.2026.108389.

Appendix

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