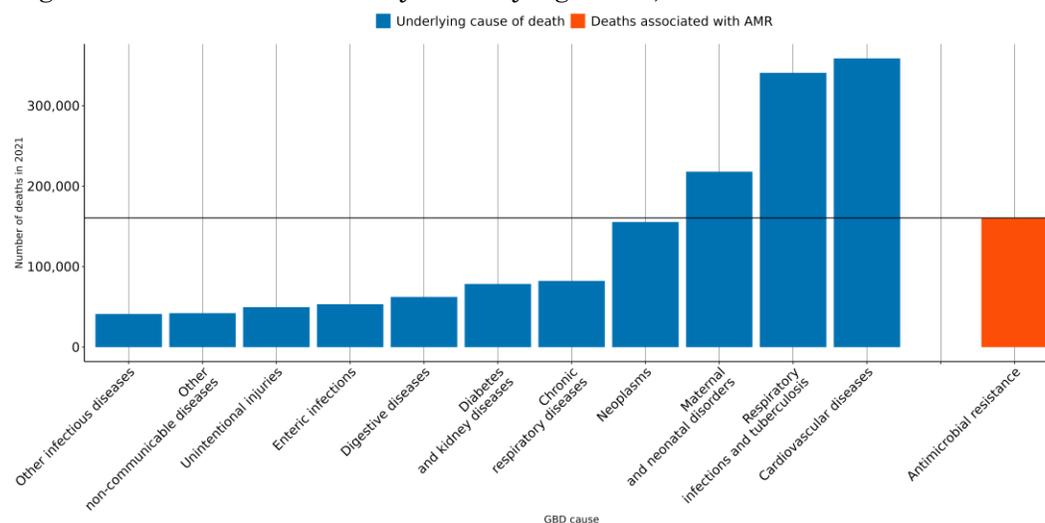


The burden of antimicrobial resistance (AMR) in Pakistan

Executive summary

- Antimicrobial Resistance (AMR) is a major global health threat, over **40,000 lives** have been lost each year since 1990 in Pakistan due to AMR.
- In 2021, there were an estimated **39,700 UI (31,000-48,300)** deaths attributable to AMR and **161,000 UI (134,000-187,000)** deaths associated with AMR in this location.
- The largest number of deaths associated with AMR in 2021 occurred among those aged **under 5** in the country.
- Among the most deadly pathogen-drug combinations in 2021 were multi-drug resistant *Mycobacterium tuberculosis* (excluding extensive drug-resistance), *Staphylococcus aureus* resistant to methicillin and *Klebsiella pneumoniae* resistant to carbapenems.

Figure 1 Number of deaths by underlying cause, and those associated with AMR in 2021



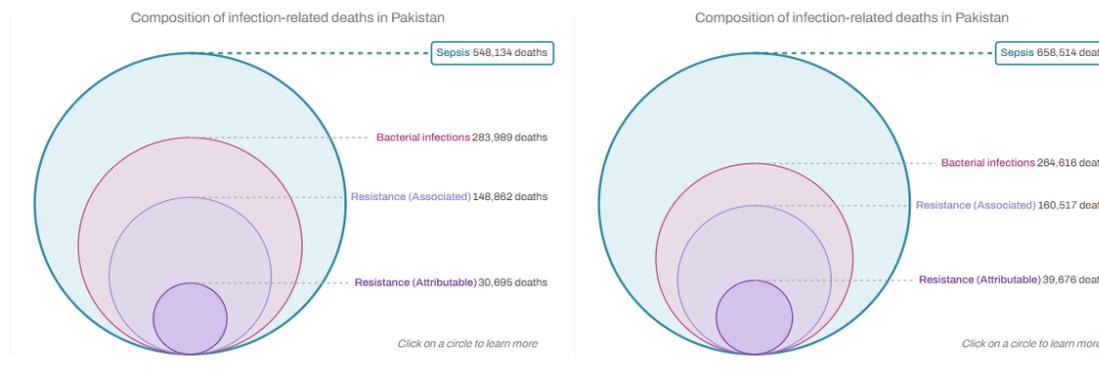
- In 2021, the number of deaths associated with AMR (orange bar in *figure 2*) were high compared to the most relevant underlying causes of death (depicted in blue) in the country. AMR associated deaths occur within multiple Global Burden of Disease (GBD) causes of death and AMR is not an underlying cause of death by itself.
- At the [2024 United Nations General Assembly high level meeting on antimicrobial resistance](#), country members agreed to aim for a **10% reduction** compared to 2019 baseline (**from 4.95 to 4.45 million**) in the global number of deaths associated with AMR by 2030. But [our forecast](#) indicates that in absence of concerted action, deaths associated with AMR could reach **5.5 million** (UI 4.8 - 6.2) if current trends continue. For Pakistan, a 10% reduction means to decrease the number of deaths associated with AMR to **159,000**, but currently the trend for this country could reach up to **168,000 UI [133,000-209,000]** AMR-associated deaths in 2030.

AMR in Pakistan

Key takeaways

- Antimicrobial Resistance (AMR) is a major global health threat, over *a million lives* have been lost each year since 1990.
- Globally, 4.71 (95% Uncertainty Interval (UI) 4.2-5.2) million deaths were associated with bacterial drug-resistant infections in 2021.
- And 1.14 (UI 1 - 1.3) million deaths were attributable to bacterial drug-resistant infection in the same year.
- *39 (UI 33 - 46) million deaths* directly attributable to bacterial AMR are projected to occur between 2025-2050 unless concerted action is taken. This equates to three deaths every minute.

Figure 2 Comparing 30 years of infection related deaths, and those associated with and attributable to AMR in Pakistan between 1990 and 2019.



- To look at these and more visualization interactively visit [Measuring Infectious Causes and Resistance Outcomes for Burden Estimation \(MICROBE\)](#)
- In **Pakistan** in 2021, there were an estimated **39,700 UI (31,000-48,300)** deaths attributable to AMR and **161,000 UI (134,000-187,000)** deaths associated with AMR. Here *“attributable deaths”* are considered to be those that would have been prevented had the drug-resistant bacteria causing the infections not been drug-resistant. *“Associated deaths”* are considered to be those that would not have occurred had the infections been prevented entirely.
- Across 204 countries, **Pakistan has the 53rd highest** age-standardized mortality rate associated with AMR in 2021.
- *Table 1* shows the bacteria which caused most deaths in 2021 (↑ indicates an increasing estimated annual rate between 1990-2021, ↓ indicates a decreasing annual trend), and *table 2* shows the pathogen-drug combinations which caused most deaths in 2021.

Table 1. Bacteria which cause most deaths in 2021 (Number of deaths in parenthesis)

Burden rank	Overall susceptible and resistant		Associated		Attributable	
	Number of deaths (UI)	Annualized rate of change (1990-2021)	Number of deaths (UI)	Annualized rate of change (1990-2021)	Number of deaths (UI)	Annualized rate of change (1990-2021)
1	Mycobacterium tuberculosis 65,400 UI (46,200-84,600)	↓	Escherichia coli 24,800 UI (20,400-29,200)	↓	Klebsiella pneumoniae 7,010 UI (5,600-8,410)	↑
2	Klebsiella pneumoniae 30,200 UI (25,300-35,200)	↑	Klebsiella pneumoniae 23,700 UI (19,600-27,800)	↑	Escherichia coli 5,890 UI (4,680-7,100)	↑
3	Escherichia coli 26,100 UI (21,500-30,800)	↓	Streptococcus pneumoniae 19,100 UI (16,000-22,200)	↓	Acinetobacter baumannii 5,090 UI (4,270-5,910)	↓
4	Streptococcus pneumoniae 23,000 UI (19,200-26,700)	↓	Staphylococcus aureus 17,600 UI (14,900-20,300)	↑	Staphylococcus aureus 4,770 UI (4,030-5,500)	↑
5	Staphylococcus aureus 20,300 UI (17,100-23,400)	↑	Acinetobacter baumannii 12,800 UI (10,700-14,900)	↓	Streptococcus pneumoniae 3,420 UI (2,590-4,240)	↓
6	Pseudomonas aeruginosa 19,700 UI (16,700-22,700)	↑	Pseudomonas aeruginosa 12,200 UI (10,100-14,200)	↑	Pseudomonas aeruginosa 3,180 UI (2,480-3,880)	↑
7	Acinetobacter baumannii 13,100 UI (11,000-15,300)	↓	Mycobacterium tuberculosis 8,090 UI (2,420-18,300)	↑	Mycobacterium tuberculosis 2,650 UI (0-7,660)	↑
8	Group B Streptococcus 11,000 UI (8,330-13,700)	↑	Salmonella Typhi 7,640 UI (2,700-12,600)	↑	Enterobacter spp. 1,240 UI (995-1,480)	↑
9	Salmonella Typhi 8,570 UI (3,090-14,000)	↓	Group B Streptococcus 5,740 UI (4,280-7,200)	↑	Serratia spp. 1,230 UI (875-1,580)	↑
10	Serratia spp. 6,930 UI (5,360-8,500)	↑	Serratia spp. 4,600 UI (3,340-5,860)	↑	Salmonella Typhi 805 UI (87-1,520)	↑

Annualized rate of change (1990-2021): <-3% (dark blue), -3% to -1.5% (medium blue), -1.5% to 0% (light blue), 0% to 1.5% (pink), 1.5% to 3% (red), 3% to 5% (dark red), >5.0% (black)

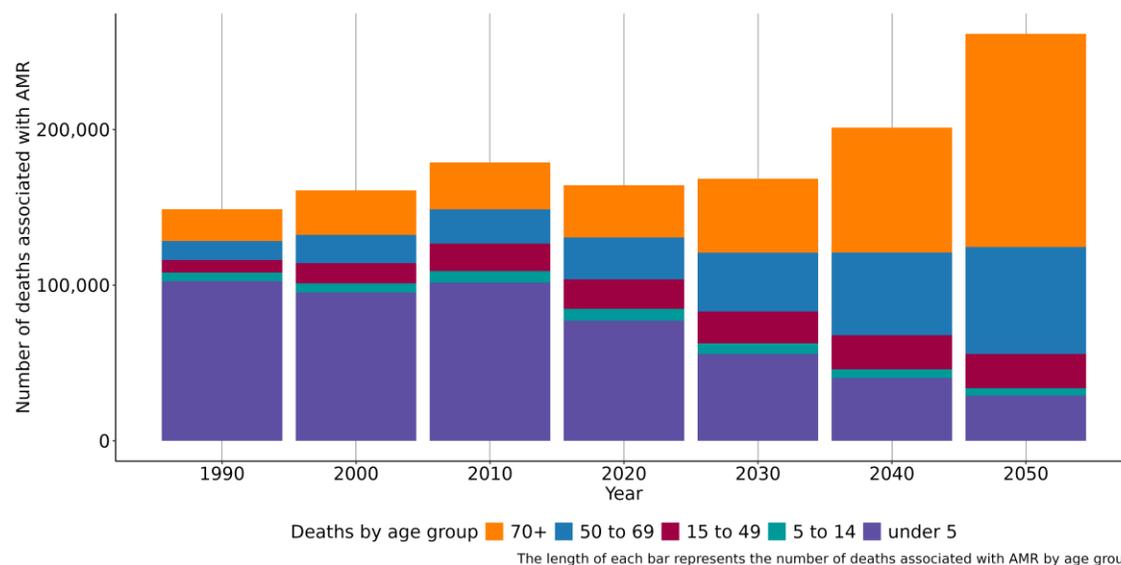
Table 2. Combinations which cause most deaths in 2021 (Number of deaths in parenthesis)

Burden Rank	Associated		Attributable	
	Number of deaths (UI)	Annualized rate of change (1990-2021)	Number of deaths (UI)	Annualized rate of change (1990-2021)
1	Escherichia coli Aminopenicillin 23,800 UI (19,500-28,200)	↑	Staphylococcus aureus Methicillin 2,940 UI (2,330-3,560)	↑
2	Klebsiella pneumoniae 3GC 20,900 UI (17,300-24,600)	↑	Mycobacterium tuberculosis MDR excluding XDR 2,490 UI (0-7,300)	↑
3	Klebsiella pneumoniae Beta-Lactam/Lactamase Inhib. 19,800 UI (15,200-24,400)	↑	Klebsiella pneumoniae Carbapenems 2,380 UI (1,790-2,960)	↑
4	Escherichia coli Fluoroquinolones 19,500 UI (15,700-23,200)	↑	Acinetobacter baumannii Carbapenems 2,360 UI (1,780-2,950)	↑
5	Escherichia coli 3GC 19,400 UI (15,800-22,900)	↑	Escherichia coli 3GC 1,630 UI (1,060-2,210)	↓
6	Escherichia coli TMP-SMX 18,800 UI (15,300-22,200)	↓	Acinetobacter baumannii Fluoroquinolones 1,400 UI (1,100-1,700)	↑
7	Klebsiella pneumoniae Fluoroquinolones 17,000 UI (13,500-20,500)	↑	Streptococcus pneumoniae Carbapenems 1,400 UI (738-2,050)	↑
8	Streptococcus pneumoniae TMP-SMX 16,700 UI (13,800-19,600)	↓	Klebsiella pneumoniae Fluoroquinolones 1,370 UI (901-1,840)	↑
9	Klebsiella pneumoniae Aminoglycosides 16,100 UI (12,900-19,300)	↑	Escherichia coli Fluoroquinolones 1,250 UI (780-1,720)	↑
10	Escherichia coli Beta-Lactam/Lactamase Inhib. 16,100 UI (12,900-19,200)	↓	Klebsiella pneumoniae 3GC 1,160 UI (718-1,600)	↑

Annualized rate of change (1990-2021): <-3% (dark blue), -3% to -1.5% (medium blue), -1.5% to 0% (light blue), 0% to 1.5% (pink), 1.5% to 3% (red), 3% to 5% (dark red), >5.0% (black)

- Independently of antimicrobial resistance, the infectious syndromes accounting for the most deaths in 2021 were as follows (estimated thousands of deaths in parenthesis) bloodstream infections (139,000 UI (110,000-168,000)), lower respiratory infection (excl. COVID) (83,800 UI (70,400-97,200)), tuberculosis (65,400 UI (46,200-84,600)), diarrhea (40,800 UI (23,900-57,800)) and meningitis (14,300 UI (10,600-18,000)).

Figure 3. Number of deaths associated with AMR by age group between 1990-2020 and 2050 projection



- In Pakistan, people aged under 5 saw the largest number of deaths associated with AMR both in 1990 and 2021, which indicates that under 5 continues to be particularly vulnerable to infections which are resistant to antibiotics. In 2021, the number of deaths associated with AMR among the under 5 was 73,300 UI (55,100-91,600), whereas the mortality rate per 100,000 was 659 UI (540-777).

Data sources for Pakistan

In total, 520 million individual records or isolates covering 19,513 study-location-years were used as input data to our estimation process. The subset of input data for this country is shown below.

Table 3. Data inputs for Pakistan by source type

Source type	Years	Sample size	Sample size units
Antibiotic use	2010-2021	12,496	Study-year datapoints
Microbial or laboratory data without outcome	1990-2021	1,124,423	Isolates
Microbial or laboratory data with outcome	2010-2021	13,236	Isolates
Literature studies	1990-2021	41,597	Cases/isolates/susceptibility tests
Single drug resistance profile data	1990-2021	417,672	Antibiotic susceptibility test

More information

About GRAM:

The purpose of the Global Research on AntiMicrobial resistance (GRAM) project is to **generate accurate and timely estimates of the magnitude and trends in antimicrobial resistance (AMR) burden** across the world, which can be used to inform treatment guidelines and agendas for decision-making and research, detect emerging problems and monitor trends to inform global strategies, as well as facilitate the assessment of interventions over time.

GRAM is the flagship project of the University of Oxford–IHME Strategic Partnership. GRAM was launched with support from the United Kingdom Department of Health and Social Care’s Fleming Fund, and the Wellcome Trust.

All resources:

For all resources on AMR analysis at IHME, visit <https://www.healthdata.org/antimicrobial-resistance>.

To look at these and more visualization interactively visit [Measuring Infectious Causes and Resistance Outcomes for Burden Estimation \(MICROBE\)](#).

Data sources:

To download the list of data input sources by country, and AMR results by region, visit the [Global Health Data Exchange \(GHDx\)](#).

Contact us:

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