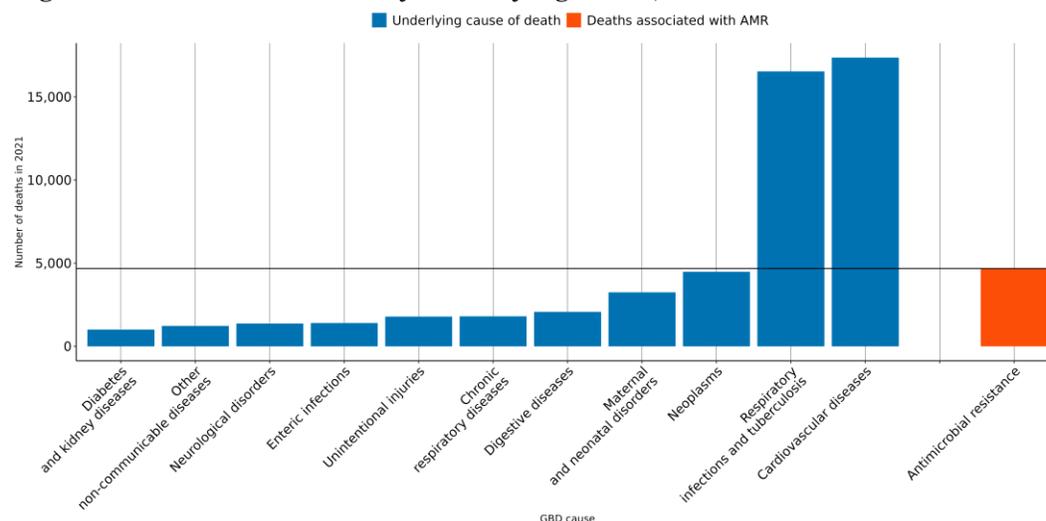


The burden of antimicrobial resistance (AMR) in Tajikistan

Executive summary

- Antimicrobial Resistance (AMR) is a major global health threat, over **1,000 lives** have been lost each year since 1990 in Tajikistan due to AMR.
- In 2021, there were an estimated **1,190 UI (885-1,480)** deaths attributable to AMR and **4,680 UI (3,700-5,660)** 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 *Streptococcus pneumoniae* resistant to carbapenems.

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



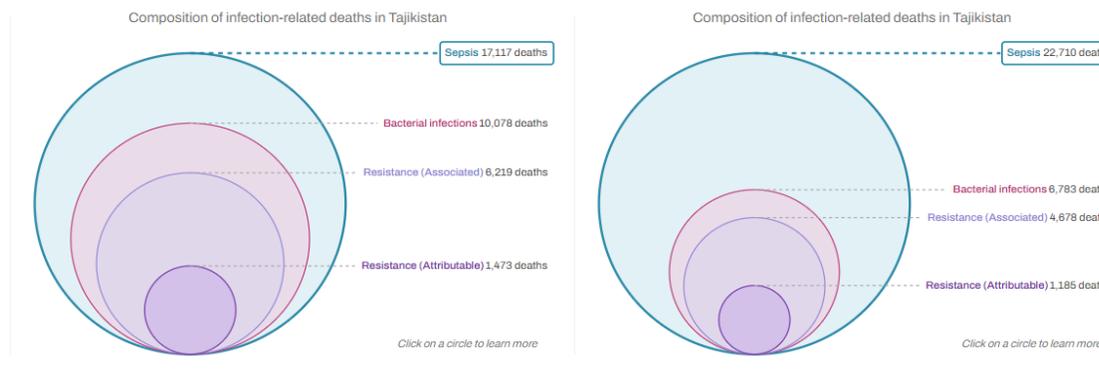
- In 2021, the number of deaths associated with AMR (orange bar in *figure 2*) were high compared to the most relevant underlying causes of death (depicted in blue) in the country. AMR associated deaths occur within multiple Global Burden of Disease (GBD) causes of death and AMR is not an underlying 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 Tajikistan, a 10% reduction means to decrease the number of deaths associated with AMR to **4,810**, but currently the trend for this country could reach up to **5,490 UI [4,090-7,090]** AMR-associated deaths in 2030.

AMR in Tajikistan

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 Tajikistan between 1990 and 2019.



- To look at these and more visualization interactively visit [Measuring Infectious Causes and Resistance Outcomes for Burden Estimation \(MICROBE\)](#)
- In **Tajikistan** in 2021, there were an estimated **1,190 UI (885-1,480)** deaths attributable to AMR and **4,680 UI (3,700-5,660)** 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, **Tajikistan has the 97th 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)

	Overall susceptible and resistant	Associated	Attributable
Burden rank	Streptococcus pneumoniae 1,560 UI (1,230-1,900) ↓	Streptococcus pneumoniae 1,220 UI (886-1,550) ↓	Streptococcus pneumoniae 294 UI (190-397) ↓
	Klebsiella pneumoniae 813 UI (686-939) ↓	Klebsiella pneumoniae 670 UI (554-786) ↓	Klebsiella pneumoniae 185 UI (150-220) ↓
	Staphylococcus aureus 765 UI (662-868) ↑	Escherichia coli 626 UI (499-753) ↓	Escherichia coli 135 UI (95-174) ↓
	Mycobacterium tuberculosis 738 UI (530-946) ↓	Staphylococcus aureus 508 UI (337-679) ↑	Acinetobacter baumannii 123 UI (106-140) ↓
	Escherichia coli 706 UI (597-815) ↓	Pseudomonas aeruginosa 362 UI (276-449) ↓	Staphylococcus aureus 114 UI (63-166) ↑
	Pseudomonas aeruginosa 574 UI (493-656) ↓	Acinetobacter baumannii 311 UI (270-352) ↓	Mycobacterium tuberculosis 97 UI (0-227) ↑
	Acinetobacter baumannii 313 UI (271-354) ↓	Mycobacterium tuberculosis 233 UI (45-421) ↑	Pseudomonas aeruginosa 92 UI (64-120) ↓
	Shigella spp. 205 UI (78-332) ↓	Enterobacter spp. 110 UI (93-128) ↓	Serratia spp. 30 UI (25-36) ↓
	Group B Streptococcus 166 UI (131-201) ↓	Serratia spp. 104 UI (86-123) ↓	Enterobacter spp. 27 UI (22-32) ↓
	Enterobacter spp. 153 UI (132-174) ↑	Shigella spp. 85 UI (15-154) ↑	Enterococcus faecalis 17 UI (9-24) ↑

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

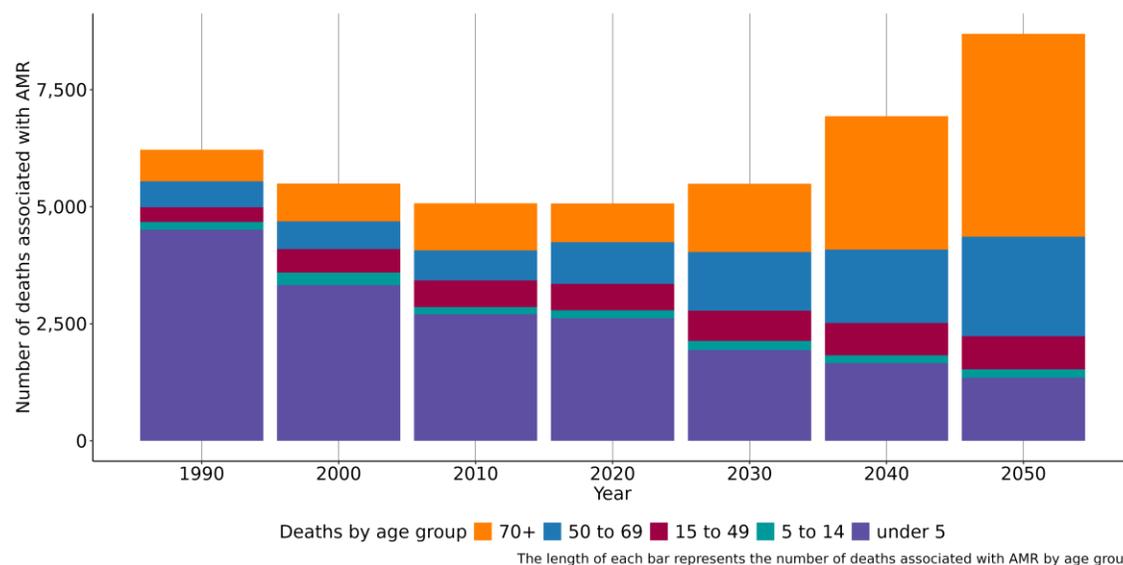
Table 2. Combinations which cause most deaths in 2021 (Number of deaths in parenthesis)

	Associated	Attributable
Burden Rank	Streptococcus pneumoniae TMP-SMX 1,010 UI (681-1,340) ↓	Streptococcus pneumoniae Carbapenems 179 UI (106-252) ↓
	Streptococcus pneumoniae Beta-Lactam/Lactamase Inhib. 836 UI (526-1,150) ↓	Mycobacterium tuberculosis MDR excluding XDR 65 UI (0-162) ↑
	Streptococcus pneumoniae Carbapenems 649 UI (403-895) ↓	Staphylococcus aureus Methicillin 59 UI (19-100) ↑
	Klebsiella pneumoniae Aminoglycosides 625 UI (514-736) ↓	Acinetobacter baumannii Carbapenems 52 UI (38-67) ↓
	Streptococcus pneumoniae Penicillin 591 UI (312-870) ↓	Klebsiella pneumoniae Carbapenems 51 UI (37-64) ↑
	Escherichia coli Aminopenicillin 562 UI (340-783) ↓	Klebsiella pneumoniae Aminoglycosides 51 UI (37-64) ↓
	Klebsiella pneumoniae 3GC 521 UI (424-618) ↑	Streptococcus pneumoniae Beta-Lactam/Lactamase Inhib. 50 UI (30-70) ↓
	Klebsiella pneumoniae TMP-SMX 515 UI (398-632) ↓	Escherichia coli 3GC 39 UI (25-53) ↑
	Klebsiella pneumoniae Fluoroquinolones 479 UI (358-599) ↑	Klebsiella pneumoniae Fluoroquinolones 36 UI (23-49) ↑
	Escherichia coli TMP-SMX 462 UI (367-558) ↓	Pseudomonas aeruginosa Carbapenems 35 UI (20-49) ↑

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

- Independently of antimicrobial resistance, the infectious syndromes accounting for the most deaths in 2021 were as follows (estimated thousands of deaths in parenthesis) lower respiratory infection (excl. COVID) (4,260 UI (3,310-5,200)), bloodstream infections (2,660 UI (2,200-3,130)), diarrhea (1,440 UI (962-1,930)), tuberculosis (738 UI (530-946)) and urinary tract infections and pyelonephritis (312 UI (234-389)).

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



- In Tajikistan, 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 2,240 UI (1,580-2,900), whereas the mortality rate per 100,000 was 403 UI (317-488).

Data sources for Tajikistan

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 Tajikistan by source type

Source type	Years	Sample size	Sample size units
Antibiotic use	1990-2021	1,307	Study-year datapoints

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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