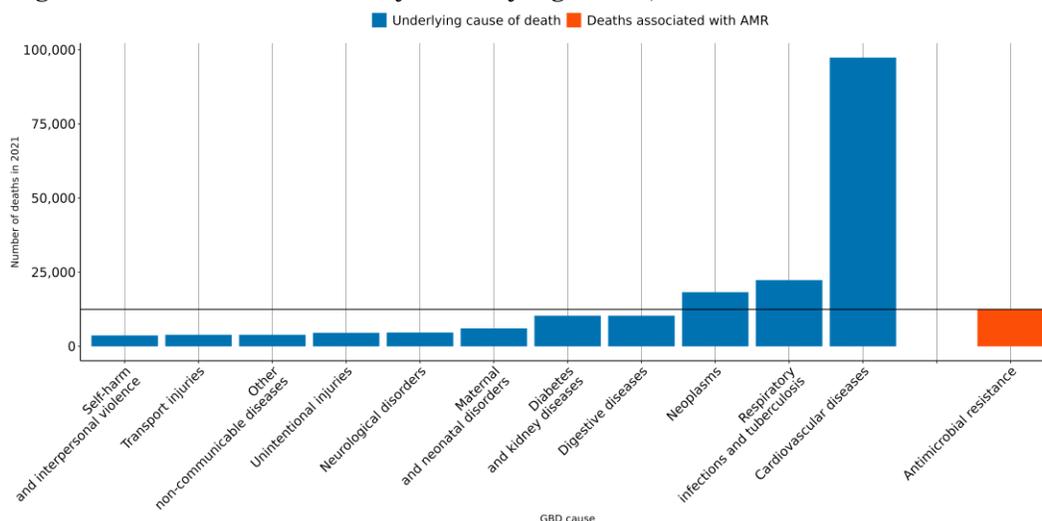


The burden of antimicrobial resistance (AMR) in Uzbekistan

Executive summary

- Antimicrobial Resistance (AMR) is a major global health threat, over **4,000 lives** have been lost each year since 1990 in Uzbekistan due to AMR.
- In 2021, there were an estimated **3,110 UI (2,350-3,870)** deaths attributable to AMR and **12,500 UI (10,100-14,800)** deaths associated with AMR in this location.
- The largest number of deaths associated with AMR in 2021 occurred among those aged **50 to 69** 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



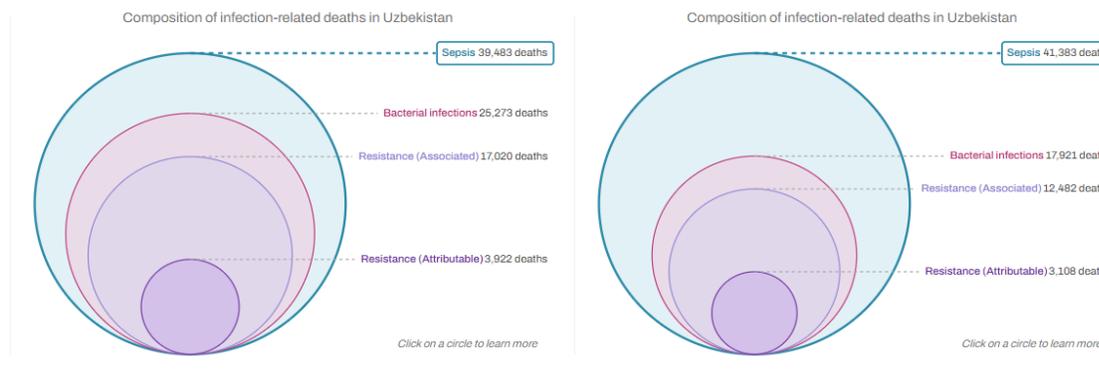
- In 2021, the number of deaths associated with AMR (orange bar in *figure 2*) were high compared to the most relevant underlying causes of death (depicted in blue) in the country. AMR associated deaths occur within multiple Global Burden of Disease (GBD) causes of death and AMR is not an underlying 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 Uzbekistan, a 10% reduction means to decrease the number of deaths associated with AMR to **12,200**, but currently the trend for this country could reach up to **14,900 UI [10,300-21,100]** AMR-associated deaths in 2030.

AMR in Uzbekistan

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 Uzbekistan between 1990 and 2019.



- To look at these and more visualization interactively visit [Measuring Infectious Causes and Resistance Outcomes for Burden Estimation \(MICROBE\)](#)
- In **Uzbekistan** in 2021, there were an estimated **3,110 UI (2,350-3,870)** deaths attributable to AMR and **12,500 UI (10,100-14,800)** 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, **Uzbekistan has the 77th lowest** 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	
	Bacteria	UI (range)	Bacteria	UI (range)	Bacteria	UI (range)
	Staphylococcus aureus	2,820 UI (2,490-3,150)	Escherichia coli	1,940 UI (1,550-2,320)	Klebsiella pneumoniae	470 UI (387-554)
	Klebsiella pneumoniae	2,320 UI (2,060-2,580)	Klebsiella pneumoniae	1,930 UI (1,660-2,200)	Escherichia coli	412 UI (293-531)
	Streptococcus pneumoniae	2,240 UI (1,980-2,490)	Staphylococcus aureus	1,860 UI (1,280-2,430)	Staphylococcus aureus	409 UI (227-591)
	Escherichia coli	2,230 UI (1,980-2,490)	Streptococcus pneumoniae	1,710 UI (1,350-2,070)	Streptococcus pneumoniae	393 UI (269-517)
	Pseudomonas aeruginosa	1,920 UI (1,700-2,130)	Pseudomonas aeruginosa	1,310 UI (1,060-1,550)	Acinetobacter baumannii	334 UI (288-381)
	Mycobacterium tuberculosis	1,370 UI (1,150-1,590)	Acinetobacter baumannii	833 UI (727-940)	Pseudomonas aeruginosa	325 UI (246-405)
	Acinetobacter baumannii	840 UI (732-947)	Mycobacterium tuberculosis	608 UI (183-1,030)	Mycobacterium tuberculosis	280 UI (0-673)
	Group A Streptococcus	536 UI (470-603)	Enterobacter spp.	390 UI (336-445)	Enterobacter spp.	118 UI (85-150)
	Group B Streptococcus	521 UI (444-597)	Serratia spp.	330 UI (276-383)	Serratia spp.	84 UI (63-104)
	Enterobacter spp.	503 UI (441-565)	Proteus spp.	249 UI (191-307)	Citrobacter spp.	54 UI (43-66)

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

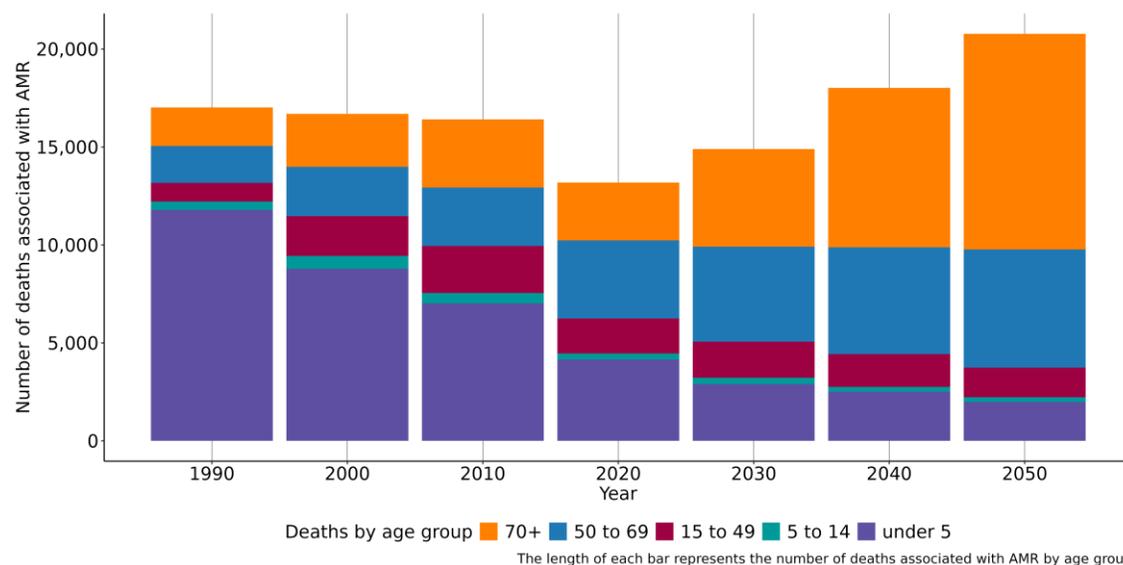
Table 2. Combinations which cause most deaths in 2021 (Number of deaths in parenthesis)

Burden Rank	Associated		Attributable	
	Combination	UI (range)	Combination	UI (range)
	Escherichia coli Aminopenicillin	1,770 UI (1,080-2,470)	Streptococcus pneumoniae Carbapenems	216 UI (127-304)
	Klebsiella pneumoniae Aminoglycosides	1,700 UI (1,440-1,950)	Staphylococcus aureus Methicillin	206 UI (66-345)
	Klebsiella pneumoniae TMP-SMX	1,650 UI (1,360-1,940)	Mycobacterium tuberculosis MDR excluding XDR	188 UI (0-479)
	Escherichia coli TMP-SMX	1,380 UI (1,060-1,710)	Acinetobacter baumannii Carbapenems	173 UI (134-211)
	Klebsiella pneumoniae Beta-Lactam/Lactamase Inhib.	1,300 UI (925-1,680)	Klebsiella pneumoniae Aminoglycosides	136 UI (104-168)
	Klebsiella pneumoniae Fluoroquinolones	1,280 UI (964-1,590)	Escherichia coli 3GC	135 UI (89-182)
	Escherichia coli 3GC	1,200 UI (784-1,630)	Pseudomonas aeruginosa Fluoroquinolones	105 UI (71-139)
	Streptococcus pneumoniae Beta-Lactam/Lactamase Inhib.	1,150 UI (760-1,550)	Pseudomonas aeruginosa Anti-pseudomonal	100 UI (75-124)
	Streptococcus pneumoniae TMP-SMX	1,120 UI (705-1,540)	Klebsiella pneumoniae Fluoroquinolones	92 UI (59-125)
	Escherichia coli Beta-Lactam/Lactamase Inhib.	1,120 UI (908-1,330)	Mycobacterium tuberculosis XDR	91 UI (0-206)

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

- 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 (10,900 UI (9,610-12,300)), lower respiratory infection (excl. COVID) (9,780 UI (8,580-11,000)), peritoneal and intra-abdominal infections (1,560 UI (1,290-1,820)), tuberculosis (1,370 UI (1,150-1,590)) and urinary tract infections and pyelonephritis (853 UI (687-1,020)).

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



- In Uzbekistan, people aged under 5 experienced the largest number of deaths associated with AMR in 1990 but this changed by 2021 as the largest number of deaths occurred among the 50 to 69. This indicates that prevention of infections among the under 5 has contributed to the reduction in the number of AMR associated deaths. In 2021, the number of deaths associated with AMR among the 50 to 69 was 4,040 UI (3,130-4,950), whereas the mortality rate per 100,000 was 312 UI (246-379).

Data sources for Uzbekistan

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 Uzbekistan by source type

Source type	Years	Sample size	Sample size units
Antibiotic use	1990-2009	62	Study-year datapoints
Microbial or laboratory data without outcome	2010-2021	43	Isolates
Literature studies	1990-2009	52	Cases/isolates/susceptibility tests

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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