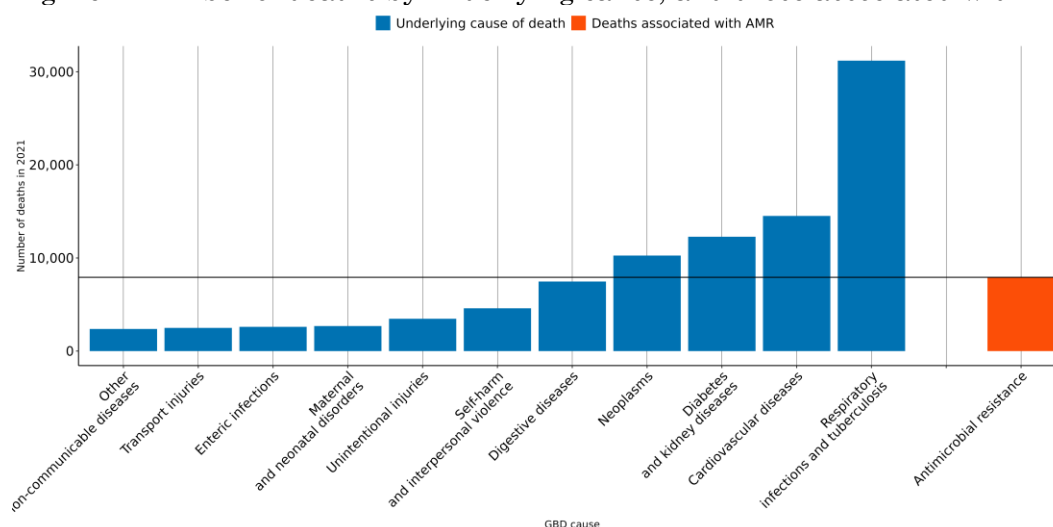


The burden of antimicrobial resistance (AMR) in Guatemala

Executive summary

- Antimicrobial Resistance (AMR) is a major global health threat, over **2,000 lives** have been lost each year since 1990 in Guatemala due to AMR.
- In 2021, there were an estimated **1,950 UI (1,640-2,270)** deaths attributable to AMR and **7,920 UI (6,630-9,220)** deaths associated with AMR in this location.
- The largest number of deaths associated with AMR in 2021 occurred among those aged **70+** in the country.
- Among the most deadly pathogen-drug combinations in 2021 were *Staphylococcus aureus* resistant to methicillin, *Klebsiella pneumoniae* resistant to carbapenems and *Acinetobacter baumannii* resistant to carbapenems.

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



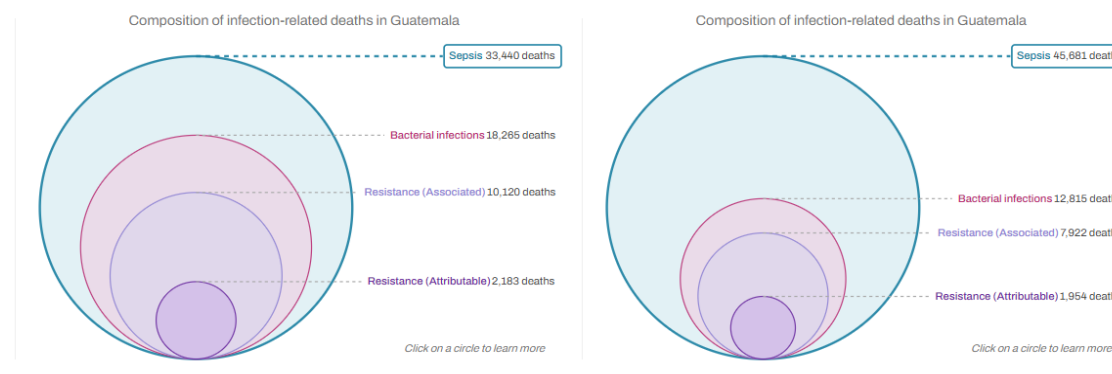
- In 2021, the number of deaths associated with AMR (orange bar in *figure 2*) were high compared to the most relevant underlying causes of death (depicted in blue) in the country. AMR associated deaths occur within multiple Global Burden of Disease (GBD) causes of death and AMR is not an underlying 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 Guatemala, a 10% reduction means to decrease the number of deaths associated with AMR to **8,590**, but currently the trend for this country could reach up to **10,500 UI [8,470-12,800]** AMR-associated deaths in 2030.

AMR in Guatemala

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 Guatemala between 1990 and 2019.



- To look at these and more visualization interactively visit [Measuring Infectious Causes and Resistance Outcomes for Burden Estimation \(MICROBE\)](#)
- In **Guatemala** in 2021, there were an estimated **1,950 UI (1,640-2,270)** deaths attributable to AMR and **7,920 UI (6,630-9,220)** 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, **Guatemala has the 81st 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		
	Streptococcus pneumoniae 2,170 UI (1,840-2,490)	↓		Klebsiella pneumoniae 1,380 UI (1,140-1,610)	↓		Klebsiella pneumoniae 401 UI (332-471)	↑	
	Staphylococcus aureus 1,880 UI (1,600-2,150)	↑		Streptococcus pneumoniae 1,230 UI (868-1,600)	↓		Acinetobacter baumannii 329 UI (281-377)	↓	
	Klebsiella pneumoniae 1,740 UI (1,470-2,000)	↓		Escherichia coli 1,230 UI (1,030-1,430)	↑		Staphylococcus aureus 318 UI (252-383)	↑	
	Pseudomonas aeruginosa 1,430 UI (1,220-1,650)	↑		Staphylococcus aureus 1,230 UI (1,020-1,440)	↑		Escherichia coli 255 UI (207-303)	↑	
	Escherichia coli 1,420 UI (1,200-1,640)	↑		Pseudomonas aeruginosa 857 UI (715-1,000)	↓		Pseudomonas aeruginosa 225 UI (175-274)	↓	
	Acinetobacter baumannii 841 UI (714-969)	↓		Acinetobacter baumannii 813 UI (690-936)	↓		Streptococcus pneumoniae 197 UI (117-278)	↓	
	Mycobacterium tuberculosis 447 UI (381-513)	↓		Enterobacter spp. 207 UI (167-246)	↓		Enterobacter spp. 52 UI (44-61)	↓	
	Group B Streptococcus 321 UI (266-377)	↓		Enterococcus faecium 180 UI (151-210)	↑		Serratia spp. 36 UI (28-44)	↓	
	Enterobacter spp. 317 UI (268-367)	↑		Proteus spp. 147 UI (113-181)	↑		Enterococcus faecium 35 UI (26-44)	↑	
	Group A Streptococcus 306 UI (252-359)	↑		Serratia spp. 146 UI (109-183)	↓		Proteus spp. 23 UI (16-29)	↑	

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% (dark red).

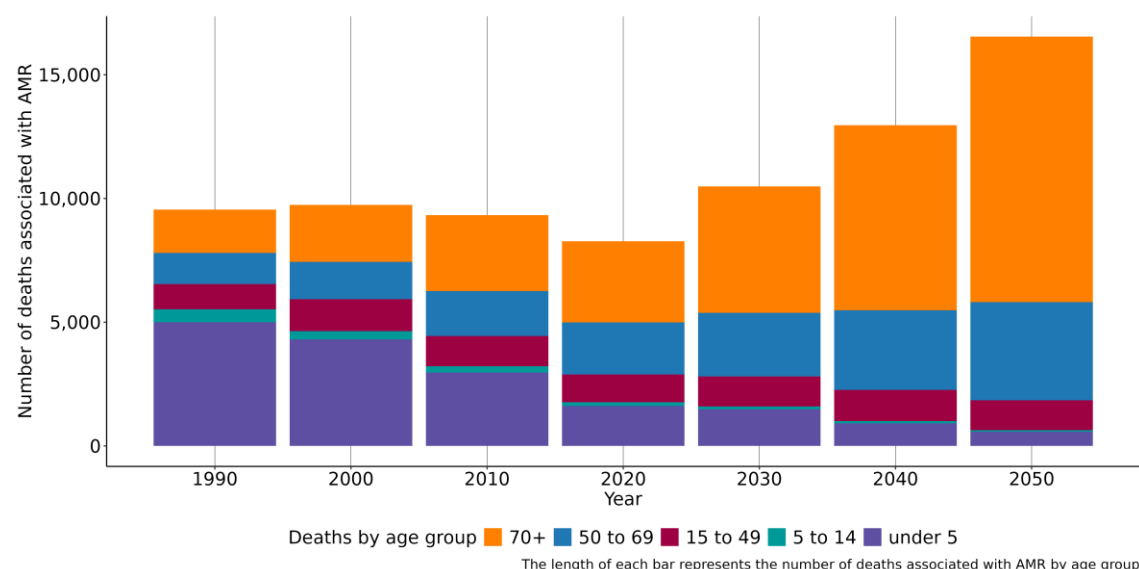
Table 2. Combinations which cause most deaths in 2021 (Number of deaths in parenthesis)

Burden Rank	Associated			Attributable		
	Klebsiella pneumoniae Aminoglycosides	1,120 UI (913-1,320)	↓	Staphylococcus aureus Methicillin	220 UI (156-283)	↑
	Escherichia coli Aminopenicillin	1,110 UI (847-1,370)	↓	Acinetobacter baumannii Carbapenems	174 UI (137-212)	↑
	Klebsiella pneumoniae Fluoroquinolones	1,100 UI (893-1,300)	↑	Klebsiella pneumoniae Carbapenems	135 UI (102-167)	↑
	Streptococcus pneumoniae TMP-SMX	1,050 UI (679-1,420)	↓	Streptococcus pneumoniae Carbapenems	93 UI (49-138)	↑
	Klebsiella pneumoniae TMP-SMX	1,000 UI (774-1,230)	↓	Pseudomonas aeruginosa Carbapenems	93 UI (56-130)	↑
	Klebsiella pneumoniae 3GC	965 UI (791-1,140)	↑	Klebsiella pneumoniae Fluoroquinolones	92 UI (63-122)	↑
	Klebsiella pneumoniae Beta-Lactam/Lactamase Inhib.	935 UI (704-1,170)	↓	Acinetobacter baumannii Fluoroquinolones	91 UI (73-109)	↑
	Staphylococcus aureus Methicillin	912 UI (669-1,150)	↑	Klebsiella pneumoniae Aminoglycosides	86 UI (63-109)	↓
	Staphylococcus aureus Macrolides	899 UI (740-1,060)	↑	Escherichia coli 3GC	57 UI (30-84)	↑
	Escherichia coli TMP-SMX	876 UI (720-1,030)	↓	Escherichia coli Fluoroquinolones	56 UI (35-76)	↑

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% (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) lower respiratory infection (excl. COVID) (9,020 UI (7,710-10,300)), bloodstream infections (5,740 UI (4,790-6,680)), diarrhea (2,620 UI (2,140-3,110)), peritoneal and intra-abdominal infections (1,410 UI (1,170-1,650)) and urinary tract infections and pyelonephritis (751 UI (634-869)).

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



- In Guatemala, 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 70+. 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 70+ was 3,200 UI (2,750-3,650), whereas the mortality rate per 100,000 was 544 UI (467-620).

Data sources for Guatemala

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 Guatemala by source type

Source type	Years	Sample size	Sample size units
Antibiotic use	2010-2021	2,319	Study-year datapoints
Microbial or laboratory data without outcome	1990-2021	194,860	Isolates
Literature studies	1990-2009	2,467	Cases/isolates/susceptibility tests
Single drug resistance profile data	1990-2021	168,236	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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