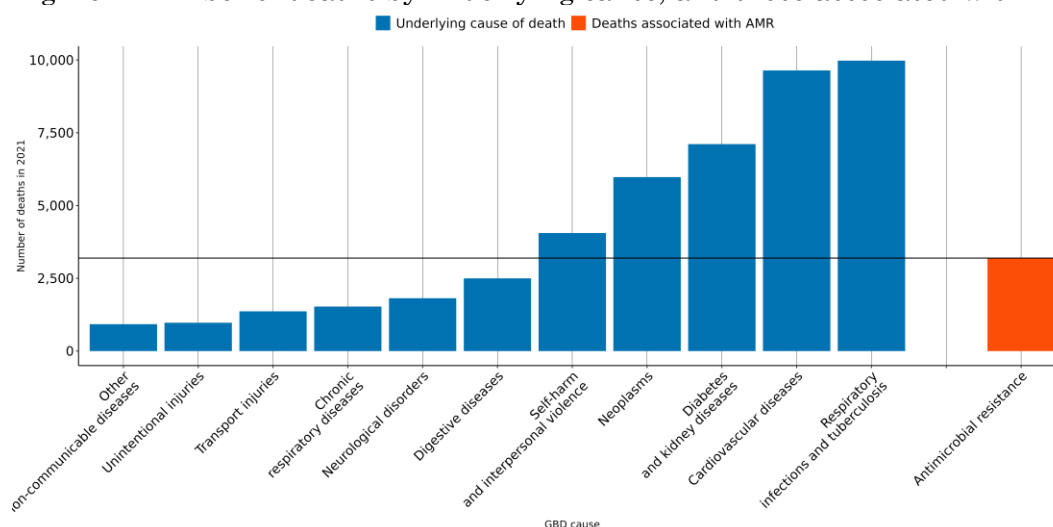


The burden of antimicrobial resistance (AMR) in El Salvador

Executive summary

- Antimicrobial Resistance (AMR) is a major global health threat, over **800 lives** have been lost each year since 1990 in El Salvador due to AMR.
- In 2021, there were an estimated **771 UI (597-946)** deaths attributable to AMR and **3,190 UI (2,460-3,930)** 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, *Acinetobacter baumannii* resistant to carbapenems and *Acinetobacter baumannii* resistant to fluoroquinolones.

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



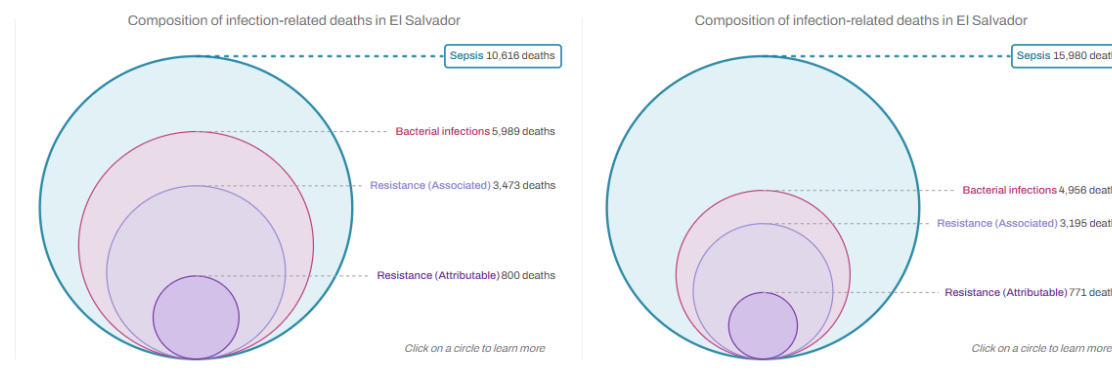
- In 2021, the number of deaths associated with AMR (orange bar in *figure 2*) were high compared to the most relevant underlying causes of death (depicted in blue) in the country. AMR associated deaths occur within multiple Global Burden of Disease (GBD) causes of death and AMR is not an underlying 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 El Salvador, a 10% reduction means to decrease the number of deaths associated with AMR to **3,120**, but currently the trend for this country could reach up to **3,820 UI [2,800-5,180]** AMR-associated deaths in 2030.

AMR in El Salvador

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 El Salvador between 1990 and 2019.



- To look at these and more visualization interactively visit [Measuring Infectious Causes and Resistance Outcomes for Burden Estimation \(MICROBE\)](#)
- In **El Salvador** in 2021, there were an estimated **771 UI (597-946)** deaths attributable to AMR and **3,190 UI (2,460-3,930)** 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, **El Salvador has the 91st 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	
	Staphylococcus aureus 904 UI (721-1,090)	↑	Staphylococcus aureus 668 UI (525-812)	↑	Staphylococcus aureus 172 UI (131-213)	↑
	Escherichia coli 627 UI (499-755)	↑	Escherichia coli 572 UI (453-691)	↑	Acinetobacter baumannii 123 UI (100-145)	↓
	Streptococcus pneumoniae 584 UI (466-701)	↓	Pseudomonas aeruginosa 402 UI (317-488)	↑	Escherichia coli 123 UI (92-153)	↑
	Klebsiella pneumoniae 582 UI (463-701)	↓	Klebsiella pneumoniae 379 UI (278-480)	↓	Pseudomonas aeruginosa 103 UI (76-129)	↑
	Pseudomonas aeruginosa 571 UI (454-687)	↑	Acinetobacter baumannii 319 UI (253-386)	↓	Klebsiella pneumoniae 99 UI (73-124)	↓
	Acinetobacter baumannii 343 UI (272-413)	↓	Streptococcus pneumoniae 308 UI (196-419)	↓	Streptococcus pneumoniae 49 UI (26-72)	↓
	Mycobacterium tuberculosis 207 UI (156-258)	↓	Enterococcus faecium 96 UI (75-118)	↑	Enterobacter spp. 20 UI (16-24)	↓
	Enterococcus faecalis 138 UI (109-167)	↑	Proteus spp. 84 UI (57-112)	↑	Enterococcus faecium 19 UI (13-24)	↑
	Enterobacter spp. 134 UI (106-161)	↑	Enterobacter spp. 83 UI (63-104)	↓	Serratia spp. 15 UI (12-19)	↓
	Proteus spp. 130 UI (104-157)	↑	Serratia spp. 60 UI (45-75)	↓	Proteus spp. 12 UI (7-18)	↑

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).

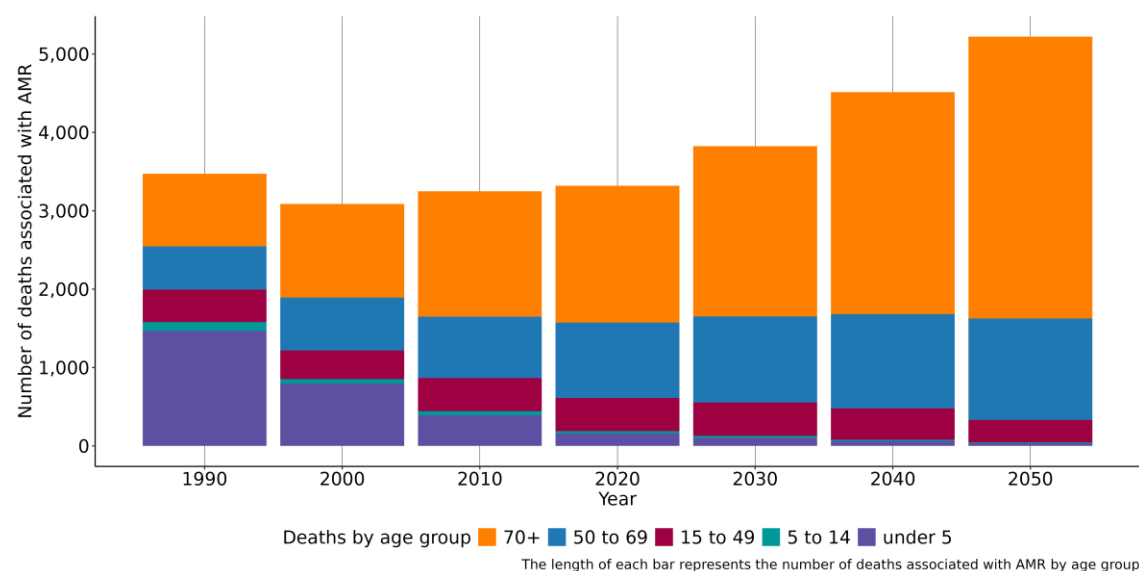
Table 2. Combinations which cause most deaths in 2021 (Number of deaths in parenthesis)

Burden Rank	Associated			Attributable		
	Escherichia coli Aminopenicillin	542 UI (396-687)	↑	Staphylococcus aureus Methicillin	120 UI (86-154)	↑
	Staphylococcus aureus Macrolides	523 UI (398-648)	↑	Acinetobacter baumannii Carbapenems	45 UI (30-60)	↑
	Staphylococcus aureus Methicillin	500 UI (354-645)	↑	Acinetobacter baumannii Fluoroquinolones	38 UI (30-46)	↑
	Escherichia coli TMP-SMX	419 UI (311-526)	↑	Pseudomonas aeruginosa Carbapenems	37 UI (19-55)	↑
	Escherichia coli Fluoroquinolones	368 UI (221-514)	↑	Pseudomonas aeruginosa Fluoroquinolones	29 UI (18-40)	↑
	Escherichia coli Beta-Lactam/Lactamase Inhib.	332 UI (250-414)	↑	Escherichia coli 3GC	26 UI (15-36)	↑
	Pseudomonas aeruginosa Fluoroquinolones	294 UI (224-365)	↓	Escherichia coli Fluoroquinolones	24 UI (9-38)	↑
	Klebsiella pneumoniae 3GC	294 UI (223-366)	↓	Klebsiella pneumoniae Carbapenems	23 UI (16-29)	↓
	Acinetobacter baumannii Fluoroquinolones	291 UI (228-354)	↑	Klebsiella pneumoniae Fluoroquinolones	22 UI (14-31)	↑
	Acinetobacter baumannii 4GC	291 UI (223-358)	↓	Staphylococcus aureus Macrolides	21 UI (13-29)	↑

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).

- 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) (2,830 UI (2,250-3,420)), bloodstream infections (2,320 UI (1,840-2,790)), peritoneal and intra-abdominal infections (706 UI (544-868)), urinary tract infections and pyelonephritis (612 UI (481-744)) and diarrhea (302 UI (166-438)).

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



- In El Salvador, 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 1,670 UI (1,300-2,040), whereas the mortality rate per 100,000 was 437 UI (340-533).

Data sources for El Salvador

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 El Salvador by source type

Source type	Years	Sample size	Sample size units
Antibiotic use	1990-2021	3,110	Study-year datapoints
Microbial or laboratory data without outcome	1990-2021	15,390	Isolates
Microbial or laboratory data with outcome	1990-2021	16	Isolates
Single drug resistance profile data	1990-2021	63,511	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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- **LinkedIn:** <https://www.linkedin.com/company/institute-for-health-metrics-and-evaluation>