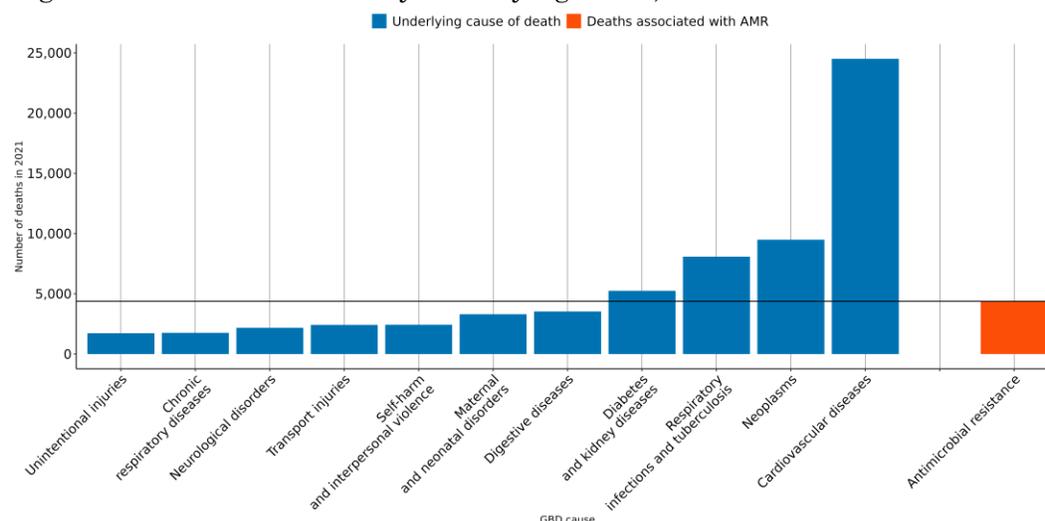


The burden of antimicrobial resistance (AMR) in the Dominican Republic

Executive summary

- Antimicrobial Resistance (AMR) is a major global health threat, over **1,000 lives** have been lost each year since 1990 in the Dominican Republic due to AMR.
- In 2021, there were an estimated **1,070 UI (840-1,290)** deaths attributable to AMR and **4,380 UI (3,410-5,340)** 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 *Streptococcus pneumoniae* resistant to carbapenems.

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



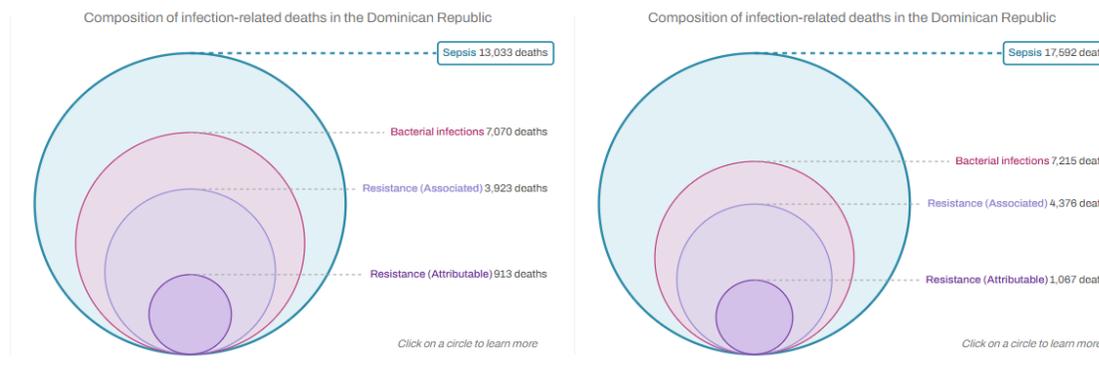
- In 2021, the number of deaths associated with AMR (orange bar in *figure 2*) were high compared to the most relevant underlying causes of death (depicted in blue) in the country. AMR associated deaths occur within multiple Global Burden of Disease (GBD) causes of death and AMR is not an underlying 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 the Dominican Rep., a 10% reduction means to decrease the number of deaths associated with AMR to **4,030**, but currently the trend for this country could reach up to **5,280 UI [3,940-7,150]** AMR-associated deaths in 2030.

AMR in the Dominican Republic

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 the Dominican Republic between 1990 and 2019.



- To look at these and more visualization interactively visit [Measuring Infectious Causes and Resistance Outcomes for Burden Estimation \(MICROBE\)](#)
- In the Dominican Republic in 2021, there were an estimated **1,070 UI (840-1,290)** deaths attributable to AMR and **4,380 UI (3,410-5,340)** 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, **the Dominican Republic has the 74th 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)

	Overall susceptible and resistant	Associated	Attributable
Burden rank	Staphylococcus aureus 1,010 UI (807-1,220) ↑	Staphylococcus aureus 824 UI (658-990) ↑	Staphylococcus aureus 230 UI (184-277) ↑
	Streptococcus pneumoniae 860 UI (675-1,050) ↓	Escherichia coli 731 UI (580-882) ↑	Acinetobacter baumannii 220 UI (176-264) ↑
	Klebsiella pneumoniae 836 UI (662-1,010) ↑	Klebsiella pneumoniae 620 UI (479-762) ↑	Streptococcus pneumoniae 139 UI (91-187) ↓
	Escherichia coli 800 UI (638-963) ↑	Acinetobacter baumannii 582 UI (452-713) ↑	Klebsiella pneumoniae 137 UI (103-171) ↑
	Acinetobacter baumannii 709 UI (563-855) ↑	Streptococcus pneumoniae 579 UI (417-741) ↓	Escherichia coli 135 UI (100-169) ↑
	Pseudomonas aeruginosa 705 UI (560-850) ↑	Pseudomonas aeruginosa 282 UI (196-367) ↓	Pseudomonas aeruginosa 67 UI (43-91) ↓
	Mycobacterium tuberculosis 689 UI (424-955) ↓	Enterobacter spp. 136 UI (102-170) ↓	Enterobacter spp. 30 UI (23-37) ↓
	Enterobacter spp. 218 UI (172-264) ↑	Enterococcus faecium 118 UI (94-143) ↑	Enterococcus faecium 24 UI (18-31) ↑
	Group B Streptococcus 200 UI (154-246) ↓	Citrobacter spp. 90 UI (65-116) ↑	Citrobacter spp. 20 UI (14-26) ↑
	Serratia spp. 198 UI (156-239) ↑	Proteus spp. 86 UI (62-111) ↑	Serratia spp. 19 UI (14-24) ↓

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

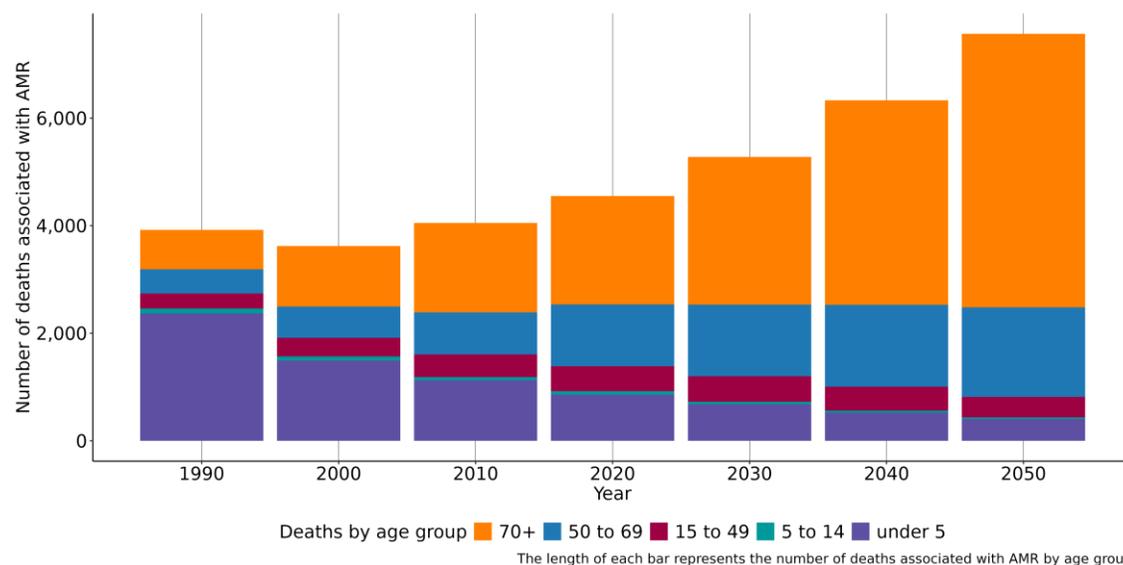
Table 2. Combinations which cause most deaths in 2021 (Number of deaths in parenthesis)

	Associated	Attributable
Burden Rank	Staphylococcus aureus Methicillin 698 UI (531-864) ↑	Staphylococcus aureus Methicillin 181 UI (135-226) ↑
	Staphylococcus aureus Macrolides 676 UI (525-827) ↑	Streptococcus pneumoniae Carbapenems 101 UI (63-140) ↑
	Escherichia coli Aminopenicillin 658 UI (458-859) ↑	Acinetobacter baumannii Carbapenems 74 UI (46-101) ↑
	Escherichia coli Fluoroquinolones 615 UI (479-752) ↑	Acinetobacter baumannii Fluoroquinolones 71 UI (56-86) ↑
	Klebsiella pneumoniae Fluoroquinolones 558 UI (427-688) ↑	Klebsiella pneumoniae Fluoroquinolones 58 UI (37-80) ↑
	Escherichia coli TMP-SMX 521 UI (399-643) ↑	Escherichia coli Fluoroquinolones 41 UI (20-63) ↑
	Acinetobacter baumannii Fluoroquinolones 516 UI (399-633) ↑	Acinetobacter baumannii Aminoglycosides 29 UI (19-39) ↓
	Klebsiella pneumoniae TMP-SMX 490 UI (369-611) ↓	Staphylococcus aureus Macrolides 27 UI (18-37) ↑
	Acinetobacter baumannii 3GC 484 UI (354-614) ↑	Acinetobacter baumannii 3GC 24 UI (20-28) ↓
	Acinetobacter baumannii 4GC 451 UI (321-581) ↑	Escherichia coli 3GC 24 UI (13-34) ↑

Annualized rate of change (1990-2021): <-3% (blue), -1.5% to 0% (light blue), 0% to 1.5% (pink), 1.5% to 3% (red), 3% to 5% (dark red), >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 (4,660 UI (3,740-5,580)), lower respiratory infection (excl. COVID) (3,070 UI (2,340-3,800)), tuberculosis (689 UI (424-955)), diarrhea (635 UI (417-853)) and peritoneal and intra-abdominal infections (625 UI (460-791)).

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



- In the Dominican Republic, 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 1,940 UI (1,450-2,420), whereas the mortality rate per 100,000 was 349 UI (262-437).

Data sources for the Dominican Republic

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 the Dominican Republic by source type

Source type	Years	Sample size	Sample size units
Antibiotic use	1990-2021	7,440	Study-year datapoints
Microbial or laboratory data without outcome	2010-2021	33,752	Isolates
Microbial or laboratory data with outcome	2010-2021	720	Isolates
Literature studies	1990-2021	60,039	Cases/isolates/susceptibility tests
Single drug resistance profile data	1990-2021	65,151	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:

- For inquiries about the analysis and questions from government officials, health departments, or research institutions: engage@healthdata.org
- For media-related inquiries: media@healthdata.org
- **Bluesky:** @ihmeuw.bsky.social
- **Twitter:** @IHME_UW
- **Facebook:** <https://www.facebook.com/IHMEUW>
- **LinkedIn:** <https://www.linkedin.com/company/institute-for-health-metrics-and-evaluation>