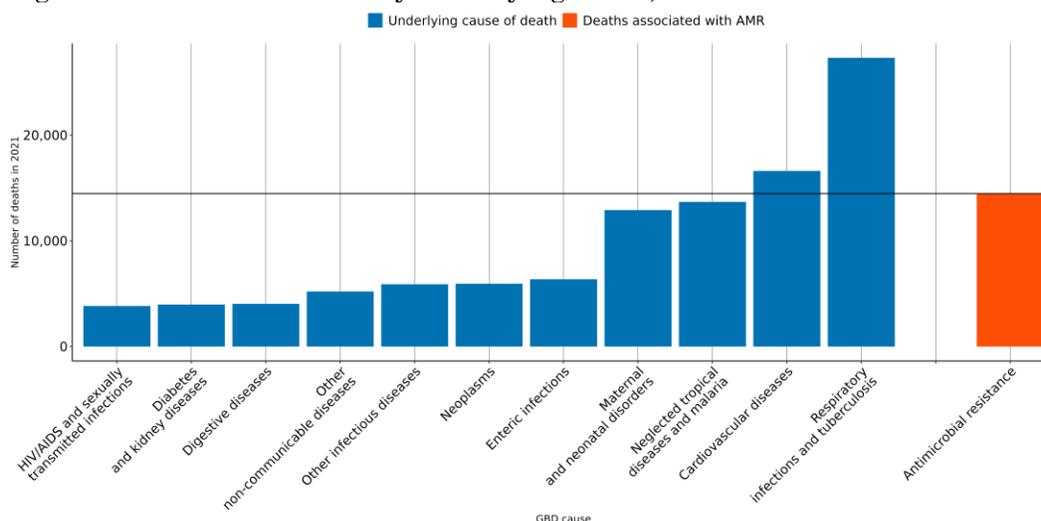


# The burden of antimicrobial resistance (AMR) in Guinea

## Executive summary

- Antimicrobial Resistance (AMR) is a major global health threat, over **4,000 lives** have been lost each year since 1990 in Guinea due to AMR.
- In 2021, there were an estimated **3,060 UI (2,100-4,020)** deaths attributable to AMR and **14,500 UI (10,400-18,500)** 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 *Staphylococcus aureus* resistant to methicillin, *Streptococcus pneumoniae* resistant to fluoroquinolones and *Streptococcus pneumoniae* resistant to penicillin.

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



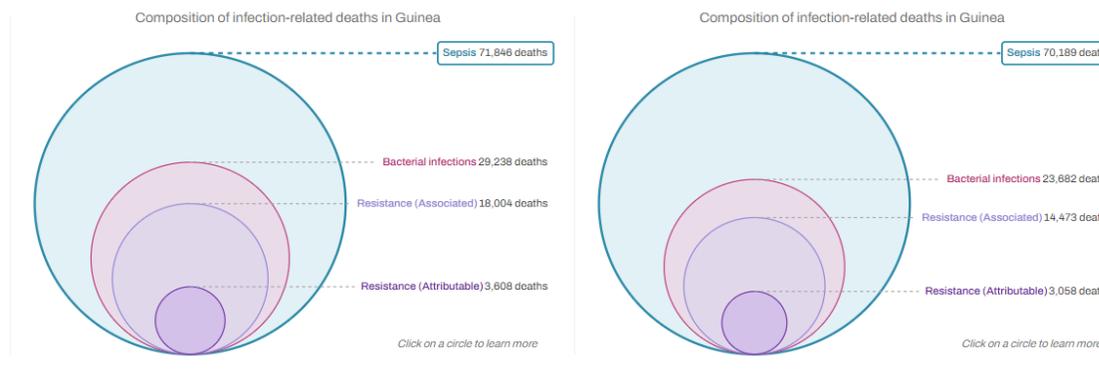
- In 2021, the number of deaths associated with AMR (orange bar in *figure 2*) were high compared to the most relevant underlying causes of death (depicted in blue) in the country. AMR associated deaths occur within multiple Global Burden of Disease (GBD) causes of death and AMR is not an underlying 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 Guinea, a 10% reduction means to decrease the number of deaths associated with AMR to **14,700**, but currently the trend for this country could reach up to **16,000 UI [11,000-22,800]** AMR-associated deaths in 2030.

## AMR in Guinea

### 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 Guinea between 1990 and 2019.



- To look at these and more visualization interactively visit [Measuring Infectious Causes and Resistance Outcomes for Burden Estimation \(MICROBE\)](#)
- In **Guinea** in 2021, there were an estimated **3,060 UI (2,100-4,020)** deaths attributable to AMR and **14,500 UI (10,400-18,500)** 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, **Guinea was among the highest 10 countries** in 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 5,140 UI (3,770-6,520) ↓	Streptococcus pneumoniae 4,190 UI (2,910-5,470) ↓	Streptococcus pneumoniae 663 UI (386-940) ↓
Mycobacterium tuberculosis 3,100 UI (2,060-4,140) ↓	Klebsiella pneumoniae 2,470 UI (1,870-3,070) ↓	Klebsiella pneumoniae 569 UI (408-731) ↑	
Klebsiella pneumoniae 2,780 UI (2,130-3,430) ↓	Escherichia coli 1,590 UI (1,140-2,050) ↓	Acinetobacter baumannii 501 UI (379-622) ↑	
Non-typhoidal Salmonella 1,910 UI (929-2,890) ↑	Acinetobacter baumannii 1,380 UI (1,000-1,760) ↑	Escherichia coli 319 UI (209-429) ↓	
Acinetobacter baumannii 1,720 UI (1,310-2,140) ↑	Pseudomonas aeruginosa 1,110 UI (781-1,430) ↓	Pseudomonas aeruginosa 269 UI (176-362) ↓	
Escherichia coli 1,710 UI (1,240-2,180) ↓	Staphylococcus aureus 1,070 UI (650-1,500) ↑	Staphylococcus aureus 253 UI (134-372) ↑	
Pseudomonas aeruginosa 1,710 UI (1,310-2,100) ↑	Enterobacter spp. 373 UI (282-463) ↑	Enterobacter spp. 107 UI (64-150) ↑	
Staphylococcus aureus 1,610 UI (1,230-1,980) ↑	Serratia spp. 330 UI (239-422) ↓	Serratia spp. 89 UI (63-114) ↑	
Group B Streptococcus 708 UI (512-904) ↓	Non-typhoidal Salmonella 327 UI (148-506) ↑	Mycobacterium tuberculosis 45 UI (0-179) ↑	
Haemophilus influenzae 470 UI (346-595) ↓	Shigella spp. 253 UI (68-438) ↓	Citrobacter spp. 36 UI (25-48) ↑	

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% (orange), 3% to 5% (brown)

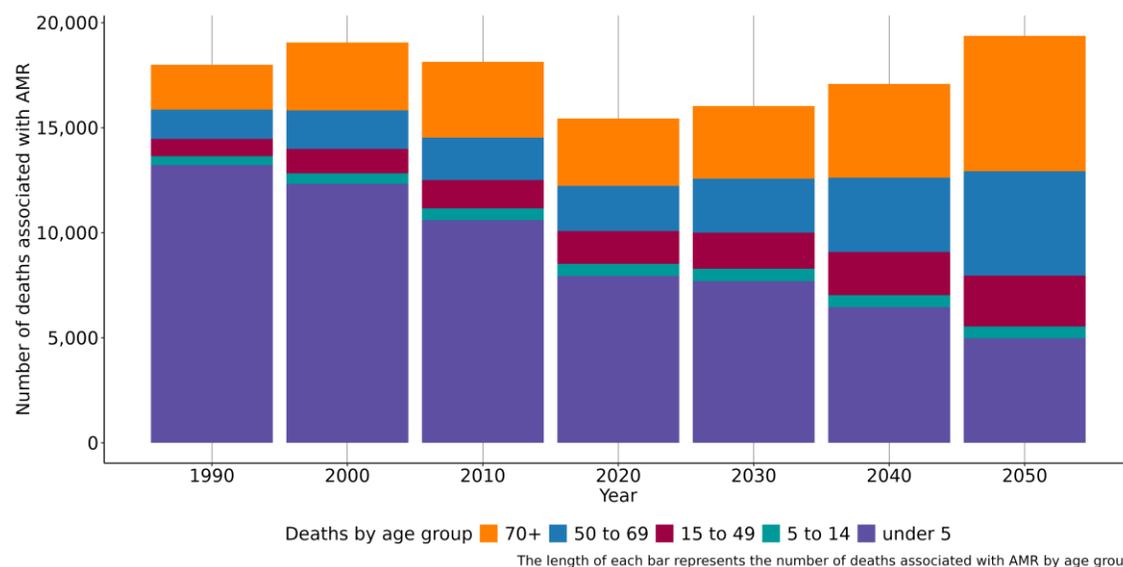
Table 2. Combinations which cause most deaths in 2021 (Number of deaths in parenthesis)

Burden Rank	Associated	Attributable
	Streptococcus pneumoniae TMP-SMX 3,840 UI (2,600-5,070) ↓	Streptococcus pneumoniae Penicillin 156 UI (77-234) ↓
Klebsiella pneumoniae TMP-SMX 2,300 UI (1,740-2,870) ↓	Streptococcus pneumoniae Fluoroquinolones 140 UI (41-238) ↓	
Klebsiella pneumoniae Beta-Lactam/Lactamase Inhib. 2,200 UI (1,610-2,790) ↓	Staphylococcus aureus Methicillin 137 UI (45-229) ↑	
Streptococcus pneumoniae Penicillin 1,820 UI (873-2,760) ↓	Klebsiella pneumoniae Beta-Lactam/Lactamase Inhib. 126 UI (45-208) ↓	
Streptococcus pneumoniae Macrolides 1,780 UI (1,060-2,500) ↑	Acinetobacter baumannii Fluoroquinolones 123 UI (90-155) ↑	
Klebsiella pneumoniae Aminoglycosides 1,690 UI (1,230-2,150) ↑	Acinetobacter baumannii Anti-pseudomonal 120 UI (92-147) ↑	
Klebsiella pneumoniae Fluoroquinolones 1,600 UI (1,100-2,090) ↑	Streptococcus pneumoniae TMP-SMX 116 UI (0-253) ↓	
Escherichia coli Aminopenicillin 1,560 UI (1,060-2,060) ↓	Klebsiella pneumoniae Fluoroquinolones 111 UI (67-156) ↑	
Streptococcus pneumoniae Fluoroquinolones 1,330 UI (514-2,150) ↓	Klebsiella pneumoniae Aminoglycosides 108 UI (71-144) ↑	
Escherichia coli TMP-SMX 1,320 UI (949-1,690) ↓	Acinetobacter baumannii Carbapenems 103 UI (53-152) ↑	

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% (orange), 3% to 5% (brown)

- 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) (12,300 UI (9,180-15,300)), bloodstream infections (9,440 UI (6,950-11,900)), diarrhea (4,390 UI (2,360-6,430)), tuberculosis (3,100 UI (2,060-4,140)) and meningitis (2,280 UI (1,330-3,230)).

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



- In Guinea, 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 7,270 UI (4,930-9,610), whereas the mortality rate per 100,000 was 1,150 UI (883-1,430).

### Data sources for Guinea

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 Guinea by source type

Source type	Years	Sample size	Sample size units
Antibiotic use	2010-2021	1,637	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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- **LinkedIn:** <https://www.linkedin.com/company/institute-for-health-metrics-and-evaluation>