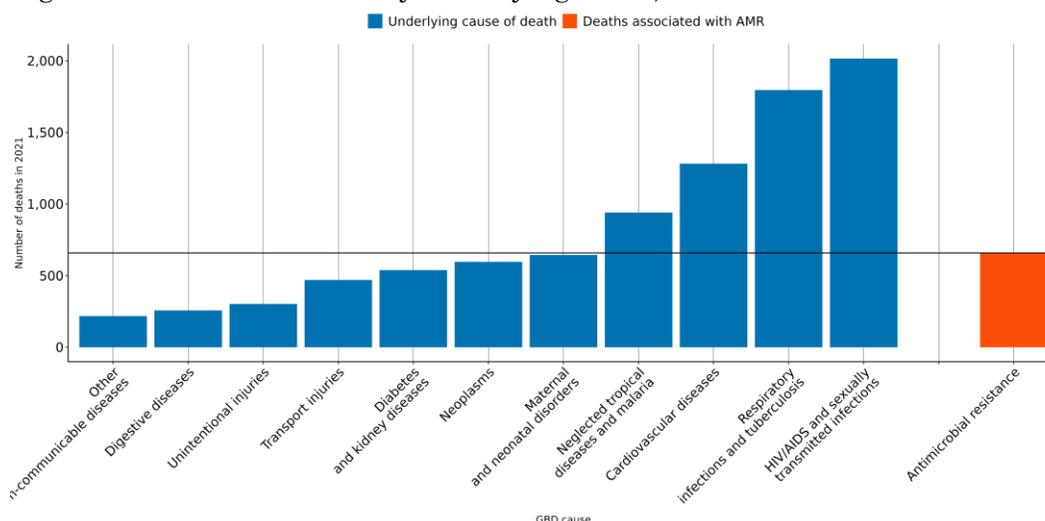


The burden of antimicrobial resistance (AMR) in Equatorial Guinea

Executive summary

- Antimicrobial Resistance (AMR) is a major global health threat, over **200 lives** have been lost each year since 1990 in Equatorial Guinea due to AMR.
- In 2021, there were an estimated **156 UI (100-213)** deaths attributable to AMR and **659 UI (423-894)** 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, *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



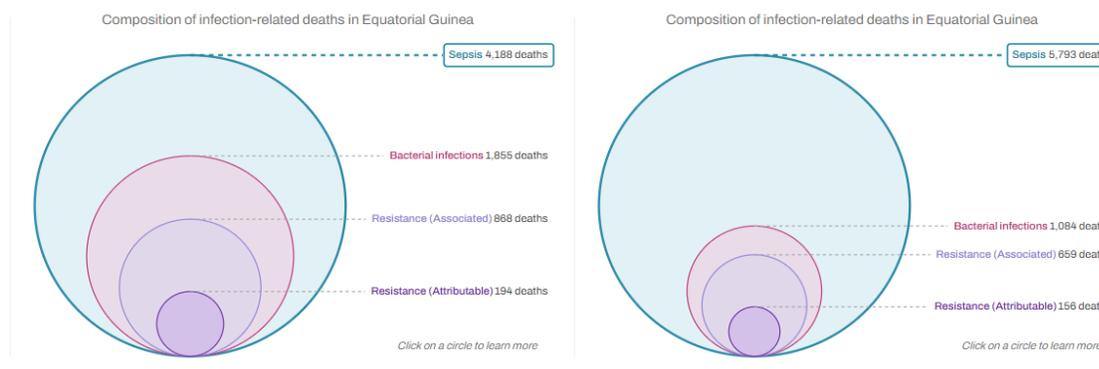
- In 2021, the number of deaths associated with AMR (orange bar in *figure 2*) were high compared to the most relevant underlying causes of death (depicted in blue) in the country. AMR associated deaths occur within multiple Global Burden of Disease (GBD) causes of death and AMR is not an underlying 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 Eq. Guinea, a 10% reduction means to decrease the number of deaths associated with AMR to **600**, but currently the trend for this country could reach up to **920 UI [567-1,440]** AMR-associated deaths in 2030.

AMR in Equatorial 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 Equatorial 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 **Equatorial Guinea** in 2021, there were an estimated **156 UI (100-213)** deaths attributable to AMR and **659 UI (423-894)** 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, **Equatorial Guinea has the 44th 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)

| | Overall susceptible and resistant | Associated | Attributable |
|-------------|---|---|---|
| Burden rank | Streptococcus pneumoniae 205 UI (133-277) ↓ | Streptococcus pneumoniae 155 UI (94-215) ↓ | Acinetobacter baumannii 35 UI (25-45) ↑ |
| | Mycobacterium tuberculosis 193 UI (96-291) ↓ | Klebsiella pneumoniae 92 UI (60-124) ↓ | Streptococcus pneumoniae 29 UI (16-43) ↓ |
| | Klebsiella pneumoniae 108 UI (71-145) ↓ | Acinetobacter baumannii 89 UI (58-120) ↑ | Klebsiella pneumoniae 20 UI (13-28) ↓ |
| | Staphylococcus aureus 108 UI (72-144) ↑ | Escherichia coli 76 UI (49-103) ↓ | Staphylococcus aureus 17 UI (9-26) ↑ |
| | Acinetobacter baumannii 93 UI (60-125) ↑ | Staphylococcus aureus 74 UI (45-103) ↑ | Escherichia coli 16 UI (10-23) ↓ |
| | Pseudomonas aeruginosa 86 UI (57-115) ↑ | Pseudomonas aeruginosa 56 UI (35-78) ↓ | Pseudomonas aeruginosa 14 UI (8-20) ↓ |
| | Escherichia coli 84 UI (56-112) ↓ | Enterobacter spp. 16 UI (10-22) ↑ | Serratia spp. 4 UI (3-6) ↓ |
| | Group B Streptococcus 26 UI (17-36) ↓ | Serratia spp. 15 UI (10-21) ↓ | Enterobacter spp. 4 UI (2-6) ↓ |
| | Enterobacter spp. 24 UI (16-32) ↑ | Enterococcus faecalis 12 UI (8-17) ↑ | Mycobacterium tuberculosis 3 UI (0-13) ↑ |
| | Haemophilus influenzae 21 UI (13-28) ↓ | Mycobacterium tuberculosis 11 UI (2-31) ↑ | Enterococcus faecalis 2 UI (1-3) ↑ |

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% (dark red)

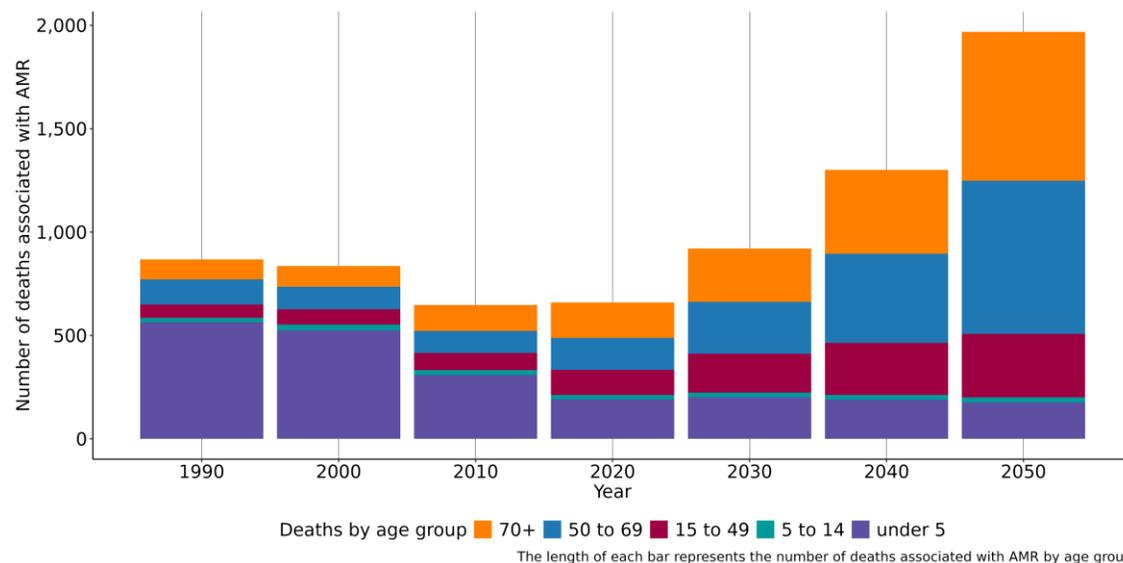
Table 2. Combinations which cause most deaths in 2021 (Number of deaths in parenthesis)

| | Associated | Attributable |
|-------------|---|--|
| Burden Rank | Streptococcus pneumoniae Macrolides 127 UI (77-178) ↑ | Acinetobacter baumannii Carbapenems 17 UI (11-23) ↑ |
| | Streptococcus pneumoniae TMP-SMX 92 UI (44-141) ↓ | Streptococcus pneumoniae Carbapenems 15 UI (7-24) ↓ |
| | Acinetobacter baumannii 4GC 86 UI (55-116) ↑ | Staphylococcus aureus Methicillin 9 UI (4-15) ↑ |
| | Acinetobacter baumannii 3GC 84 UI (54-113) ↑ | Acinetobacter baumannii Fluoroquinolones 9 UI (7-12) ↑ |
| | Klebsiella pneumoniae TMP-SMX 81 UI (53-110) ↓ | Escherichia coli 3GC 6 UI (3-9) ↑ |
| | Acinetobacter baumannii Anti-pseudomonal 81 UI (52-109) ↑ | Acinetobacter baumannii Aminoglycosides 6 UI (3-8) ↑ |
| | Acinetobacter baumannii Beta-Lactam/Lactamase Inhib. 80 UI (52-108) ↑ | Streptococcus pneumoniae Macrolides 5 UI (3-8) ↑ |
| | Acinetobacter baumannii Carbapenems 77 UI (49-106) ↑ | Klebsiella pneumoniae Fluoroquinolones 5 UI (3-7) ↓ |
| | Acinetobacter baumannii Fluoroquinolones 76 UI (49-103) ↑ | Pseudomonas aeruginosa Carbapenems 5 UI (2-8) ↑ |
| | Klebsiella pneumoniae Beta-Lactam/Lactamase Inhib. 76 UI (47-105) ↓ | Klebsiella pneumoniae Aminoglycosides 5 UI (3-7) ↑ |

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% (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) (504 UI (332-676)), bloodstream infections (504 UI (320-688)), tuberculosis (193 UI (96-291)), diarrhea (115 UI (53-176)) and meningitis (88 UI (51-125)).

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



- In Equatorial 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 182 UI (106-258), whereas the mortality rate per 100,000 was 894 UI (653-1,130).

Data sources for Equatorial 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 Equatorial Guinea by source type

| Source type | Years | Sample size | Sample size units |
|--------------------|-----------|-------------|-------------------------------------|
| Literature studies | 2010-2021 | 25 | 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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