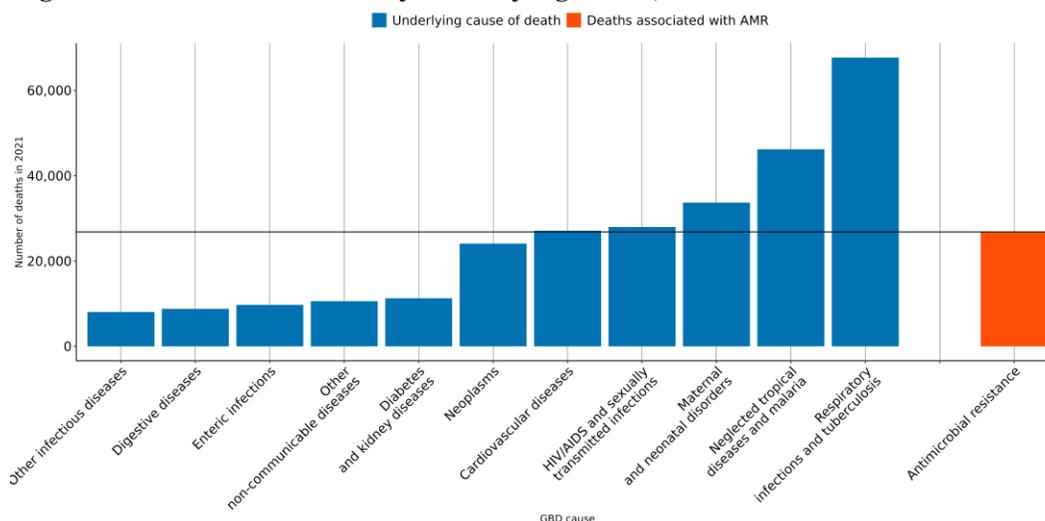


The burden of antimicrobial resistance (AMR) in Uganda

Executive summary

- Antimicrobial Resistance (AMR) is a major global health threat, over **7,000 lives** have been lost each year since 1990 in Uganda due to AMR.
- In 2021, there were an estimated **5,620 UI (4,020-7,210)** deaths attributable to AMR and **26,800 UI (20,400-33,300)** 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 multi-drug resistant *Mycobacterium tuberculosis* (excluding extensive drug-resistance), *Klebsiella pneumoniae* resistant to third-generation cephalosporins and *Streptococcus pneumoniae* resistant to penicillin.

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



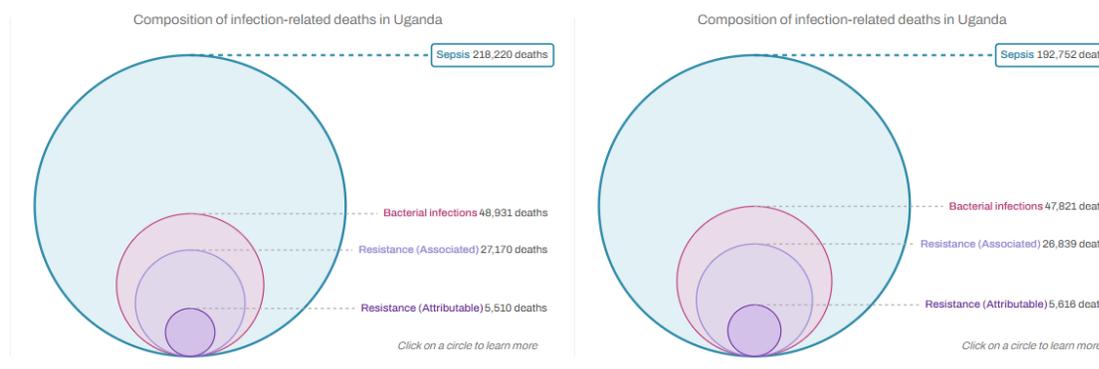
- In 2021, the number of deaths associated with AMR (orange bar in *figure 2*) were high compared to the most relevant underlying causes of death (depicted in blue) in the country. AMR associated deaths occur within multiple Global Burden of Disease (GBD) causes of death and AMR is not an underlying 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 Uganda, a 10% reduction means to decrease the number of deaths associated with AMR to **25,500**, but currently the trend for this country could reach up to **30,100 UI [21,700-40,800]** AMR-associated deaths in 2030.

AMR in Uganda

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 Uganda between 1990 and 2019.



- To look at these and more visualization interactively visit [Measuring Infectious Causes and Resistance Outcomes for Burden Estimation \(MICROBE\)](#)
- In **Uganda** in 2021, there were an estimated **5,620 UI (4,020-7,210)** deaths attributable to AMR and **26,800 UI (20,400-33,300)** 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, **Uganda has the 37th 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		
	Bacteria	UI (range)	Change	Bacteria	UI (range)	Change	Bacteria	UI (range)	Change
	Mycobacterium tuberculosis	11,900 UI (7,950-15,800)	↑	Streptococcus pneumoniae	5,300 UI (4,030-6,570)	↓	Klebsiella pneumoniae	1,090 UI (816-1,360)	↑
	Streptococcus pneumoniae	6,060 UI (4,810-7,320)	↓	Klebsiella pneumoniae	4,800 UI (3,790-5,800)	↑	Escherichia coli	857 UI (572-1,140)	↓
	Klebsiella pneumoniae	5,610 UI (4,510-6,710)	↑	Escherichia coli	4,090 UI (2,980-5,200)	↓	Streptococcus pneumoniae	783 UI (476-1,090)	↓
	Escherichia coli	4,440 UI (3,280-5,610)	↓	Staphylococcus aureus	2,800 UI (2,060-3,540)	↑	Acinetobacter baumannii	691 UI (548-833)	↑
	Staphylococcus aureus	3,950 UI (3,210-4,690)	↑	Pseudomonas aeruginosa	2,300 UI (1,660-2,950)	↑	Staphylococcus aureus	553 UI (377-729)	↑
	Pseudomonas aeruginosa	3,800 UI (3,070-4,530)	↑	Acinetobacter baumannii	2,000 UI (1,540-2,450)	↑	Pseudomonas aeruginosa	553 UI (365-741)	↑
	Acinetobacter baumannii	2,460 UI (1,970-2,940)	↑	Mycobacterium tuberculosis	888 UI (221-2,180)	↑	Mycobacterium tuberculosis	274 UI (0-843)	↑
	Group B Streptococcus	1,870 UI (1,400-2,340)	↑	Serratia spp.	754 UI (571-937)	↑	Serratia spp.	204 UI (153-256)	↑
	Serratia spp.	1,110 UI (857-1,360)	↑	Group B Streptococcus	724 UI (511-937)	↑	Enterobacter spp.	160 UI (124-197)	↑
	Haemophilus influenzae	1,050 UI (800-1,300)	↓	Enterobacter spp.	623 UI (486-760)	↑	Haemophilus influenzae	85 UI (40-130)	↓

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

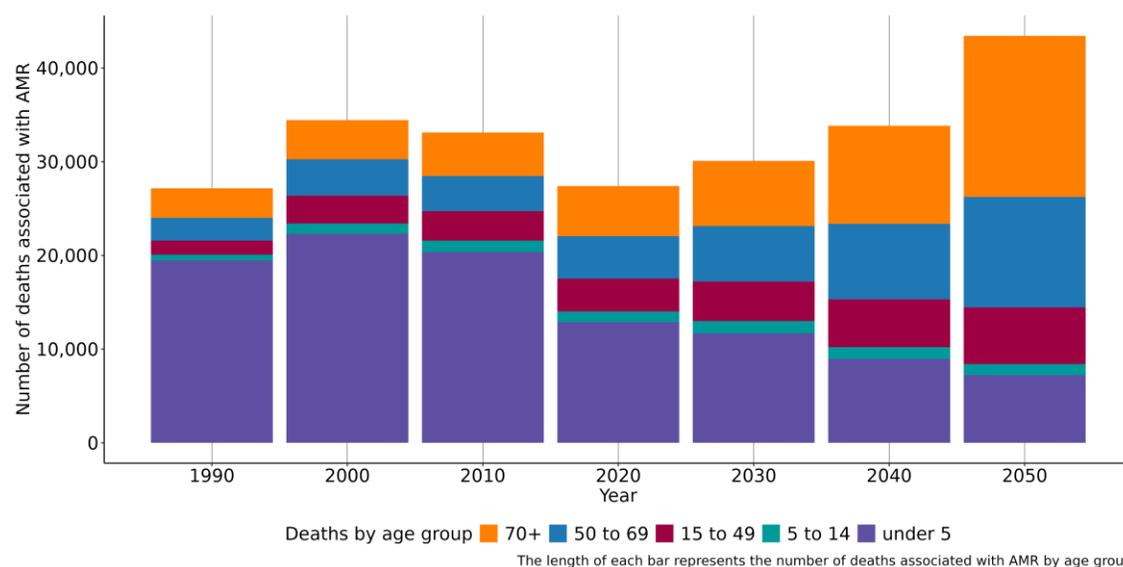
Table 2. Combinations which cause most deaths in 2021 (Number of deaths in parenthesis)

Burden Rank	Associated			Attributable		
	Combination	UI (range)	Change	Combination	UI (range)	Change
	Streptococcus pneumoniae TMP-SMX	5,120 UI (3,870-6,370)	↓	Klebsiella pneumoniae 3GC	311 UI (175-447)	↓
	Klebsiella pneumoniae TMP-SMX	4,610 UI (3,650-5,570)	↑	Mycobacterium tuberculosis MDR excluding XDR	269 UI (0-830)	↑
	Klebsiella pneumoniae Beta-Lactam/Lactamase Inhib.	3,760 UI (2,750-4,770)	↑	Streptococcus pneumoniae Penicillin	246 UI (132-359)	↓
	Escherichia coli TMP-SMX	3,660 UI (2,690-4,630)	↓	Staphylococcus aureus Methicillin	237 UI (123-351)	↑
	Klebsiella pneumoniae 3GC	3,610 UI (2,810-4,410)	↑	Klebsiella pneumoniae TMP-SMX	233 UI (114-351)	↑
	Escherichia coli Aminopenicillin	3,480 UI (2,170-4,800)	↓	Klebsiella pneumoniae Fluoroquinolones	226 UI (138-313)	↑
	Klebsiella pneumoniae Fluoroquinolones	2,970 UI (2,180-3,760)	↑	Escherichia coli 3GC	198 UI (88-309)	↓
	Escherichia coli Beta-Lactam/Lactamase Inhib.	2,700 UI (1,940-3,460)	↓	Escherichia coli TMP-SMX	198 UI (133-263)	↓
	Escherichia coli Fluoroquinolones	2,550 UI (1,500-3,590)	↑	Staphylococcus aureus TMP-SMX	177 UI (103-251)	↑
	Escherichia coli 3GC	2,450 UI (1,520-3,370)	↑	Streptococcus pneumoniae TMP-SMX	163 UI (0-354)	↓

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

- 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 (23,100 UI (17,800-28,400)), lower respiratory infection (excl. COVID) (18,800 UI (15,100-22,500)), tuberculosis (11,900 UI (7,950-15,800)), diarrhea (9,080 UI (4,690-13,500)) and meningitis (4,230 UI (2,680-5,770)).

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



- In Uganda, 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 12,300 UI (8,340-16,300), whereas the mortality rate per 100,000 was 881 UI (675-1,090).

Data sources for Uganda

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 Uganda by source type

Source type	Years	Sample size	Sample size units
Antibiotic use	1990-2021	4,744	Study-year datapoints
Microbial or laboratory data without outcome	1990-2021	21,551	Isolates
Microbial or laboratory data with outcome	2010-2021	918	Isolates
Literature studies	1990-2021	5,946	Cases/isolates/susceptibility tests
Single drug resistance profile data	2010-2021	6,761	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>