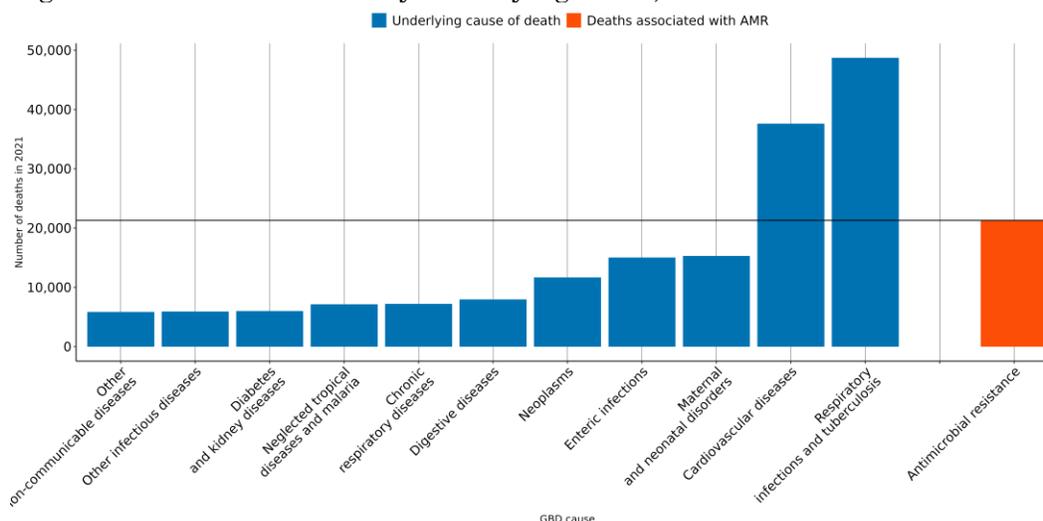


The burden of antimicrobial resistance (AMR) in Madagascar

Executive summary

- Antimicrobial Resistance (AMR) is a major global health threat, over **6,000 lives** have been lost each year since 1990 in Madagascar due to AMR.
- In 2021, there were an estimated **4,760 UI (3,560-5,950)** deaths attributable to AMR and **21,300 UI (16,900-25,700)** 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 *Klebsiella pneumoniae* resistant to fluoroquinolones, *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



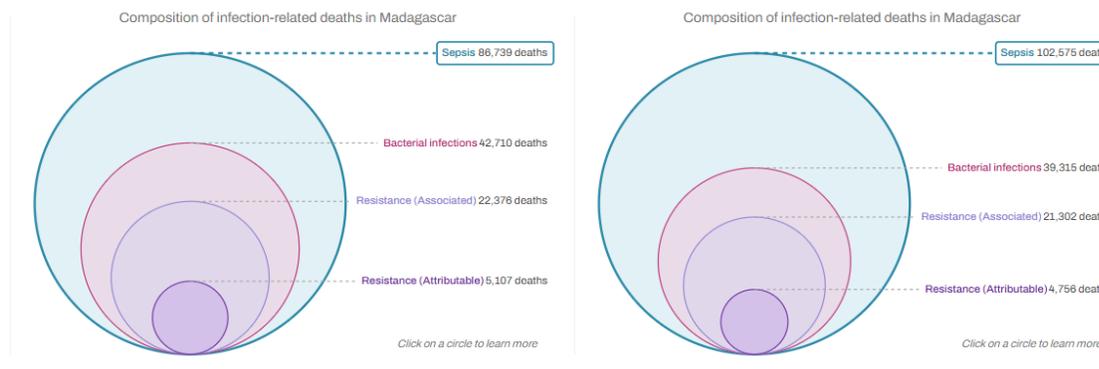
- In 2021, the number of deaths associated with AMR (orange bar in *figure 2*) were high compared to the most relevant underlying causes of death (depicted in blue) in the country. AMR associated deaths occur within multiple Global Burden of Disease (GBD) causes of death and AMR is not an underlying 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 Madagascar, a 10% reduction means to decrease the number of deaths associated with AMR to **20,900**, but currently the trend for this country could reach up to **24,100 UI [18,400-31,500]** AMR-associated deaths in 2030.

AMR in Madagascar

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 Madagascar between 1990 and 2019.



- To look at these and more visualization interactively visit [Measuring Infectious Causes and Resistance Outcomes for Burden Estimation \(MICROBE\)](#)
- In **Madagascar** in 2021, there were an estimated **4,760 UI (3,560-5,950)** deaths attributable to AMR and **21,300 UI (16,900-25,700)** 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, **Madagascar has the 14th 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	10,800 UI (7,220-14,400)	↓	Streptococcus pneumoniae	4,280 UI (3,300-5,250)	↓	Streptococcus pneumoniae	922 UI (612-1,230)	↓
	Streptococcus pneumoniae	5,000 UI (4,030-5,980)	↓	Escherichia coli	3,770 UI (2,710-4,820)	↓	Klebsiella pneumoniae	884 UI (664-1,100)	↑
	Klebsiella pneumoniae	4,380 UI (3,600-5,160)	↑	Klebsiella pneumoniae	3,760 UI (3,040-4,480)	↑	Escherichia coli	711 UI (451-970)	↓
	Escherichia coli	4,100 UI (2,990-5,210)	↓	Staphylococcus aureus	2,020 UI (1,470-2,570)	↑	Acinetobacter baumannii	633 UI (525-741)	↑
	Pseudomonas aeruginosa	2,880 UI (2,360-3,390)	↑	Pseudomonas aeruginosa	1,880 UI (1,440-2,330)	↑	Pseudomonas aeruginosa	452 UI (322-582)	↑
	Staphylococcus aureus	2,640 UI (2,160-3,120)	↑	Acinetobacter baumannii	1,670 UI (1,360-1,980)	↑	Staphylococcus aureus	386 UI (277-496)	↑
	Acinetobacter baumannii	1,750 UI (1,430-2,070)	↓	Mycobacterium tuberculosis	642 UI (124-1,780)	↑	Mycobacterium tuberculosis	188 UI (0-673)	↑
	Shigella spp.	1,730 UI (615-2,840)	↓	Enterobacter spp.	515 UI (418-612)	↑	Enterobacter spp.	139 UI (104-175)	↑
	Group B Streptococcus	1,130 UI (900-1,370)	↑	Serratia spp.	453 UI (348-558)	↑	Serratia spp.	117 UI (89-145)	↑
	Haemophilus influenzae	767 UI (615-919)	↓	Haemophilus influenzae	422 UI (240-605)	↓	Haemophilus influenzae	74 UI (32-116)	↓

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)

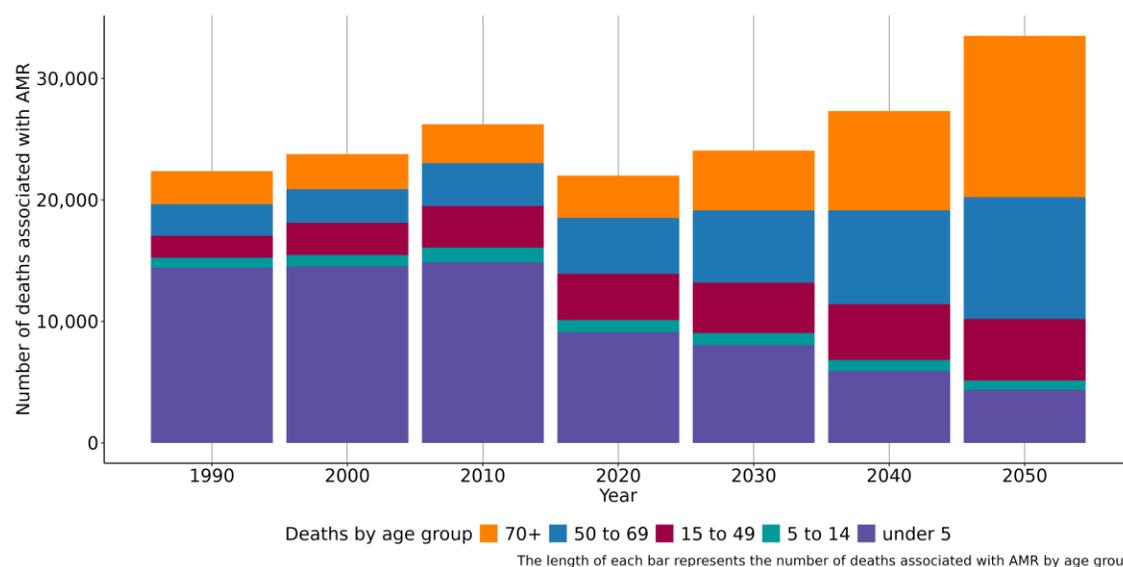
Table 2. Combinations which cause most deaths in 2021 (Number of deaths in parenthesis)

Burden Rank	Associated			Attributable		
	Combination	UI (range)	Change	Combination	UI (range)	Change
	Streptococcus pneumoniae TMP-SMX	3,880 UI (2,890-4,860)	↓	Streptococcus pneumoniae Carbapenems	460 UI (269-651)	↓
	Klebsiella pneumoniae Beta-Lactam/Lactamase Inhib.	3,530 UI (2,780-4,280)	↑	Acinetobacter baumannii Carbapenems	241 UI (159-323)	↑
	Escherichia coli Aminopenicillin	3,380 UI (2,250-4,500)	↓	Klebsiella pneumoniae Fluoroquinolones	187 UI (119-255)	↑
	Escherichia coli TMP-SMX	3,270 UI (2,380-4,170)	↓	Mycobacterium tuberculosis MDR excluding XDR	185 UI (0-663)	↑
	Klebsiella pneumoniae TMP-SMX	3,110 UI (2,490-3,740)	↑	Escherichia coli Beta-Lactam/Lactamase Inhib.	183 UI (46-321)	↓
	Escherichia coli Beta-Lactam/Lactamase Inhib.	2,950 UI (2,120-3,770)	↓	Klebsiella pneumoniae 3GC	182 UI (105-259)	↑
	Klebsiella pneumoniae Fluoroquinolones	2,610 UI (2,000-3,230)	↑	Escherichia coli TMP-SMX	171 UI (115-227)	↓
	Klebsiella pneumoniae 3GC	2,460 UI (1,930-2,980)	↑	Pseudomonas aeruginosa Anti-pseudomonal	170 UI (119-222)	↑
	Klebsiella pneumoniae Aminoglycosides	2,340 UI (1,760-2,910)	↑	Streptococcus pneumoniae Fluoroquinolones	169 UI (70-267)	↓
	Escherichia coli Fluoroquinolones	2,110 UI (1,140-3,080)	↑	Staphylococcus aureus TMP-SMX	166 UI (96-235)	↑

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) lower respiratory infection (excl. COVID) (18,000 UI (14,300-21,700)), diarrhea (15,000 UI (8,790-21,200)), bloodstream infections (13,300 UI (10,900-15,700)), tuberculosis (10,800 UI (7,220-14,400)) and meningitis (2,740 UI (2,070-3,420)).

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



- In Madagascar, 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 8,380 UI (6,080-10,700), whereas the mortality rate per 100,000 was 950 UI (722-1,180).

Data sources for Madagascar

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 Madagascar by source type

Source type	Years	Sample size	Sample size units
Antibiotic use	1990-2021	2,971	Study-year datapoints
Microbial or laboratory data without outcome	2010-2021	9,409	Isolates
Literature studies	1990-2021	5,060	Cases/isolates/susceptibility tests
Single drug resistance profile data	2010-2021	34,436	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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