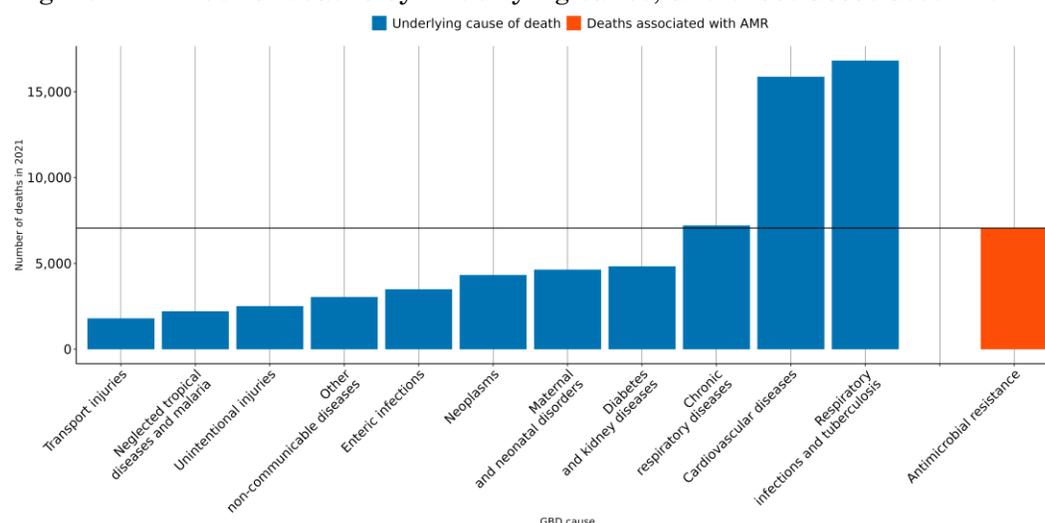


The burden of antimicrobial resistance (AMR) in Papua New Guinea

Executive summary

- Antimicrobial Resistance (AMR) is a major global health threat, over **1,000 lives** have been lost each year since 1990 in Papua New Guinea due to AMR.
- In 2021, there were an estimated **1,640 UI (1,170-2,100)** deaths attributable to AMR and **7,060 UI (5,420-8,700)** 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 *Acinetobacter baumannii* resistant to carbapenems, *Streptococcus pneumoniae* resistant to carbapenems and *Streptococcus pneumoniae* resistant to macrolides.

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



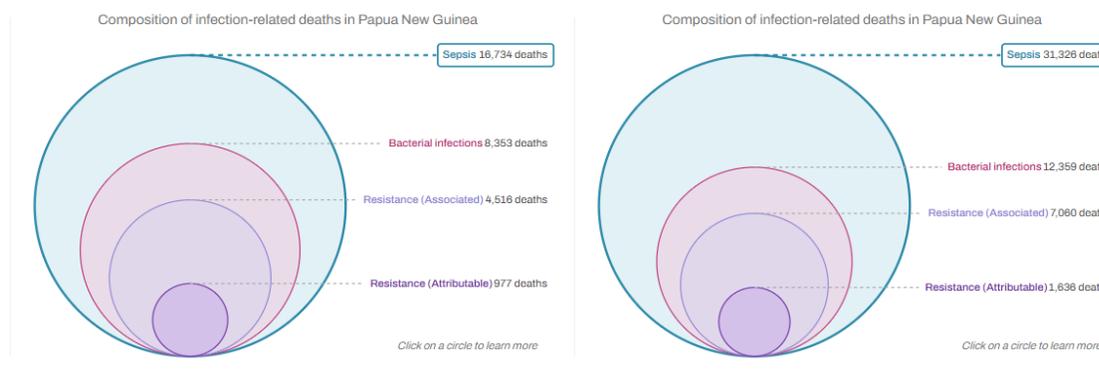
- In 2021, the number of deaths associated with AMR (orange bar in *figure 2*) were high compared to the most relevant underlying causes of death (depicted in blue) in the country. AMR associated deaths occur within multiple Global Burden of Disease (GBD) causes of death and AMR is not an underlying 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 Papua New Guinea, a 10% reduction means to decrease the number of deaths associated with AMR to **6,840**, but currently the trend for this country could reach up to **9,480 UI [6,770-12,800]** AMR-associated deaths in 2030.

AMR in Papua New 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 Papua New 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 **Papua New Guinea** in 2021, there were an estimated **1,640 UI (1,170-2,100)** deaths attributable to AMR and **7,060 UI (5,420-8,700)** 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, **Papua New Guinea has the 52nd 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	
	Burden rank	UI (range)	Burden rank	UI (range)	Burden rank	UI (range)
	Mycobacterium tuberculosis	2,620 UI (1,980-3,260)	Streptococcus pneumoniae	2,270 UI (1,800-2,750)	Streptococcus pneumoniae	481 UI (328-634)
	Streptococcus pneumoniae	2,490 UI (2,000-2,970)	Klebsiella pneumoniae	1,050 UI (807-1,290)	Klebsiella pneumoniae	249 UI (188-311)
	Klebsiella pneumoniae	1,380 UI (1,140-1,620)	Escherichia coli	689 UI (520-857)	Acinetobacter baumannii	209 UI (163-256)
	Pseudomonas aeruginosa	919 UI (758-1,080)	Acinetobacter baumannii	564 UI (437-691)	Escherichia coli	146 UI (103-189)
	Staphylococcus aureus	844 UI (697-992)	Pseudomonas aeruginosa	541 UI (397-685)	Pseudomonas aeruginosa	135 UI (89-180)
	Escherichia coli	773 UI (616-930)	Staphylococcus aureus	494 UI (316-672)	Staphylococcus aureus	112 UI (54-169)
	Acinetobacter baumannii	690 UI (566-814)	Mycobacterium tuberculosis	225 UI (64-506)	Mycobacterium tuberculosis	83 UI (0-233)
	Salmonella Typhi	519 UI (163-874)	Serratia spp.	175 UI (142-209)	Serratia spp.	51 UI (40-61)
	Shigella spp.	351 UI (111-592)	Salmonella Typhi	162 UI (0-323)	Enterobacter spp.	44 UI (32-56)
	Group B Streptococcus	253 UI (200-305)	Enterobacter spp.	145 UI (116-174)	Haemophilus influenzae	20 UI (5-36)

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

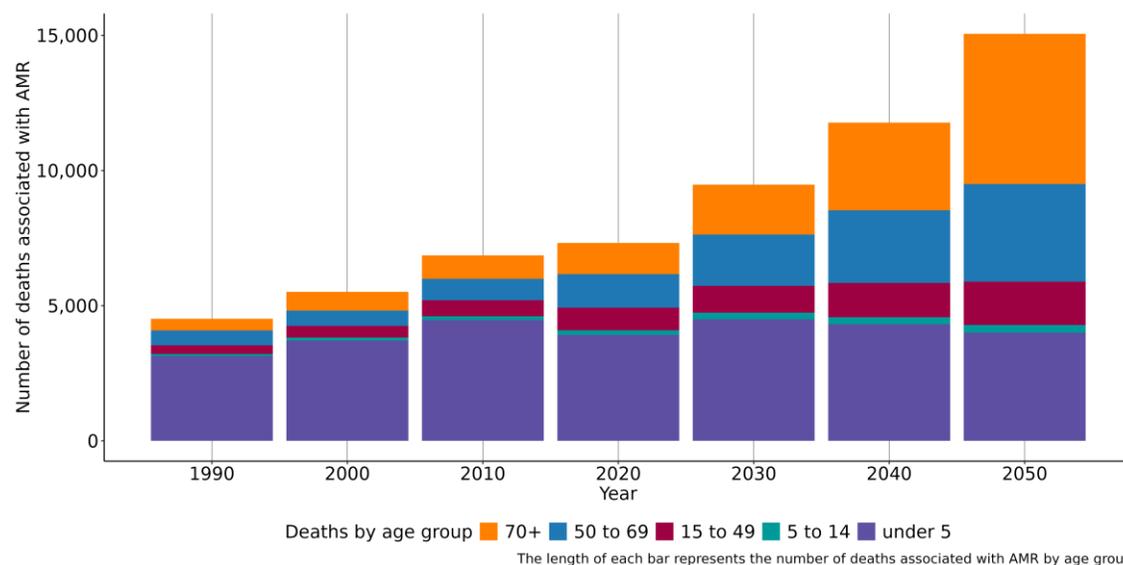
Table 2. Combinations which cause most deaths in 2021 (Number of deaths in parenthesis)

Burden Rank	Associated		Attributable	
	Burden Rank	UI (range)	Burden Rank	UI (range)
	Streptococcus pneumoniae Macrolides	2,160 UI (1,700-2,610)	Streptococcus pneumoniae Carbapenems	265 UI (155-375)
	Streptococcus pneumoniae TMP-SMX	1,500 UI (965-2,040)	Streptococcus pneumoniae Macrolides	81 UI (44-117)
	Streptococcus pneumoniae Beta-Lactam/Lactamase Inhib.	1,110 UI (632-1,580)	Acinetobacter baumannii Carbapenems	74 UI (43-105)
	Streptococcus pneumoniae Carbapenems	992 UI (598-1,390)	Klebsiella pneumoniae Aminoglycosides	71 UI (50-91)
	Klebsiella pneumoniae TMP-SMX	834 UI (616-1,050)	Mycobacterium tuberculosis MDR excluding XDR	65 UI (0-192)
	Klebsiella pneumoniae Aminoglycosides	807 UI (610-1,000)	Acinetobacter baumannii Fluoroquinolones	62 UI (48-76)
	Streptococcus pneumoniae 3GC	797 UI (528-1,070)	Escherichia coli 3GC	59 UI (38-80)
	Klebsiella pneumoniae Beta-Lactam/Lactamase Inhib.	762 UI (505-1,020)	Staphylococcus aureus Methicillin	57 UI (16-97)
	Klebsiella pneumoniae 3GC	656 UI (498-815)	Pseudomonas aeruginosa Carbapenems	48 UI (25-72)
	Escherichia coli Aminopenicillin	612 UI (342-882)	Klebsiella pneumoniae Carbapenems	45 UI (31-59)

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

- 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) (6,950 UI (5,620-8,290)), bloodstream infections (3,980 UI (3,190-4,770)), diarrhea (2,990 UI (1,950-4,020)), tuberculosis (2,620 UI (1,980-3,260)) and typhoid fever, paratyphoid fever, and invasive non-typhoidal salmonella (601 UI (213-988)).

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



- In Papua New 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 3,650 UI (2,650-4,650), whereas the mortality rate per 100,000 was 658 UI (494-821).

Data sources for Papua New 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 Papua New Guinea by source type

Source type	Years	Sample size	Sample size units
Antibiotic use	1990-2021	668	Study-year datapoints
Microbial or laboratory data without outcome	1990-2021	293	Isolates
Literature studies	1990-2021	112	Cases/isolates/susceptibility tests
Single drug resistance profile data	1990-2009	565	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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