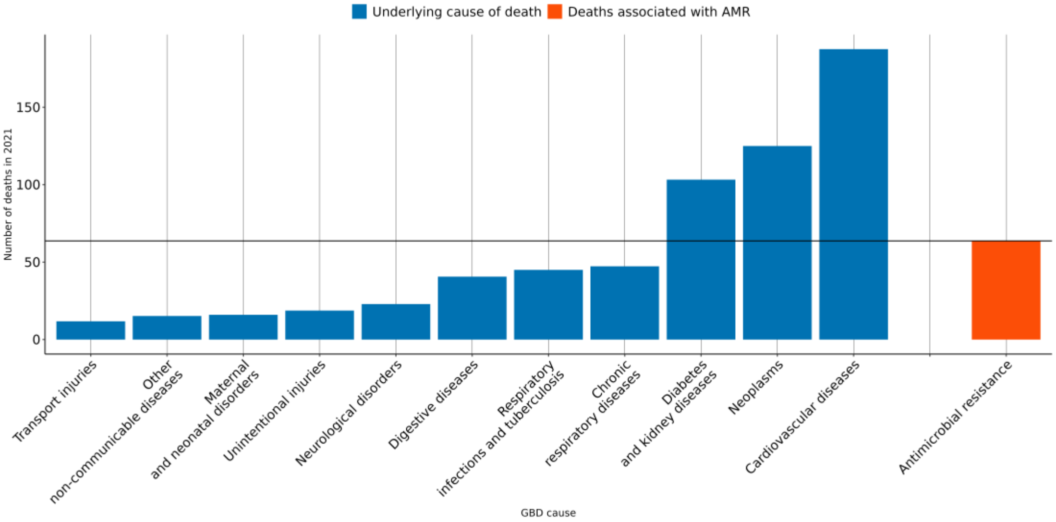
The burden of antimicrobial resistance (AMR) in Tonga

Executive summary

- Antimicrobial Resistance (AMR) is a major global health threat, over **20 lives** have been lost each year since 1990 in Tonga due to AMR.
- In 2021, there were an estimated **17 UI (12-22)** deaths attributable to AMR and **64 UI (46-81)** deaths associated with AMR in this location.
- The largest number of deaths associated with AMR in 2021 occurred among those aged **70+** 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



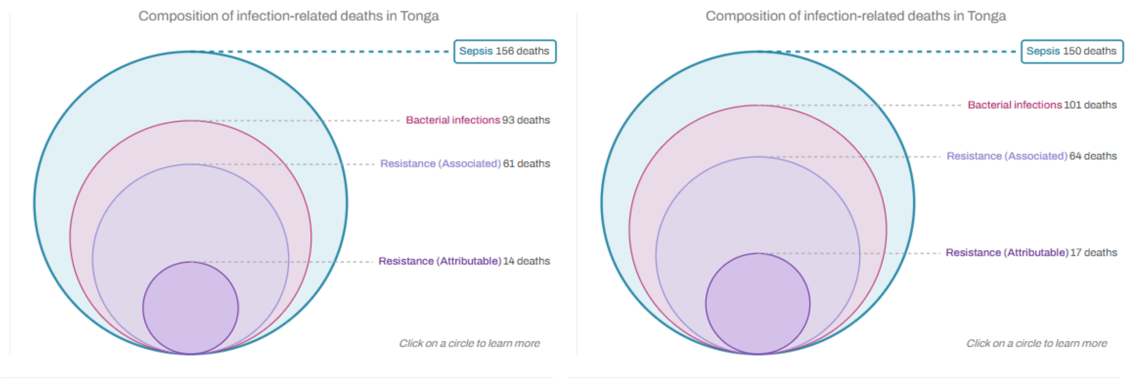
- In 2021, the number of deaths associated with AMR (orange bar in *figure 2*) were high compared to the most relevant underlying causes of death (depicted in blue) in the country. AMR associated deaths occur within multiple Global Burden of Disease (GBD) causes of death and AMR is not an underlying 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 Tonga, a 10% reduction means to decrease the number of deaths associated with AMR to **58**, but currently the trend for this country could reach up to **64 UI [46-86]** AMR-associated deaths in 2030.

AMR in Tonga

Key takeaways

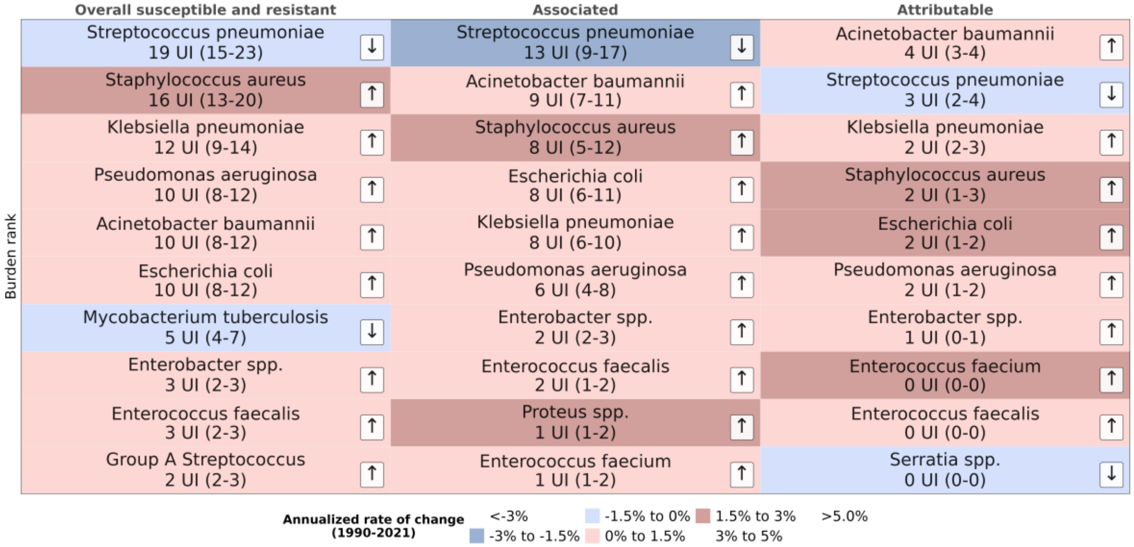
- Antimicrobial Resistance (AMR) is a major global health threat, over *a million lives* have been lost each year since 1990.
- Globally, 4.71 (95% Uncertainty Interval (UI) 4.2-5.2) million deaths were associated with bacterial drug-resistant infections in 2021.
- And 1.14 (UI 1 - 1.3) million deaths 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 Tonga between 1990 and 2019.



- To look at these and more visualization interactively visit [Measuring Infectious Causes and Resistance Outcomes for Burden Estimation (MICROBE)]
- In **Tonga** in 2021, there were an estimated **17 UI (12-22)** deaths attributable to AMR and **64 UI (46-81)** 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, **Tonga has the 74th 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.

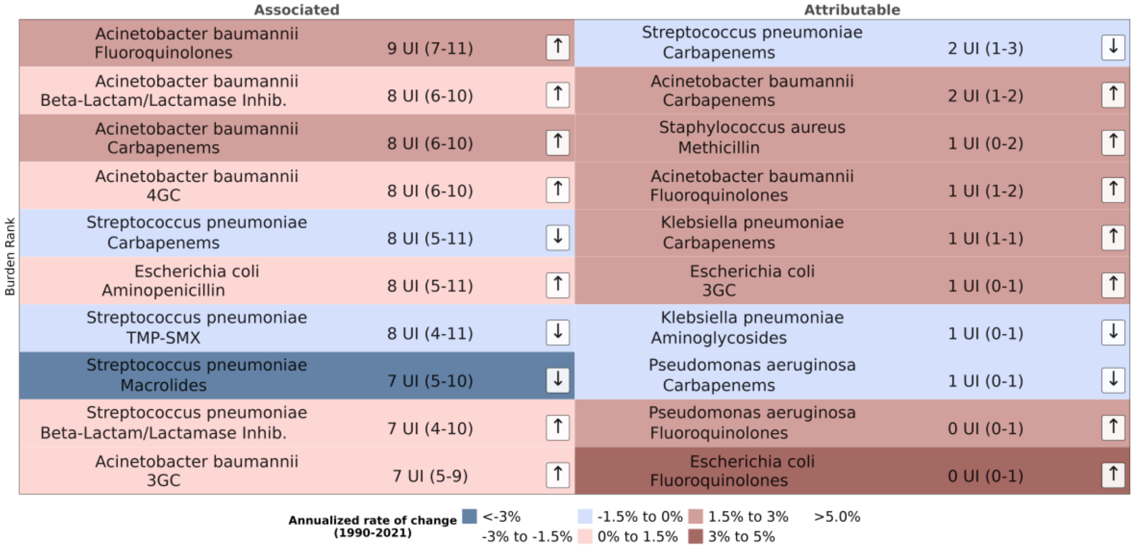
Table 1. Bacteria which cause most deaths in 2021 (Number of deaths in parenthesis)



Burden rank	Overall susceptible and resistant		Associated		Attributable	
	Streptococcus pneumoniae 19 UI (15-23)	↓	Streptococcus pneumoniae 13 UI (9-17)	↓	Acinetobacter baumannii 4 UI (3-4)	↑
	Staphylococcus aureus 16 UI (13-20)	↑	Acinetobacter baumannii 9 UI (7-11)	↑	Streptococcus pneumoniae 3 UI (2-4)	↓
	Klebsiella pneumoniae 12 UI (9-14)	↑	Staphylococcus aureus 8 UI (5-12)	↑	Klebsiella pneumoniae 2 UI (2-3)	↑
	Pseudomonas aeruginosa 10 UI (8-12)	↑	Escherichia coli 8 UI (6-11)	↑	Staphylococcus aureus 2 UI (1-3)	↑
	Acinetobacter baumannii 10 UI (8-12)	↑	Klebsiella pneumoniae 8 UI (6-10)	↑	Escherichia coli 2 UI (1-2)	↑
	Escherichia coli 10 UI (8-12)	↑	Pseudomonas aeruginosa 6 UI (4-8)	↑	Pseudomonas aeruginosa 2 UI (1-2)	↑
	Mycobacterium tuberculosis 5 UI (4-7)	↓	Enterobacter spp. 2 UI (2-3)	↑	Enterobacter spp. 1 UI (0-1)	↑
	Enterobacter spp. 3 UI (2-3)	↑	Enterococcus faecalis 2 UI (1-2)	↑	Enterococcus faecium 0 UI (0-0)	↑
	Enterococcus faecalis 3 UI (2-3)	↑	Proteus spp. 1 UI (1-2)	↑	Enterococcus faecalis 0 UI (0-0)	↑
	Group A Streptococcus 2 UI (2-3)	↑	Enterococcus faecium 1 UI (1-2)	↑	Serratia spp. 0 UI (0-0)	↓

Annualized rate of change (1990-2021) <-3% | -3% to -1.5% | -1.5% to 0% | 0% to 1.5% | 1.5% to 3% | 3% to 5% | >5.0%

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



Burden Rank	Associated			Attributable		
	Acinetobacter baumannii Fluoroquinolones	9 UI (7-11)	↑	Streptococcus pneumoniae Carbapenems	2 UI (1-3)	↓
	Acinetobacter baumannii Beta-Lactam/Lactamase Inhib.	8 UI (6-10)	↑	Acinetobacter baumannii Carbapenems	2 UI (1-2)	↑
	Acinetobacter baumannii Carbapenems	8 UI (6-10)	↑	Staphylococcus aureus Methicillin	1 UI (0-2)	↑
	Acinetobacter baumannii 4GC	8 UI (6-10)	↑	Acinetobacter baumannii Fluoroquinolones	1 UI (1-2)	↑
	Streptococcus pneumoniae Carbapenems	8 UI (5-11)	↓	Klebsiella pneumoniae Carbapenems	1 UI (1-1)	↑
	Escherichia coli Aminopenicillin	8 UI (5-11)	↑	Escherichia coli 3GC	1 UI (0-1)	↑
	Streptococcus pneumoniae TMP-SMX	8 UI (4-11)	↓	Klebsiella pneumoniae Aminoglycosides	1 UI (0-1)	↓
	Streptococcus pneumoniae Macrolides	7 UI (5-10)	↓	Pseudomonas aeruginosa Carbapenems	1 UI (0-1)	↓
	Streptococcus pneumoniae Beta-Lactam/Lactamase Inhib.	7 UI (4-10)	↑	Pseudomonas aeruginosa Fluoroquinolones	0 UI (0-1)	↑
	Acinetobacter baumannii 3GC	7 UI (5-9)	↑	Escherichia coli Fluoroquinolones	0 UI (0-1)	↑

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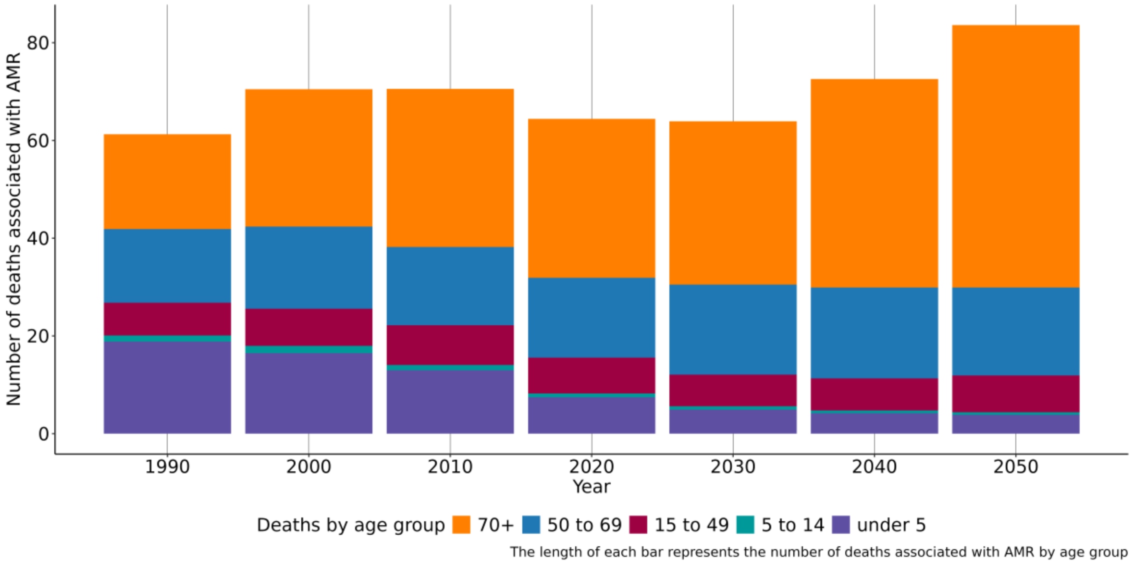
- Independently of antimicrobial resistance, the infectious syndromes accounting for the most deaths in 2021 were as follows (estimated thousands of deaths in parenthesis) lower respiratory infection (excl. COVID) (60 UI (47-73)), bloodstream infections (42 UI (33-52)), peritoneal and intra-abdominal infections (9 UI (6-11)), urinary tract infections and pyelonephritis (7 UI (5-9)) and infections of the skin and subcutaneous systems (6 UI (4-8)).

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



- In Tonga, people aged 70+ saw the largest number of deaths associated with AMR both in 1990 and 2021, which indicates that 70+ continues to be particularly vulnerable to infections which are resistant to antibiotics. In 2021, the number of deaths associated with AMR among the 70+ was 32 UI (24-41), whereas the mortality rate per 100,000 was 738 UI (548-928).

Data sources for Tonga

In total, 520 million individual records or isolates covering 19,513 study-location-years were used as input data to our estimation process. There was no input data accessible for this country. Estimates were informed by results from the Global Burden of Disease study and data from the surrounding region. Any datasets that could be used to improve these estimates in the future are welcome.

Table 3. Data inputs for Tonga by source type

Source type	Years	Sample size	Sample size units
No other source but GBD study input	None		GBD study input

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