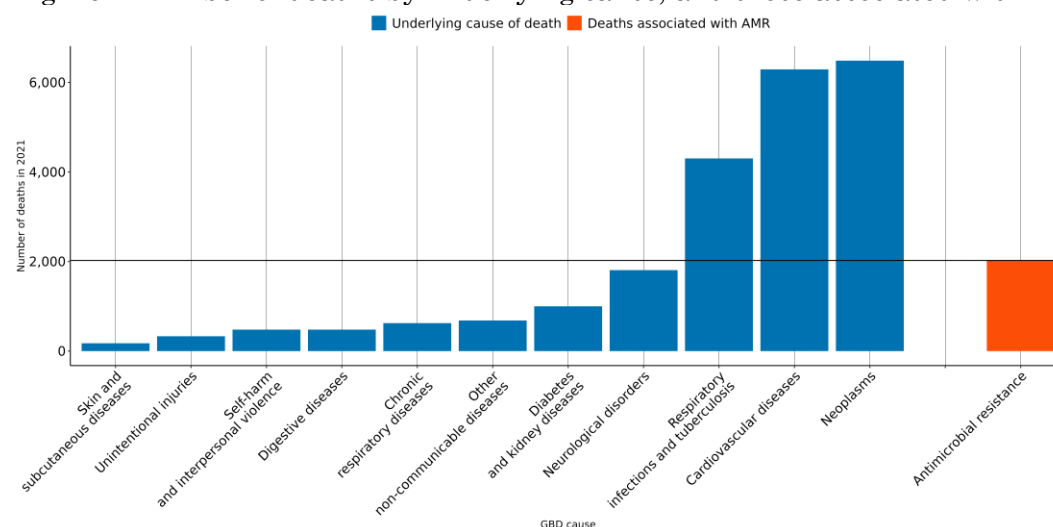


The burden of antimicrobial resistance (AMR) in Singapore

Executive summary

- Antimicrobial Resistance (AMR) is a major global health threat, over **400 lives** have been lost each year since 1990 in Singapore due to AMR.
- In 2021, there were an estimated **437 UI (352-521)** deaths attributable to AMR and **2,020 UI (1,700-2,340)** 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



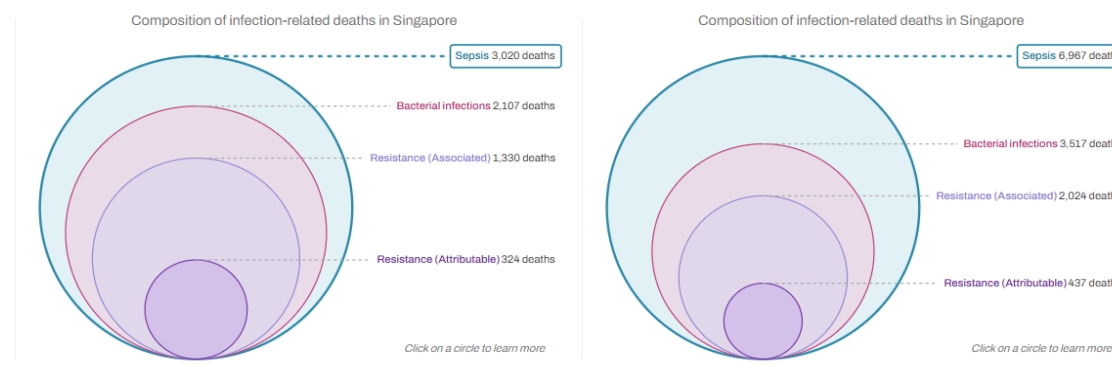
- In 2021, the number of deaths associated with AMR (orange bar in *figure 2*) were high compared to the most relevant underlying causes of death (depicted in blue) in the country. AMR associated deaths occur within multiple Global Burden of Disease (GBD) causes of death and AMR is not an underlying 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 Singapore, a 10% reduction means to decrease the number of deaths associated with AMR to **1,930**, but currently the trend for this country could reach up to **3,460 UI [2,660-4,170]** AMR-associated deaths in 2030.

AMR in Singapore

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 Singapore between 1990 and 2019.



- To look at these and more visualization interactively visit [Measuring Infectious Causes and Resistance Outcomes for Burden Estimation \(MICROBE\)](#)
- In **Singapore** in 2021, there were an estimated **437 UI (352-521)** deaths attributable to AMR and **2,020 UI (1,700-2,340)** 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, **Singapore has the 29th lowest** 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)	Bacteria	UI (range)	Bacteria	UI (range)
	Staphylococcus aureus	904 UI (806-1,000)	Staphylococcus aureus	484 UI (395-573)	Staphylococcus aureus	108 UI (81-134)
	Streptococcus pneumoniae	608 UI (540-676)	Streptococcus pneumoniae	472 UI (395-549)	Streptococcus pneumoniae	85 UI (58-111)
	Escherichia coli	446 UI (391-502)	Escherichia coli	334 UI (289-378)	Escherichia coli	62 UI (50-73)
	Pseudomonas aeruginosa	332 UI (297-367)	Pseudomonas aeruginosa	163 UI (128-198)	Acinetobacter baumannii	54 UI (47-60)
	Klebsiella pneumoniae	300 UI (265-334)	Klebsiella pneumoniae	140 UI (114-165)	Pseudomonas aeruginosa	42 UI (31-53)
	Acinetobacter baumannii	151 UI (136-165)	Acinetobacter baumannii	136 UI (121-151)	Klebsiella pneumoniae	32 UI (25-40)
	Group A Streptococcus	126 UI (110-142)	Enterococcus faecium	68 UI (60-76)	Enterococcus faecium	16 UI (12-19)
	Proteus spp.	94 UI (82-107)	Proteus spp.	60 UI (44-75)	Enterobacter spp.	9 UI (7-10)
	Haemophilus influenzae	82 UI (73-92)	Enterobacter spp.	34 UI (29-39)	Proteus spp.	9 UI (6-12)
	Enterococcus faecalis	82 UI (73-91)	Enterococcus faecalis	28 UI (23-33)	Enterococcus faecalis	5 UI (3-7)

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)

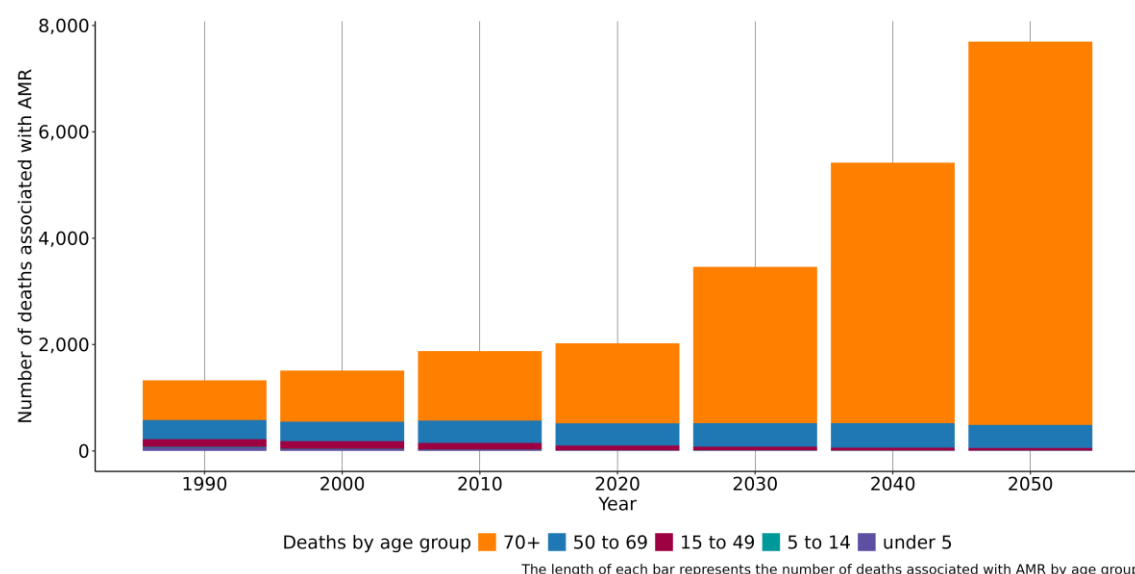
Table 2. Combinations which cause most deaths in 2021 (Number of deaths in parenthesis)

Burden Rank	Associated			Attributable		
	Bacteria	UI (range)	Rate of change	Bacteria	UI (range)	Rate of change
	Streptococcus pneumoniae Macrolides	356 UI (294-418)	↑	Staphylococcus aureus Methicillin	63 UI (43-83)	↑
	Streptococcus pneumoniae TMP-SMX	354 UI (266-443)	↓	Streptococcus pneumoniae Carbapenems	52 UI (31-74)	↓
	Staphylococcus aureus Fluoroquinolones	328 UI (249-406)	↑	Acinetobacter baumannii Carbapenems	27 UI (21-32)	↓
	Staphylococcus aureus Macrolides	310 UI (252-369)	↑	Staphylococcus aureus Fluoroquinolones	22 UI (7-38)	↑
	Escherichia coli Aminopenicillin	288 UI (239-338)	↑	Pseudomonas aeruginosa Carbapenems	18 UI (12-25)	↑
	Staphylococcus aureus Methicillin	275 UI (186-364)	↑	Escherichia coli Fluoroquinolones	16 UI (10-23)	↑
	Escherichia coli Fluoroquinolones	220 UI (181-258)	↑	Acinetobacter baumannii Fluoroquinolones	14 UI (12-17)	↑
	Streptococcus pneumoniae Carbapenems	194 UI (126-262)	↓	Streptococcus pneumoniae Macrolides	14 UI (8-20)	↑
	Escherichia coli TMP-SMX	172 UI (134-211)	↑	Klebsiella pneumoniae Fluoroquinolones	13 UI (9-17)	↑
	Escherichia coli Beta-Lactam/Lactamase Inhib.	148 UI (117-178)	↑	Staphylococcus aureus Macrolides	13 UI (9-17)	↑

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) (3,490 UI (3,070-3,900)), bloodstream infections (816 UI (737-895)), urinary tract infections and pyelonephritis (638 UI (540-735)), peritoneal and intra-abdominal infections (310 UI (275-345)) and infections of the skin and subcutaneous systems (215 UI (186-244)).

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



- In Singapore, 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 1,530 UI (1,260-1,800), whereas the mortality rate per 100,000 was 317 UI (261-373).

Data sources for Singapore

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 Singapore by source type

Source type	Years	Sample size	Sample size units
Microbial or laboratory data without outcome	1990-2021	129,988	Isolates
Literature studies	1990-2009	549	Cases/isolates/susceptibility tests
Single drug resistance profile data	1990-2021	179,707	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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