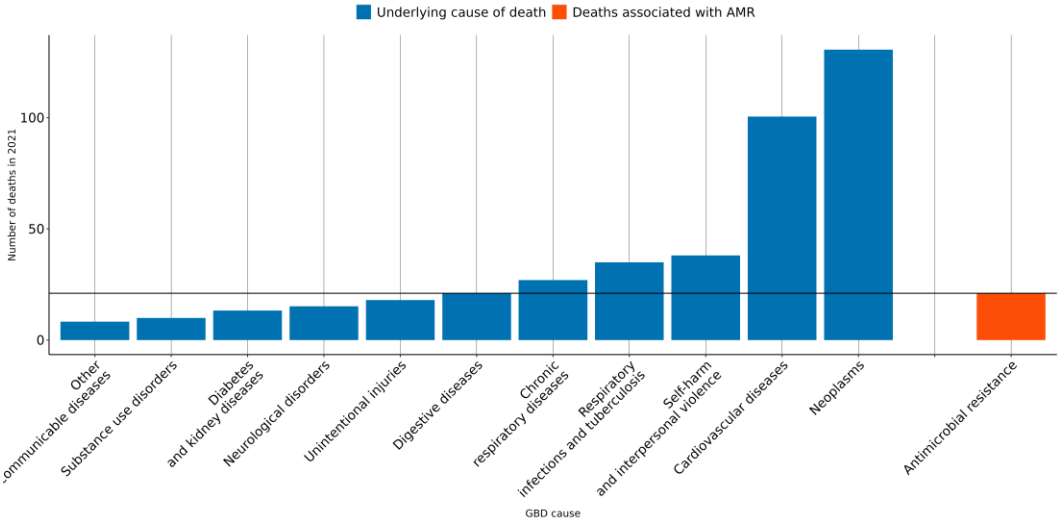
The burden of antimicrobial resistance (AMR) in Greenland

Executive summary

- Antimicrobial Resistance (AMR) is a major global health threat, over **5 lives** have been lost each year since 1990 in Greenland due to AMR.
- In 2021, there were an estimated **5 UI (3-6)** deaths attributable to AMR and **21 UI (14-28)** deaths associated with AMR in this location.
- The largest number of deaths associated with AMR in 2021 occurred among those aged **50 to 69** in the country.
- Among the most deadly pathogen-drug combinations in 2021 were *Staphylococcus aureus* resistant to fluoroquinolones, *Staphylococcus aureus* resistant to methicillin and *Pseudomonas aeruginosa* resistant to carbapenems.

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



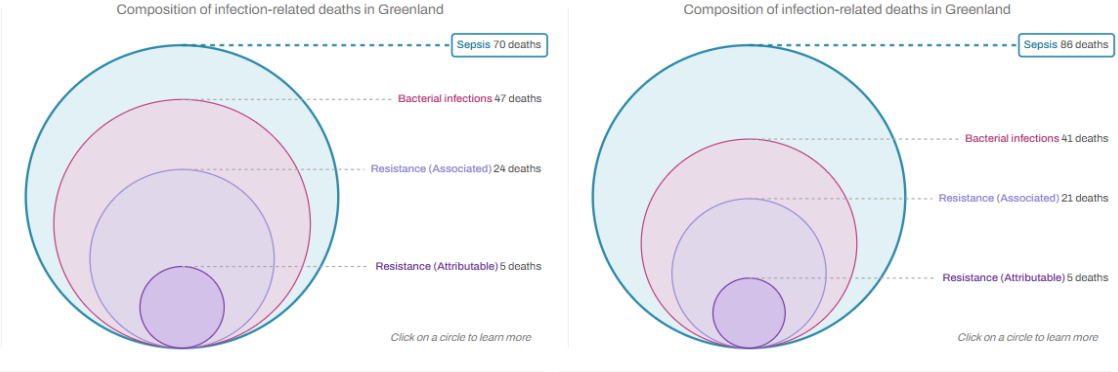
- In 2021, the number of deaths associated with AMR (orange bar in *figure 2*) were high compared to the most relevant underlying causes of death (depicted in blue) in the country. AMR associated deaths occur within multiple Global Burden of Disease (GBD) causes of death and AMR is not an underlying 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 Greenland, a 10% reduction means to decrease the number of deaths associated with AMR to **20**, but currently the trend for this country could reach up to **29 UI [20-40]** AMR-associated deaths in 2030.

AMR in Greenland

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 Greenland between 1990 and 2019.



- To look at these and more visualization interactively visit [Measuring Infectious Causes and Resistance Outcomes for Burden Estimation (MICROBE)]
- In **Greenland** in 2021, there were an estimated **5 UI (3-6)** deaths attributable to AMR and **21 UI (14-28)** 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, **Greenland has the 55th 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
1	Staphylococcus aureus 9 UI (7-10) ↑	Staphylococcus aureus 5 UI (3-6) ↑	Staphylococcus aureus 1 UI (1-2) ↑
2	Escherichia coli 6 UI (5-7) ↑	Escherichia coli 4 UI (2-6) ↑	Escherichia coli 1 UI (0-1) ↑
3	Pseudomonas aeruginosa 5 UI (4-5) ↓	Klebsiella pneumoniae 3 UI (2-3) ↓	Klebsiella pneumoniae 1 UI (0-1) ↓
4	Klebsiella pneumoniae 5 UI (4-5) ↓	Pseudomonas aeruginosa 3 UI (2-3) ↓	Pseudomonas aeruginosa 1 UI (0-1) ↓
5	Streptococcus pneumoniae 4 UI (3-4) ↓	Streptococcus pneumoniae 1 UI (1-2) ↓	Acinetobacter baumannii 0 UI (0-0) ↓
6	Mycobacterium tuberculosis 3 UI (2-3) ↓	Acinetobacter baumannii 1 UI (1-1) ↓	Streptococcus pneumoniae 0 UI (0-0) ↓
7	Enterococcus faecalis 1 UI (1-2) ↑	Enterobacter spp. 1 UI (1-1) ↓	Enterobacter spp. 0 UI (0-0) ↓
8	Enterobacter spp. 1 UI (1-1) ↓	Enterococcus faecium 1 UI (1-1) ↑	Enterococcus faecium 0 UI (0-0) ↑
9	Enterococcus faecium 1 UI (1-1) ↑	Enterococcus faecalis 1 UI (1-1) ↓	Serratia spp. 0 UI (0-0) ↓
10	Acinetobacter baumannii 1 UI (1-1) ↓	Proteus spp. 1 UI (0-1) ↑	Enterococcus faecalis 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%

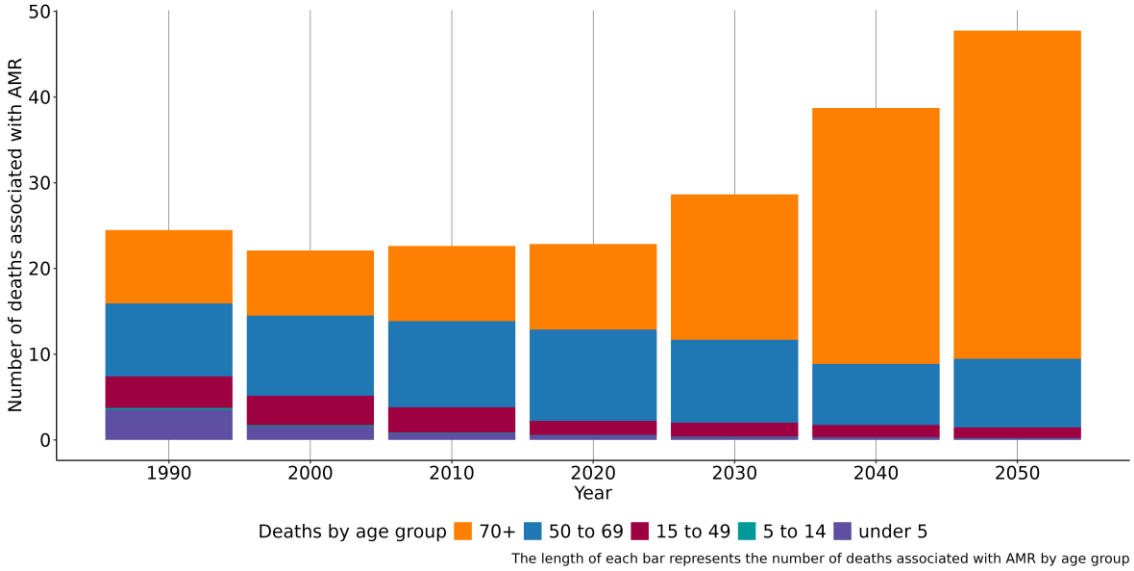
Table 2. Combinations which cause most deaths in 2021 (Number of deaths in parenthesis)

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

- 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 UI (20-26)), lower respiratory infection (excl. COVID) (18 UI (15-21)), peritoneal and intra-abdominal infections (7 UI (6-8)), urinary tract infections and pyelonephritis (4 UI (3-5)) and tuberculosis (3 UI (2-3)).

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



- In Greenland, people aged 70+ experienced the largest number of deaths associated with AMR in 1990 but this changed by 2021 as the largest number of deaths occurred among the 50 to 69. This indicates that prevention of infections among the 70+ has contributed to the reduction in the number of AMR associated deaths. In 2021, the number of deaths associated with AMR among the 50 to 69 was 10 UI (7-13), whereas the mortality rate per 100,000 was 306 UI (201-410).

Data sources for Greenland

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.

[1] “There was no input data accessible for Greenland.”

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
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