

# **Global sewage situation report**

## **May 2020**

**The Global Sewage Surveillance Project Consortium**



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## Background

Antimicrobial resistance (AMR) is a cross-cutting and increasing threat to global health, and it threatens to undermine decades of progress in the treatment of infectious diseases. AMR is a complex problem with multiple and interconnected drivers, which may include changing dynamics in travel, trade, climate change, and populations. Reliable information that accurately describes and characterizes the global occurrence and transmission of AMR is essential to address this challenge and to support national and global priority setting, public health actions, and treatment decisions.

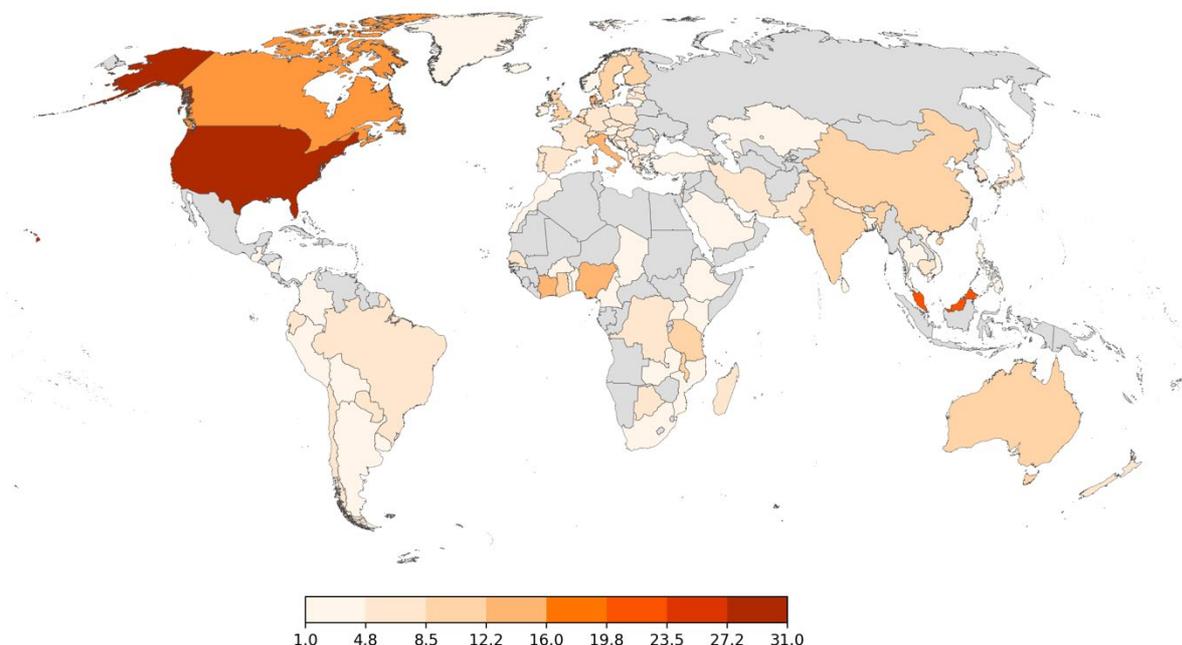
Current surveillance of AMR is often focusing on a few pathogens only and mainly based on passive reporting of phenotypic laboratory results for specific pathogens isolated from human clinical infections. This procedure leads to significant time delays, often incomparable data, and a narrow pathogen spectrum not capturing all relevant AMR genes, where the major part might be present in the commensal bacterial flora of healthy individuals. However, obtaining fecal samples from healthy humans is logistically difficult.

From a surveillance point of view, urban sewage is attractive because it provides sampling material from a large and mostly healthy population, which otherwise would not be feasible to monitor. Globally, a rapidly increased proportion of the human population live in urban areas and an increasing proportion is connected to a sewer system. In addition, analyzing sewage samples does not require informed consent, thus limiting ethical concerns and has limited practical and logistical barriers for sampling.

The Global Sewage Surveillance Project was initiated in 2016 with the purpose to explore the potential of using sewage for continuous monitoring of AMR. The first results were published in 2019, based on samples collected in 2016 ([www.nature.com/articles/s41467-019-08853-3](http://www.nature.com/articles/s41467-019-08853-3).)

All sequence data have been mapped to known databases for antimicrobial resistance genes (ARGs) and bacteria (16S). The abundance of each individual ARG relative to bacterial content in the sample has been calculated. The data have then been analyzed for overall diversity and abundance between the different countries and regions.

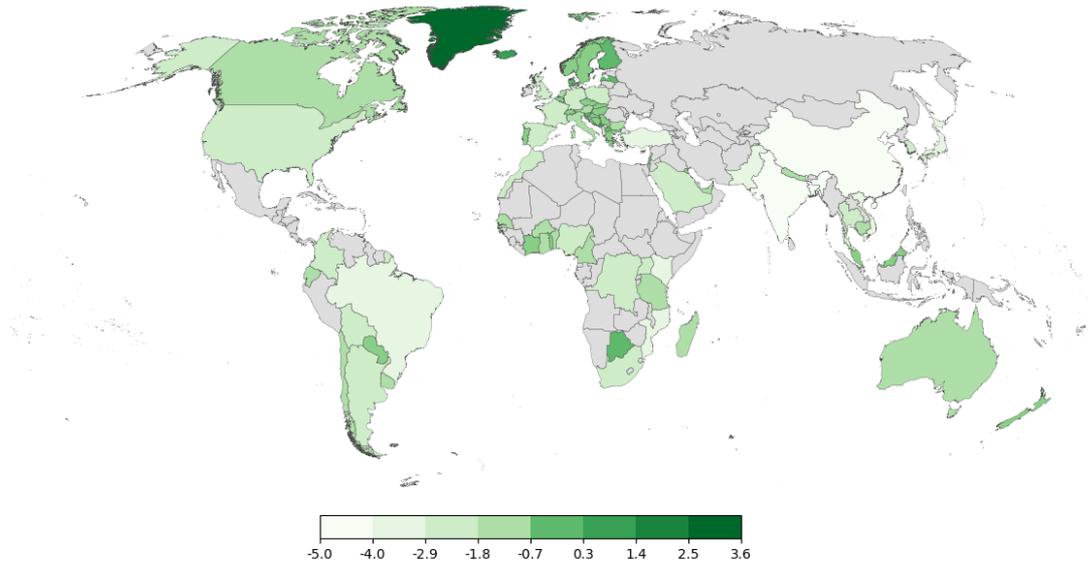
## Number of samples obtained 2016-2018



**Number of countries sampled: 102**

**Number of samples obtained: 570**

## Number of samples per million people (log)



### Next steps

We are currently in the process of finalizing figures and analyses for the next publication that will also include an analysis of the genetic diversity of the flanking regions of the most abundant ARGs.

The samples have also been stored for virome analysis, but we have not until recently been able to secure funding for this, which unfortunately also was delayed due to the COVID-19 outbreak.

All the recent COVID-19 related interventions have created a unique opportunity to document the effects on other diseases as well. The Global Sewage Surveillance Project is one of the few projects where surveillance on a global scale has been ongoing also before the COVID-19 outbreak. Thus, we would very much like to continue the global sampling and hope that all of you will participate also in the next round we are planning for the fall 2020 and spring 2021.

### Additional information

More information and links can be found at:

[www.globalsurveillance.eu](http://www.globalsurveillance.eu)

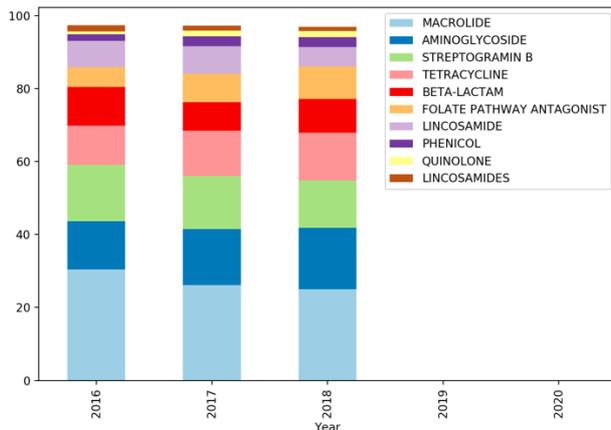
### Funding:

Novo Nordisk Fonden

The World health Organization

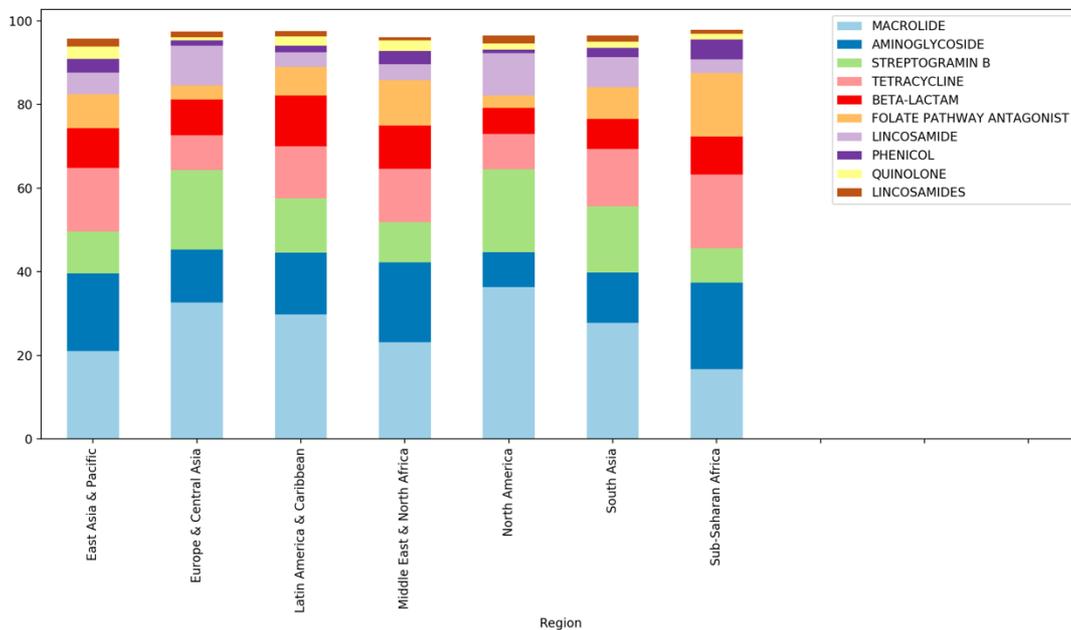
## Global resistome composition per year

This plot shows the annual global resistome compositions amalgamated on phenotypical resistance class level. Genes giving resistance to a total of 19 different classes are found in the entire dataset. Here we show the, on average, 10 most abundant classes.



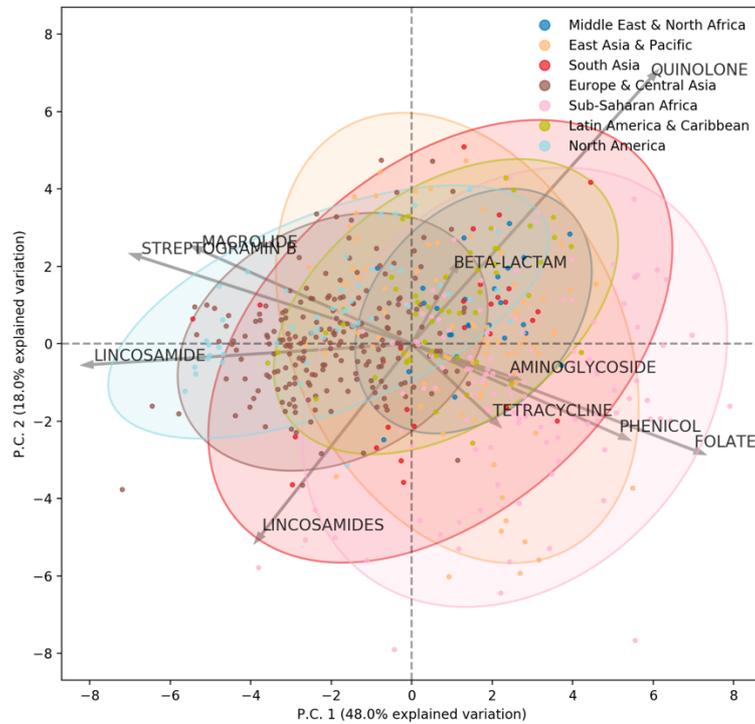
## Global resistome composition per region

Same as above, but per region over all years.

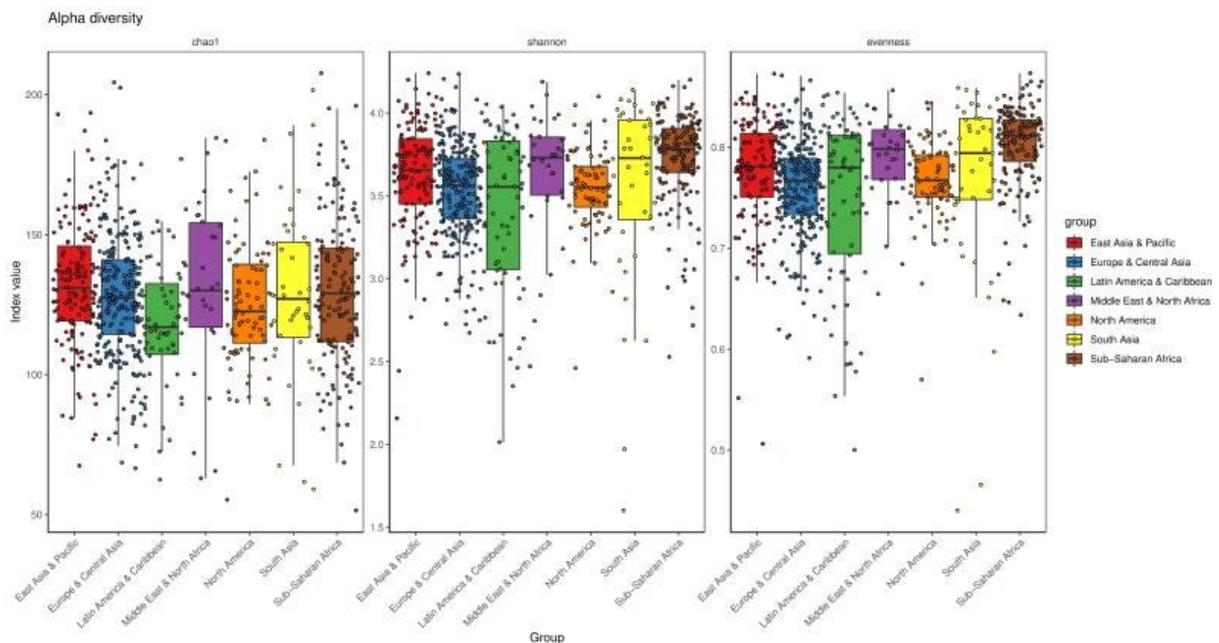


## Global resistome PCA over the entire sampling period

The entire class amalgamated data set, shown projected on the principal components. The samples have been grouped on region level across sampling rounds.



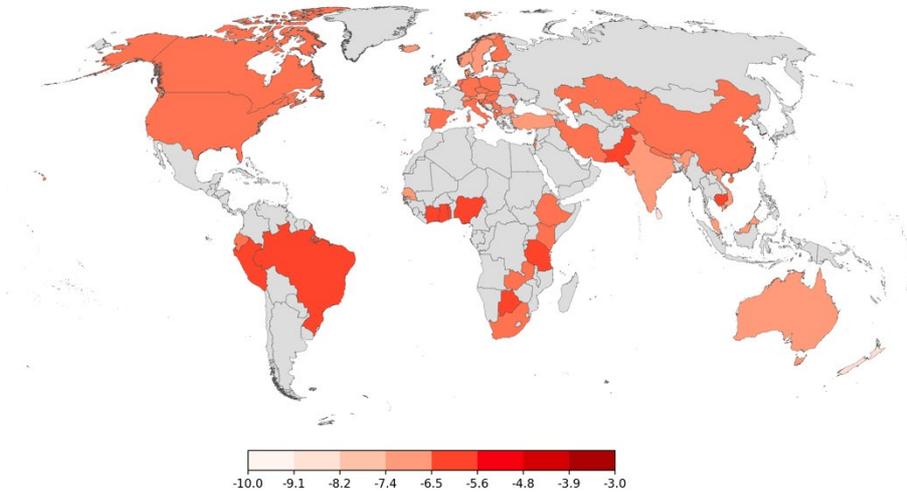
## Diversity indicators per region



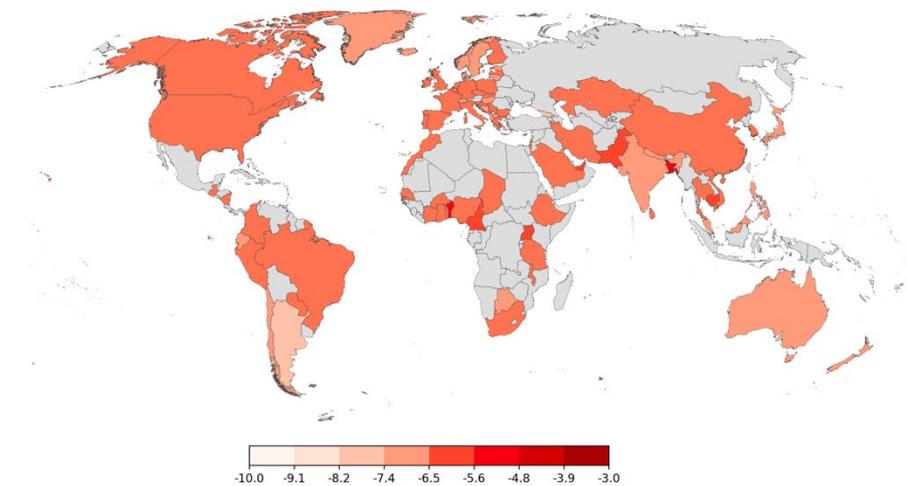
## Total resistance gene abundance per year (ARG/16S)

These maps show the global distribution of AMR load, i.e., the fraction of bacteria reads that can be assigned to an ARG reference. This ratio is log-transformed to bring it onto a linear scale, which explains the negative values in the legend (ARG count << 16S count). Each map shows the country sum per year.

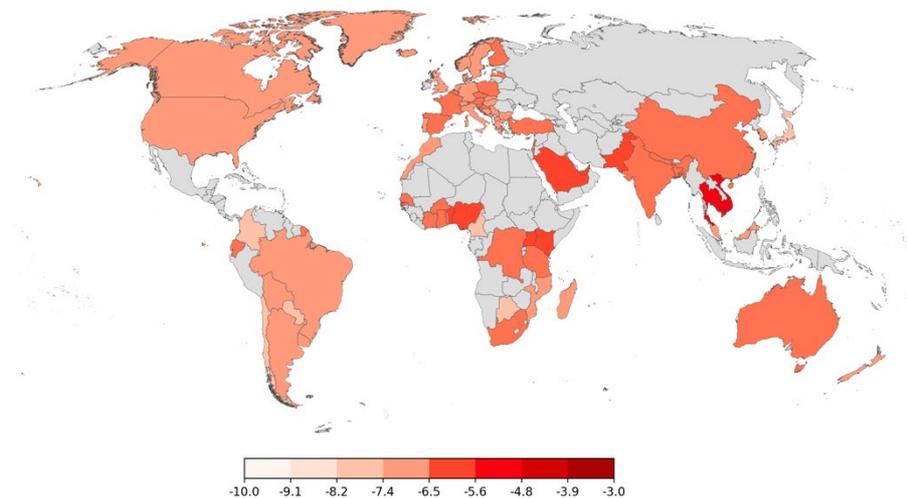
2016



2017



2018



# Change in resistance abundance over time per country

The following pages show linear regressions over time of the AMR load in each individual country. Only countries with more than two samples are shown here. The regression analysis should be treated with caution, particularly for countries with a low number of samples, because we have not taken the uncertainty associated with each individual sample into account here.

