Global monitoring of antimicrobial resistance based on metagenomics analyses of urban sewage

Date: Wednesday 13th March 2019
Source: Hendriksen RS [...] Frank M. Aarestrup
https://www.nature.com/articles/s41467-019-08853-3

Abstract
Antimicrobial resistance (AMR) is a serious threat to global public health, but obtaining representative data on AMR for healthy human populations is difficult. Here, we use metagenomic analysis of untreated sewage to characterize the bacterial resistome from 79 sites in 60 countries. We find systematic differences in abundance and diversity of AMR genes between Europe/North-America/Oceania and Africa/Asia/South-America. Antimicrobial use data and bacterial taxonomy only explains a minor part of the AMR variation that we observe. We find no evidence for cross-selection between antimicrobial classes, or for effect of air travel between sites. However, AMR gene abundance strongly correlates with socio-economic, health and environmental factors, which we use to predict AMR gene abundances in all countries in the world. Our findings suggest that global AMR gene diversity and abundance vary by region, and that improving sanitation and health could potentially limit the global burden of AMR. We propose metagenomic analysis of sewage as an ethically acceptable and economically feasible approach for continuous global surveillance and prediction of AMR.

Comment
Urban sewage is attractive as a surveillance tool because it provides unbiased, population samples. Thus it provides information on the total burden of AMR genes in the population including healthy individuals. Sewage has proven useful for surveillance in the global polio eradication program.
The results are nicely summarized in Figure 1b, which shows the number of AMR reads per kilogram material in different regions of the world. Africa has the highest number followed by South America with Asia as third.
It is perhaps surprising that Africa is the continent with the highest burden, as more studies on AMR are published from Asia compared to Africa, but this study highlight a silent epidemic of AMR in Africa.
The approach is not easy. Strengthen of microbiology service to provide information on bacteria and susceptibility pattern everywhere is mandatory, antibiotic stewardship is key to limit the use of broad spectrum antibiotics, but will fail without a reliable microbiology service.

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