Wastewater as a breeding ground for antibiotic resistance

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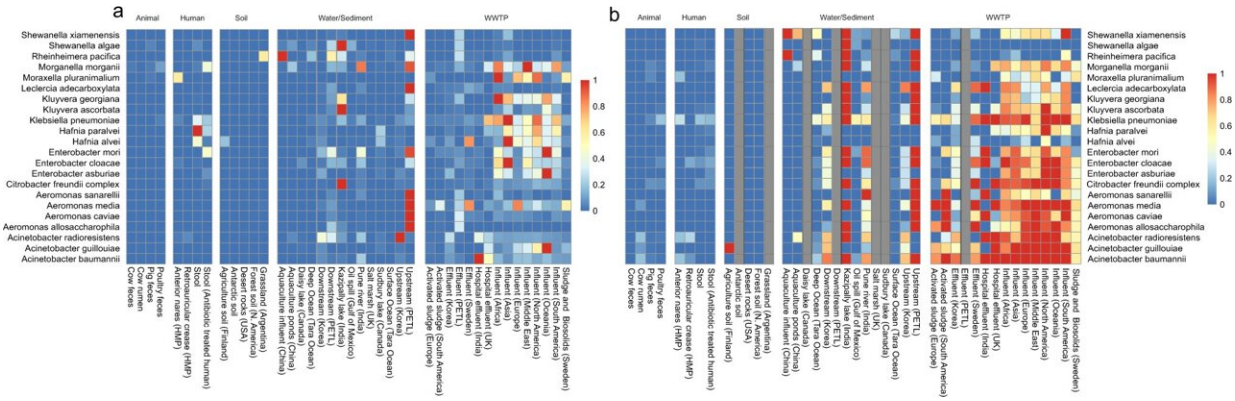

Relative abundance and prevalence of 22 known origin species. Average relative abundance of the 22 investigated origin species in different environments (2496 samples) normalized by each species' highest relative abundance (a), and the prevalence of the 22 investigated origin species as fraction of samples with detectable levels of the corresponding species within each environment type (b). Some environments are excluded from the analysis in (b) due to too few identified bacterial fragments. Credit: *Communications Biology* (2023). DOI: 10.1038/s42003-023-04676-7

Wastewater is a more potent environment for antibiotic resistance to evolve than has been previously realized. A study from the University of Gothenburg, Sweden, shows that wastewaters have unique characteristics, allowing resistance genes to start their journey from harmless bacteria to those that cause disease.

Microorganisms produced antibiotic molecules long before we started to use them as medicines. Accordingly, the ability of many environmental bacteria to defend themselves against antibiotics is ancient.

Since the introduction of antibiotics in clinics, disease-causing bacteria have also started to accumulate more and more resistance genes in their DNA. This still-ongoing process requires that genes, which were previously well anchored in the chromosomes of certain bacterial species, first gain the ability to move around and eventually jump between species.

In a study published in the journal *Communications Biology*, researchers at the Centre for Antibiotic Resistance Research (CARe) in Gothenburg, Sweden, present evidence for where the genes could gain their ability to move.

Important to prevent emergence

It is known that wastewaters contain residues of antibiotics and could favor the development of antibiotic-resistant bacteria. New evidence show that wastewaters also have characteristics that allow the resistance genes to start their journey from harmless bacteria to disease-causing bacteria.

The researchers acknowledged that it is not sufficient for antibiotics to drive the process. The species carrying the resistance genes in their chromosomes also needs to be present, as well as specific sequences of DNA that could provide the ability to move the resistance genes.

By studying DNA from thousands of samples from different environments, the researchers could identify where all the key components came together. To the authors' surprise, it was not in the gut of humans or animals, it was in wastewaters sampled across the world.

"In order to fight antibiotic resistance we cannot focus only on preventing the spread of those types of resistant bacteria that are already in circulation, we also need to prevent or delay the emergence of new ones," says Fanny Berglund, researcher at the Sahlgrenska academy at University of Gothenburg, and the lead author of the study.

More focus on wastewater

The same research team has published several other studies showing that the environment harbors a huge variety of different resistance genes, many more than the resistance genes that we see today in bacteria causing disease.

This makes the environment a vast source for new resistance genes that one after the other acquire the ability to jump between species, to eventually end up in pathogens. The authors conclude that favoring this development by polluting the environment with antibiotics is not a good idea.

"There is a lot of focus on reducing antibiotic use in humans and animals. This is of course important, but our study shows that we also need to pay attention to our waste streams, as this seems to be a place where new variants of antibiotic resistance could emerge," concludes Berglund.

More information: Fanny Berglund et al, Evidence for wastewaters as environments where mobile antibiotic resistance genes emerge, *Communications Biology* (2023). DOI: 10.1038/s42003-023-04676-7

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