



When rain overwhelms the sewers, antibiotic-resistant bacteria flood the river

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Topics: Wastewater | Pollutants

Wastewater treatment plants are ‘hotspots’ for antibiotic resistance genes and bacteria but sewer overflows exacerbate the problem by disseminating them into rivers. Researchers at Eawag suggest ways to minimise these effects.

Antibiotic resistance is an emerging threat to public health, and now a leading cause of [death worldwide](#), killing close to five million people in 2019. Due partly to the overuse and abuse of antibiotics since their commercialisation in the early 20th century, the scale of the problem has continued to grow. Wastewater has been recognised as one of the most important routes by which bacteria and genes resistant to antibiotics are released into the environment.

Even after processing in a wastewater treatment plant, non-disinfected wastewaters contain orders of magnitude more antibiotic-resistant bacteria and antibiotic resistance genes than is naturally found in rivers and lakes. Raw sewage contains yet again much higher levels, and thus discharge of untreated sewage can be expected to contaminate the environment even more severely. One way this can happen, even in countries with otherwise excellent sanitation infrastructure, is when heavy rain leads to sewage volumes that exceed the capacities of sewer systems or wastewater treatment plants. A mixture of excess rainwater and sewage is then discharged into receiving water bodies, bypassing conventional treatment processes.

Our Microbial Ecology research group at Eawag investigates community-level microbial processes in natural and engineered systems, including [environmental antibiotic resistance](#). Recently we published a paper in [Water Research](#), which details our investigation into antibiotic resistance contamination during stormwater events in the river Murg near Münchwilen in Switzerland.



**Sampling wastewater-bypass during stormwater events in a wastewater treatment plant in Münchwilen, Thurgau, Switzerland.
(Source: Eawag)**

We wanted to document and quantify the extent of such contamination during heavy rainfall. This is challenging, because such events are relatively rare, and you have to be on site when they happen. For instance, even though these events occurred in Münchwilen on 118 calendar days in 2019, most did not last long. During heavy rains, many other potential sources of antibiotic resistance contamination enter the river, complicating our research further. This includes surface runoff that transports soil into the river, such as from fields and meadows that may have been manured. Sediment within the river is also resuspended by the faster flow.

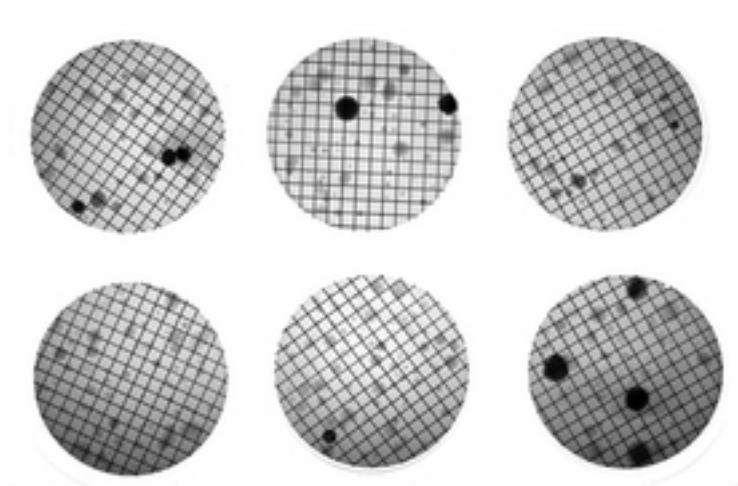
Using modern sequencing techniques to distinguish microbes from different sources, we disentangled these inputs. Our results show that the sewage overflow, so-called 'wastewater bypass', was clearly the major source of antibiotic resistance in the river. In many wastewater plants, including the one in Münchwilen, the bypass at least undergoes a sedimentation process before it is discharged to the river. However, post-sedimentation levels of antibiotic resistance were still very high.



Deploying an auto-sampler at the wastewater receiving river during stormwater events.
 (Source: Eawag)

We were surprised that the increased levels of antibiotic resistance genes in the river persisted for quite a while (for 22 hours) even after the storm had moved on. While there are no other wastewater treatment plants along the river, there are many discharge points upstream where combined sewer overflows can contaminate the river. This implies that antibiotic resistance contamination entered the river at various points and the upstream inputs kept being transported to our sampling points.

We also detected multi-resistant bacteria, i.e., bacteria with resistance against multiple types of antibiotics. Many genetic fragments found in our samples contained multiple antibiotic resistance genes. These fragments were especially abundant in bypass and bypass-impacted river water. Therefore, the risk of public exposure to antibiotic-resistant and even multi-resistant bacteria increases during and after stormwater events. We also found that a high portion of multi-resistance genetic fragments were associated with plasmids - small DNA molecules that can be transferred between bacteria. Those multi-resistance plasmids could persist in the environment.



An example of cultivated multi-resistant bacteria from wastewater bypass.
 (Source: Eawag)

How much is wastewater bypass contributing to antibiotic resistance contamination in Swiss rivers? According to a different Eawag project - '[Diffuse micropollutant emissions from urban areas \(DIMES\)](#)' performed by Dr Christoph Ort and Dr Max Maurer - combined sewer overflows comprise approximately four percent of the total wastewater discharges in Switzerland (see articles in [Water Research](#) and [Aqua & Gas](#)). At a glance, this proportion looks small. However, bypass contains two to three orders of magnitude higher levels of antibiotic resistance than treated wastewater. The actual contribution made by bypass and sewage overflows might therefore be comparable to that of treated effluents over the whole year.

What can we do to reduce this impact? In our [Water Research paper](#), we suggest increasing


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discharged by wastewater treatme
nt plants to receiving rivers during stormwater events, where it may contrib
ute to increased levels of antibiotic resistance genes (ARGs) and multi-resi
stance risk factors (multi-resistant bacteria and multi-resistance genomic d
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h as soil runoff and resuspended river sediment could also play a role durin
g stormwater events. Here we report on stormwater event-based sampling campa
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s in bypass, treated effluent, and the receiving river, as well as complimen
tary data on catchment soils and surface sediments. Both indicator ARGs (qPC
R) and resistome (ARG profiles revealed by metagenomics) indicated bypass as
the main contributor to the increased levels of ARGs in the river during st
ormwater events. Furthermore, we showed for the first time that the risk of
exposure to bypass-borne multi-resistance risk factors increase under stormw

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ater events and that many of these MGDs were plasmid associated and thus potentially mobile. In addition, elevated resistance risk factors persisted for some time (up to 22 h) in the receiving water after stormwater events, likely due to inputs from distributed overflows in the catchment. This indicates temporal dynamics should be considered when interpreting the risks of exposure to resistance from event-based contamination. We propose that reducing bypass from wastewater treatment plants may be an important intervention option for reducing dissemination of antibiotic resistance.' (1652 chars) serialnumber => protected'0043-1354' (9 chars) doi => protected'10.1016/j.watres.2021.117827' (28 chars) uid => protected23890 (integer) _localizedUid => protected23890 (integer)modified _languageUid => protectedNULL _versionedUid => protected23890 (integer)modified pid => protected124 (integer) Lee, J.; Beck, K.; Bürgmann, H. (2022) Wastewater bypass is a major temporary point-source of antibiotic resistance genes and multi-resistance risk factors in a Swiss river, *Water Research*, 208, 117827 (12 pp.), doi:10.1016/j.watres.2021.117827, Institutional Repository

<https://www.sciencedirect.com/science/article/pii/S0043135421010216?via%3Dihub>

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Related Links

Eawag- Factsheet on the Spread of antibiotic resistance in the aquatic environment

Eawag project: Antibiotic resistance as an emerging environmental contaminant

National Research Programme NRP 72 – Antimicrobial Resistance



The article was originally published by [Water Science Policy](#).

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