

What can river biofilms tell us after an environmental event?

With help from citizen scientists, 231 biofilm samples were collected across four rivers to explore how microbial communities change following rainfall, discharges and other environmental events.

By Erin Doyle | September 2026

231 FIELD SAMPLES	23 SAMPLING SITES	4 RIVERS	25 EVENTS
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What is a river biofilm?

The brown, green or slippery coating on a submerged stone is a biofilm: a living community of bacteria, fungi and algae. Biofilms support river food webs and nutrient cycling. They can also respond to changing conditions and trap or accumulate some substances from the surrounding water.

This study investigated how bacterial communities change after environmental events and whether any bacterial groups respond consistently enough to support future river monitoring.

Citizen scientists made the study possible

Short-lived events are difficult for a small research team to capture. During autumn and winter 2025, volunteers used their local knowledge to identify events and collected 231 biofilm samples from 23 sites on the Rivers Chess, Misbourne, Ver and Red. Together, the samples represented 25 events.

These included first-flush rainfall - the wash-off of accumulated material at the start of rain - as well as rain associated with reported sewage, stormwater or balancing-tank discharges, and a car crash that caused a petrochemical spill. Rainfall was involved in every event, which is important when interpreting the results.

At each visit, volunteers scrubbed biofilm from three submerged stones using new toothbrushes. The toothbrushes were sealed and frozen, and sampling was repeated weekly for the following three weeks where possible. The first sample was collected between zero and seven days after the reported event.

Sampling in action



River biofilms form visible or slippery coatings on submerged stones and contain diverse microorganisms. [River Chess, July 2025. Photo by Erin Doyle]



A thick biofilm being collected by scrubbing a stone using a new toothbrush. [Photo by Erin Doyle].

From river stone to DNA

In the laboratory, the biofilm was rinsed from the toothbrushes and into collection tubes. DNA was extracted from the biofilms and the V3-V4 region of the bacterial 16S rRNA gene was sequenced.

What the sequencing tells us: It shows which bacterial groups contributed DNA and their relative abundance - their share of the sequences detected. It does not provide absolute cell numbers or, by itself, show whether bacteria were alive, active, harmful or carrying out a particular function.

What have we found so far?

Initial comparisons suggested that bacterial community profiles differed according to dominant upstream land use. Agricultural and forest-fragment samples contained larger shares of bacterial families commonly associated with plants and soils, while urban samples contained higher proportions of some families that include anaerobic organisms.

Among the 25 most frequently detected genus-level groups were *Aquirickettsiella*, *Nocardioides*, *Aquamicrobium* and *Novosphingobium*, alongside groups commonly found in water and soil. Ten could not be identified reliably to genus level. Particular species or strains within some of these genera have previously been associated with freshwater invertebrates, low-nutrient habitats, polluted environments or the breakdown of organic chemicals. Those characteristics cannot be assigned to the organisms detected here as we do not have species level identifications.

On the River Misbourne, *Aquirickettsiella* and *Sphingorhabdus* accounted for larger shares of sequence reads downstream of the wastewater treatment works than upstream. On the River Chess, however, *Aquirickettsiella* accounted for a smaller share downstream. Several bacterial families previously reported in sewage sludge were more prominent in the second and third post-event samples than in the first. These observations are useful leads, but they do not establish the bacteria's source or the cause of the changes.

Is there a consistent post-event signal?

PRELIMINARY FINDING

No single bacterial genus responded consistently across the three larger rivers. The River Red provided an intriguing lead, but further testing is needed.

The initial analysis found no consistent genus-specific response across the Rivers Ver, Misbourne and Chess after similar event types. Seven genera followed a consistent change between sites on the River Red. However, this is not yet a firm result. There were only two sites sampled on the River Red, and these were close together, which may have resulted in these sites having started with similar communities. The River Red is also much shorter and experiences a less varied mixture of pressures compared with the other rivers. More sites and events are needed to distinguish these explanations.

Why is the answer complicated?

Every event was related to rainfall to some degree, with ongoing rain throughout the sampling period resulting in all samples being collected within 48 hours of rainfall within the catchment. We therefore cannot yet separate the effects of rainfall and flow from those of sewage, stormwater, or other events. At each site, the first sample was collected zero-to-seven-days after the initial event. This delay means rapid changes may have happened before sampling. Because there were no pre-event baseline samples, we also cannot say that a community later 'recovered' or returned to its original state. However, comparison with additional samples which were collected from these rivers may help to answer this question with further analysis.

What happens next?

The next analysis will combine the DNA results with Defra rainfall and river-flow data and account for the exact interval between each event and sampling. It will also test whether changes across the whole bacterial community provide a more reliable signal than any single genus. The data discussed here will also be compared with data from separate samples collected from these rivers as part of a seasonal sampling campaign carried out in 2025.

There may not be one universal bacterial 'alarm bell' for every river or event. Biofilm communities appear to reflect a combination of local land use, rainfall, flow, event type and sampling time. That complexity makes repeated local observations especially valuable.

THANK YOU

This study depended on volunteers responding at short notice and returning over the following weeks. Your samples and local knowledge allowed events to be observed across four rivers on a scale that a small research team could not have achieved alone.

Detailed heatmaps follow: Pages 4-5 retain the site names so participants can locate their samples. Within each figure, red and orange cells indicate a larger share of bacterial DNA sequences and blue cells a smaller share. The colours do not represent pollution severity or health risk.

Detailed heatmaps: Rivers Chess and Misbourne

Site names from the original plots have been retained so that volunteers can locate their samples. Each column is a sample and each row is a bacterial group.

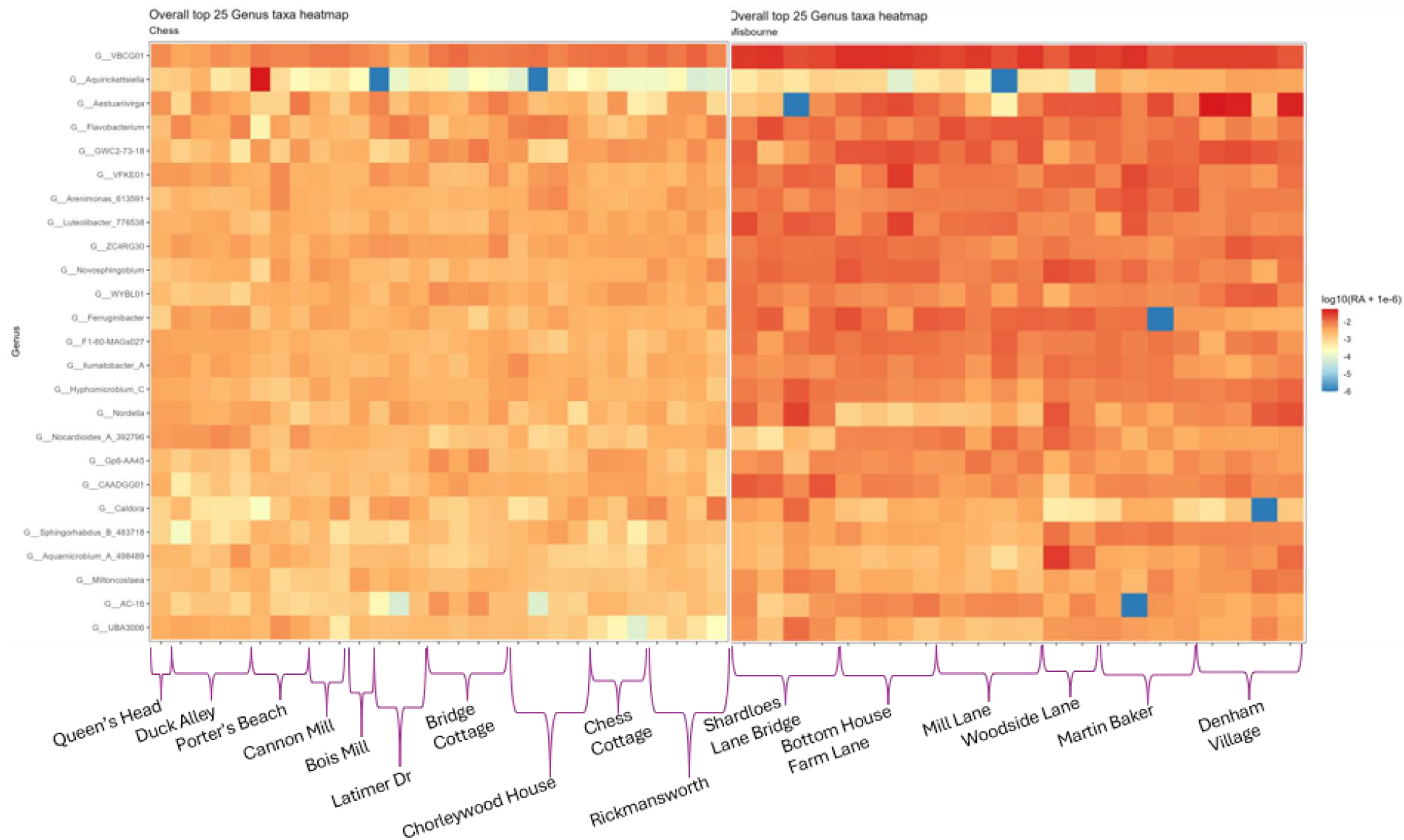


Figure 1a. Relative abundance heatmaps for the Rivers Chess and Misbourne. Rows show bacterial groups and columns show samples grouped by site. Red and orange indicate a larger share of sequence reads; blue indicates a smaller share. Colour does not indicate pollution severity or health risk.

Detailed heatmaps: Rivers Ver and Red

The original colour scales are retained. Because the scale ranges differ between this figure and Figure 1a, compare patterns within each figure rather than colour intensity between figures.

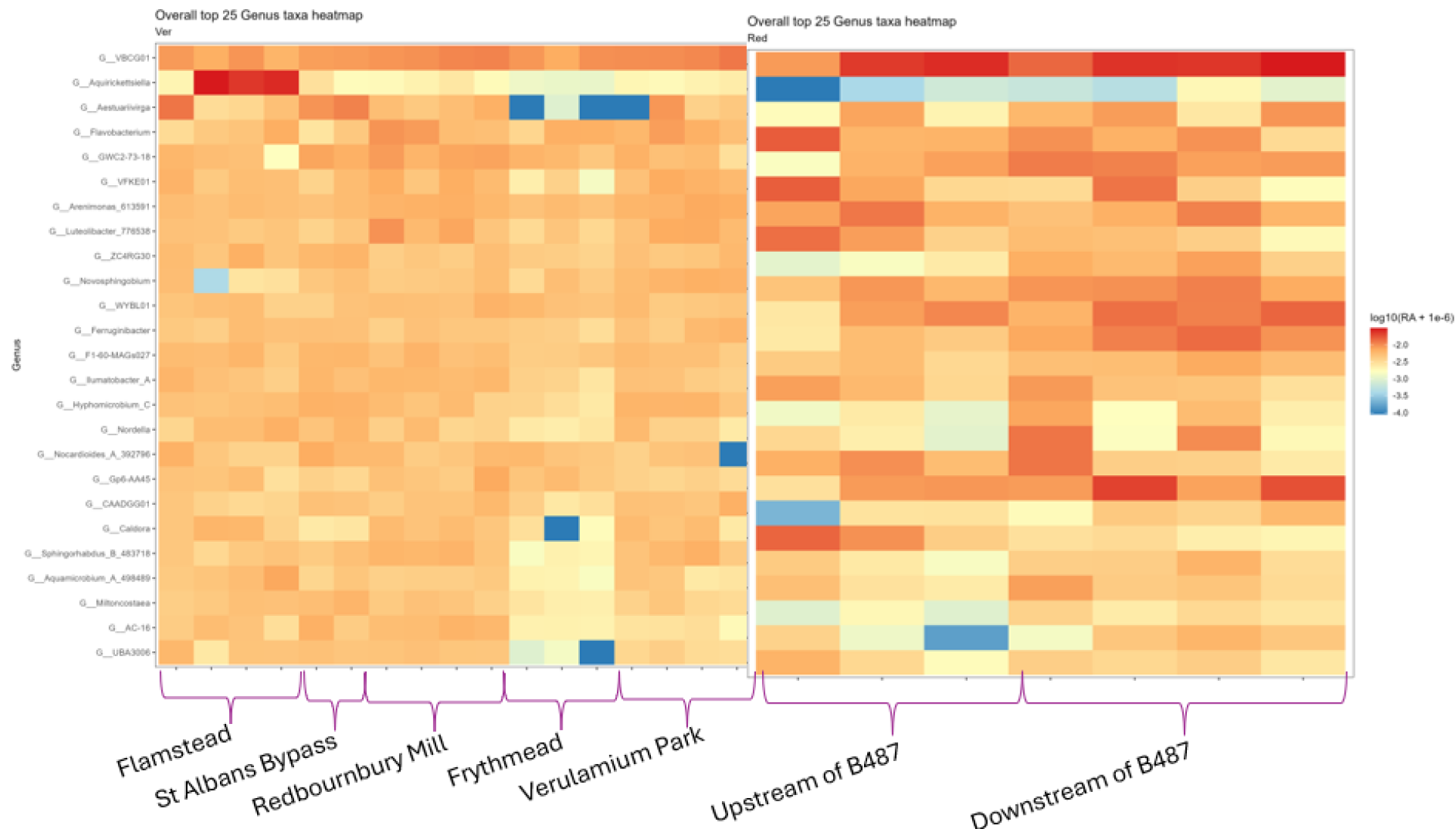


Figure 1b. Relative abundance heatmaps for the Rivers Ver and Red. Rows show bacterial groups and columns show samples grouped by site. Red and orange indicate a larger share of sequence reads; blue indicates a smaller share. Colour does not indicate pollution severity or health risk.