Research Statement

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Antibiotic resistance rarely appears out of nowhere. In hospitals, resistance genes move between bacteria on mobile pieces of DNA called plasmids, and they often reach the wastewater before they show up in a patient's blood culture. My research asks how we can read those signals in wastewater early enough, and cheaply enough, for hospitals to act on them. The long-term aim is surveillance that warns of rising resistance before it is seen at the bedside.

During my PhD at the University of Manchester, I sequenced wastewater from four hospitals every week for eighteen months and built an analysis pipeline that links each resistance gene to the plasmid carrying it, rather than counting genes in isolation. This made it possible to follow plasmids, not only genes, over time. One family of plasmids carried 41% of all the carbapenem resistance genes we detected, which suggests that surveillance focused on a few carriers could capture much of the risk.

Since 2023, as a postdoctoral researcher, I have worked to make that approach usable outside a research group. I rebuilt the pipeline in Nextflow so that it runs on standard hardware, and the analysis time for one sample fell from three days to six hours. A regional surveillance programme now uses it for its routine samples. Across this work I have published seven papers, three as first author, and co-supervised two MSc students.

My next five years would follow three directions. The first asks which plasmids will spread. By linking wastewater signals to the bacteria isolated from patients in the same hospitals, I want to test whether features of a plasmid seen in wastewater predict its later appearance in clinical samples; the first step is a matched dataset built with a hospital microbiology laboratory. The second asks whether hospitals without sequencing can still benefit. From my existing data I have chosen 12 marker genes that together track most of the plasmid activity I observed, and I will test whether a simple qPCR panel for these genes follows the full sequencing picture, starting with stored samples. The third is an open, documented version of the pipeline for public health laboratories, beginning with a short training course.

The University of Bath is a natural home for this programme because of the department's strengths in microbial evolution and its links with regional health protection teams, which would make the matched datasets of the first direction realistic. I would also be glad to contribute to teaching. I have run a four-day Python workshop for biologists four times, and I would like to develop a module on analysing sequencing data for students who have never programmed.

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