“Rapid and precise detection of gastrointestinal infections using metagenome sequencing”.

The gut microbiome is a community of microscopic organisms in our intestines that live in the colon, including viruses, bacteria, fungi and parasites. Many of these microorganisms in the gut are harmless, going unnoticed in our day-to-day lives, but sometimes people can become infected with some that are more dangerous, which can lead to an infection. In my project, I am focusing on bacterial infections in the gut. Some infections do not require medical interventions, but sometimes, a person may need to be treated with medications like antibiotics.

In hospitals, the current way to determine which bacteria are causing gastrointestinal illnesses is by culturing from stool samples. This is a method of growing the microorganisms on jelly full of nutrients that help them to grow; this is known as a culture-dependent method. This can be a time-consuming process, delaying the infection's diagnosis and treatment. There have been some developments towards more sophisticated technologies that identify microbes; however, many still require the step of growing bacteria before using and an idea of what may be causing the infection. In research, there has been a move away from culturing bacteria to identify harmful microbes towards culture-independent methods where scientists directly use a patient's sample for identification, with no prior assumption of what could be causing an infection is needed.

My research is trying to develop these culture-independent bacterial identification methods from a stool by looking at the DNA in the sample. DNA is like a fingerprint, unique to each microbe and can be used to work out what is present in a sample. When we culture microorganisms, we look at a single type of bacteria each time, whereas my research looks at the collection of all DNA belonging to all the microorganisms in the stool sample through sequencing. Sequencing is like a jigsaw puzzle, piecing tiny bits of information together to complete a bigger picture. When a jigsaw contains many small pieces of a puzzle, it can be hard to assemble because the details can be very similar- this is like short-

read sequencing. We are more likely to place puzzle pieces in the correct sections using larger jigsaw pieces as they have fewer similarities- this is like long-read sequencing. My research uses long-read sequencing to piece together the information from the genetic soup of the stool sample and pinpoint what is in there. I want to show if there are improvements in the new technology of long-read sequencing to make it easier to identify microbes from patient samples.

Providing proof of improved ways to identify infection-causing microbes could be used as evidence and justification to develop protocols to use long-read sequencing in hospitals, which would positively patients by reducing diagnosis time and improving antibiotic treatment.