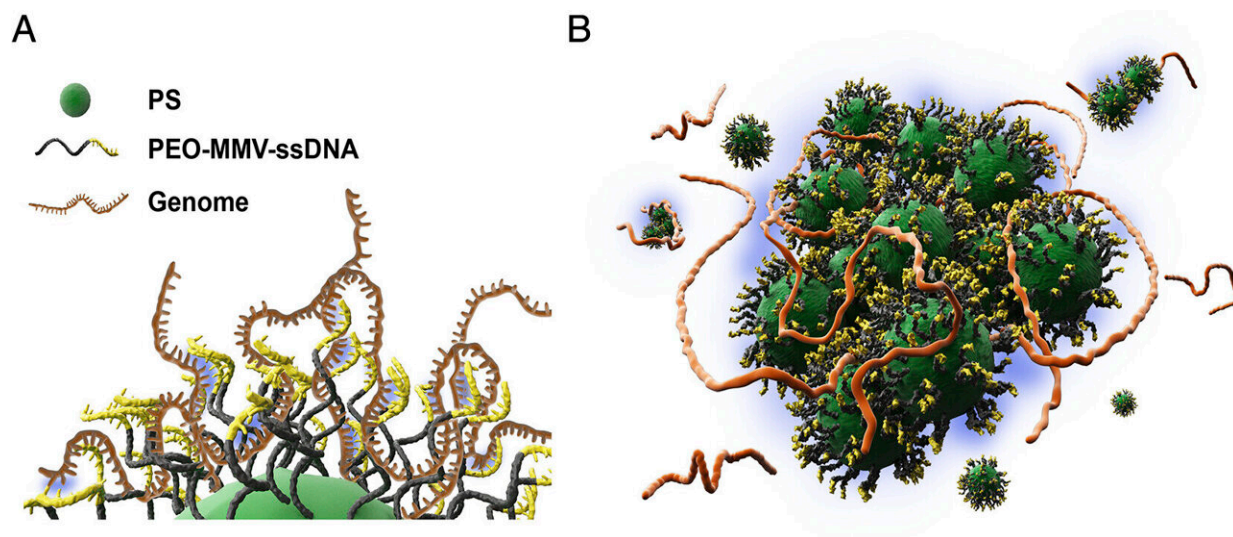


# New method for identifying bacteria more easily

November 28 2023, by Steinar Brandslet



(A) Cartoon of a DNA-coated colloidal particle bound to parts of a long bacterial genomic DNA. Short single-stranded DNA probes, which are grafted on the surface of a colloid, form complementary connections with the target genomic DNA. (B) Colloidal aggregation and subsequent sedimentation resulted from the cooperative binding of many DNA-coated particles to denatured bacterial DNA. Credit: *Proceedings of the National Academy of Sciences* (2023). DOI: 10.1073/pnas.2305995120

Far too many antibiotics are used around the world. As a result, bacteria are becoming resistant to these drugs. Curing bacterial diseases is becoming more difficult than before because antibiotics are perhaps our

foremost weapons in the fight against them.

An important step towards using fewer antibiotics is to find better methods for identifying pathogens, and here is the good news.

"We have developed a simple tool that can identify all of the [genetic material](#) in bacteria. This allows us to find out more quickly what kind of bacteria a [sick person](#) or animal is affected by, or what kind of bacteria are found in food or the environment. We can then also decide whether it is necessary to use antibiotics against the bacterium, and if so what kind, so we don't have to use as much medication," says Professor Erika Eiser at NTNU's Department of Physics.

## **No need to copy genetic material**

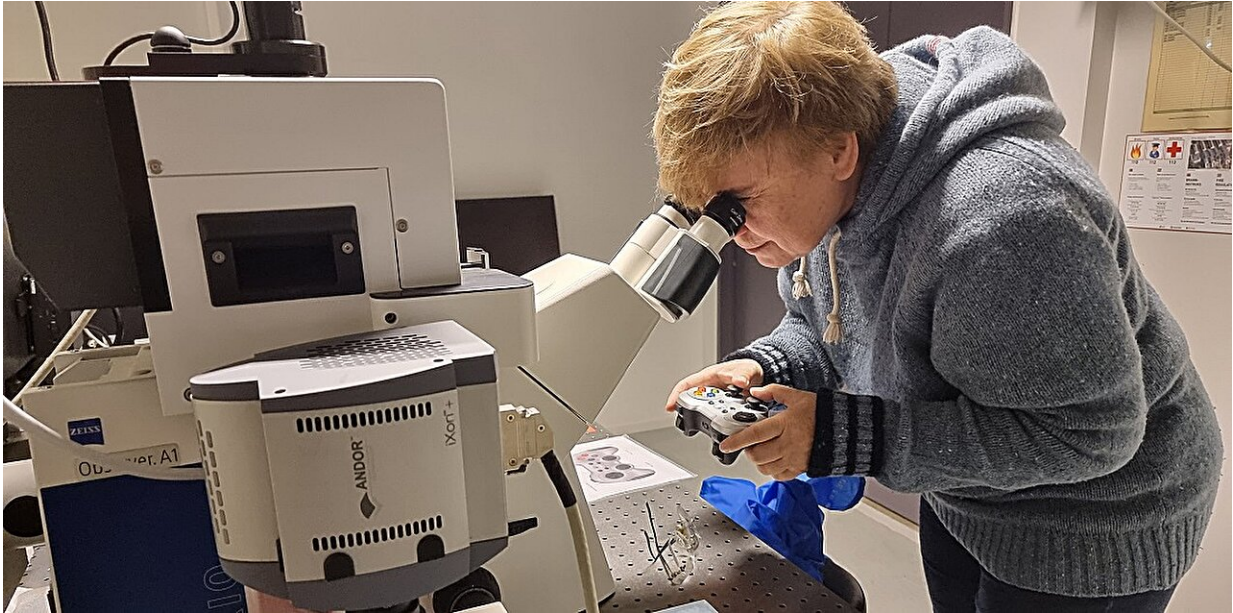
An international research group is behind the latest findings. The results have been [published](#) in the *Proceedings of the National Academy of Sciences*. Playing a key role in the work was Peicheng Xu from the Institute of Physics Chinese Academy of Sciences in Beijing, for whom Eiser was previously an academic supervisor.

One reason why the new method is faster is that users do not have to go through a step called "gene amplification." This involves making several copies of the genetic material so it is easier to analyze, but this step can now be skipped.

"We can analyze all of the bacterium's DNA without gene amplification by using a method previously used in simulations," says Professor Eiser.

Eiser was part of a research group led by Tine Curk from Johns Hopkins University that developed the [theory behind the method](#), which also works in reality.

"We get excellent results when we apply the theoretical method to real samples," says Eiser.



Professor Erika Eiser was in the group that proved that it is possible to identify bacteria and viruses more effectively with a new method. Credit: Marie-Laure Olivier, PoreLab, NTNU

## **The method creates clumps**

This paragraph might be a bit difficult to understand, but basically, DNA is made up of rows of so-called nucleotides. The new method enables researchers to find short sequences of the bacteria's DNA. They do this by seeing how these sequences bind to different variants of DNA that are grafted onto colloids, which are particles dissolved in a liquid.

If you are interested in finding out more, you can read about the process in more detail [here](#). What it means, however, is that researchers can

quickly identify the bacteria, because they bind themselves to these colloids in various ways and cause them to clump together.

The bottom line is that you don't have to analyze so much material. You can skip the step of having to copy them, and this saves time and money.

"Using this method, we saw how as few as five E. coli bacteria caused the colloids to create clusters," says Professor Eiser.

## Still a way to go

All of this is currently in its early stages. Eiser has published a proof-of-principle experiment. This means that there is still a lot of work to be done before it becomes a widely used method.

"The findings can provide us with a [reliable method](#) for identifying pathogens in disciplines such as [food safety](#), [disease control](#) and [environmental monitoring](#)," says Professor Eiser.

In a world where more and more [bacteria](#) are becoming resistant to antibiotics, this is particularly good news.

**More information:** Peicheng Xu et al, Whole-genome detection using multivalent DNA-coated colloids, *Proceedings of the National Academy of Sciences* (2023). [DOI: 10.1073/pnas.2305995120](https://doi.org/10.1073/pnas.2305995120)

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