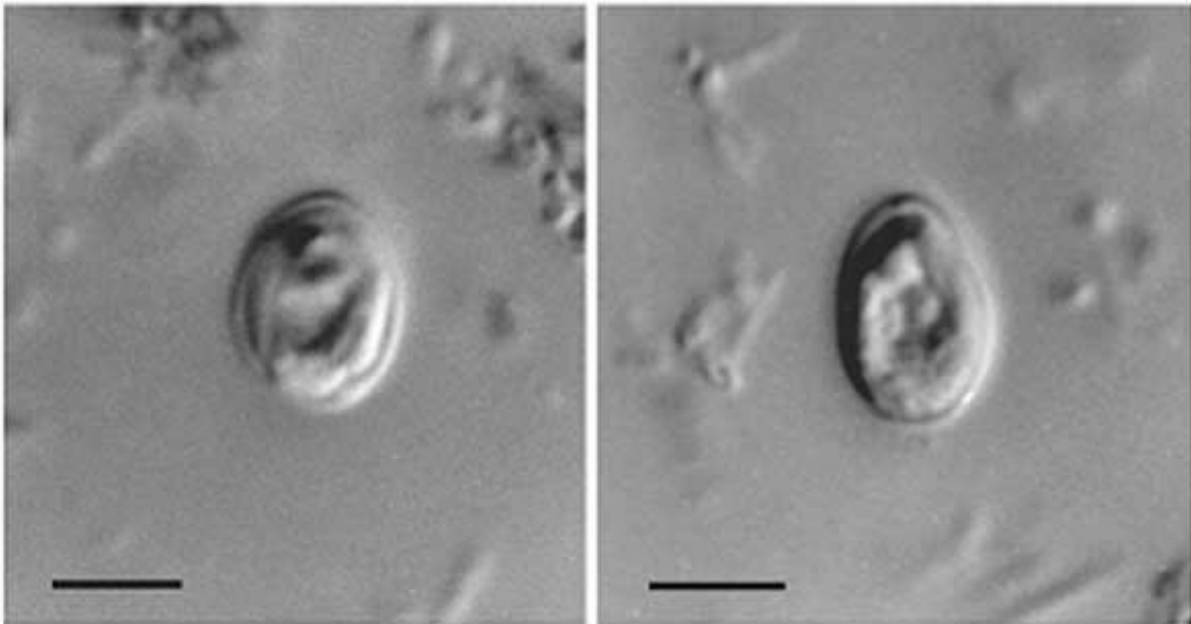


# Scientists expose hidden risks of diarrhoeal disease

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*Cryptosporidium muris*. Credit: public domain image

A rapidly evolving new subspecies of the cryptosporidium parasite—a leading cause of diarrhoeal disease in children worldwide—has been revealed by scientists at the University of East Anglia.

The study, published in *Nature Microbiology*, sheds new light on how this parasite has evolved the ability to spread more easily between people.

Researchers sequenced and compared whole genomes from over 20 different [cryptosporidium](#) cases to find out more about the parasite and how it infects people.

Their work will help [public health interventions](#) aimed at preventing the spread of the disease.

The *Cryptosporidium* parasite is one of several microorganisms that cause diarrhoeal disease. It is responsible for around 57,000 deaths each year, 80 per cent of which are among children under five years old.

The vast majority of these are in low-income countries, but outbreaks also occur in the UK and elsewhere in Europe. There is no effective drug or vaccine available, so understanding the transmission of this parasite is critical in tackling outbreaks.

Spread primarily through contact with faeces, *Cryptosporidium* can be contracted either from animals or from people. Scientists had previously thought there were just two main species of the parasite—one transmitted between humans and one from animals to humans.

In this study, the UEA team report their discovery of a recently evolved, human specialised subspecies.

Dr. Kevin Tyler, one of the senior authors of the study from UEA's Norwich Medical School, said: "Identifying this emerging subspecies of *Cryptosporidium* could be extremely significant to public health bodies tasked with stopping the spread of disease.

"Although they are genetically more akin to the species normally contracted from livestock animals, these forms are typically passed from person to person, so preventing their spread will require a different public health focus—putting resources into improving sanitation, or

issuing advice to boil water before drinking it, rather than improving the separation of people and animals."

Most remarkably, the team showed that the new subspecies has evolved rapidly by hybridising with another *Cryptosporidium* species. The [genetic exchange](#) happened only recently, probably around the time of the Industrial Revolution when urbanisation became widespread.

Since then, the new genes that were incorporated into the genome of the new subspecies have evolved rapidly, adapting themselves to their new human host.

Prof Cock van Oosterhout, from UEA's School of Environmental Sciences, said: "Human-adapted strains of [parasites](#) can evolve and emerge readily within just a few decades by exchanging genes with each other.

"You could say that these hybridising pathogens are cheating the co-evolutionary arms race by sharing genes with one another. That way, they can use genes that are adapted to infect one species for infecting another species—and in this case, humans were in their crosshairs."

The team is now putting together a "diagnostic toolbox" to specifically discriminate the different forms, enabling public health bodies to identify the new form of *Cryptosporidium*, and design local strategies to prevent the spread of infection.

Dr. Tyler said: "Using the data we provide in the paper it will be possible for these kinds of *Cryptosporidium* to be identified in microbiology laboratories using specific probes and standard techniques—facilitating straightforward, but effective interventions to be planned. Understanding what approach is likely to be most effective, particularly during outbreaks, will help public health organisations concentrate resources

and deliver the best outcomes."

'Evolutionary genomics of anthroponosis in *Cryptosporidium*' is published in the journal *Nature Microbiology* on Monday, March 4, 2019.

**More information:** Evolutionary genomics of anthroponosis in *Cryptosporidium*, *Nature Microbiology* (2019). [DOI: 10.1038/s41564-019-0377-x](https://doi.org/10.1038/s41564-019-0377-x) , [www.nature.com/articles/s41564-019-0377-x](https://www.nature.com/articles/s41564-019-0377-x)

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