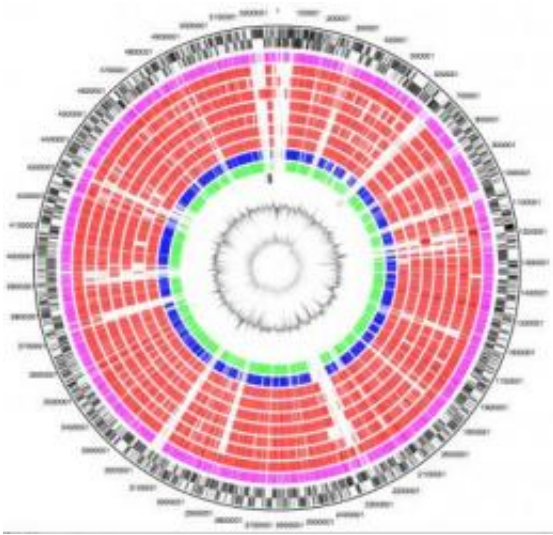


Crowd-sourcing the *E. coli* O104:H4 outbreak

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Circular diagram comparing the chromosomes of *E. coli* strains. The red circles show genes shared between different *E. coli* strains, with the outermost red circle being *E. coli* 55989. The magenta circle shows the 2001 outbreak strain, whilst the blue and green circles show genes shared with a *Salmonella* and a *Shigella*, respectively. Matches to the Shiga toxin encoding virus are shown in black under the green circle. This virus was present in the 2001 outbreak strain, and in *E. coli* O157:H7, but not in 55989. Credit: Lisa Crossman

Ten variants of the deadly *Escherichia coli* strain that hit Germany in May 2011 have been sequenced across the world. The unprecedented level of collaboration across the scientific community should give insight into how the outbreak arose, says a scientist at the Society for General

Microbiology's Autumn Conference 2011.

Sequencing of the bacterium started in early June at BGI, China. Their sequence was provided in draft form to the scientific community as a crowd-sourcing project. This allowed scientists, including those at The [Genome Analysis](#) Centre (TGAC) in Norwich to identify key disease-causing genes. Dr Lisa Crossman, Microbial [Genome Project](#) Leader at TGAC, explained, "We have found that the *E. coli* strain responsible for the [outbreak](#) carries a very high number of genes known to be involved in disease. These include genes that influence the bacterium's ability to attach to surfaces and survival genes that increase tolerance to high acidity, low oxygen, UV light and antibiotics."

The outbreak of *E. coli* O104:H4 resulted in a large number of cases of [bloody diarrhoea](#) and haemolytic uraemic syndrome (HUS) in Germany, and in 15 other countries in Europe and North America. The earliest studies suggested contaminated cucumbers were to blame. However by 10 June, raw beansprouts were identified as the source of infection. Over 4,000 cases and around 50 deaths have occurred so far across 16 countries in Europe and North America. The outbreak has also had a very high economic impact on the fresh vegetable market, especially in Spain and across Europe.

Crowd-sourcing researchers found that the outbreak strain is most closely related to a strain of *E. coli* originally isolated in Central Africa some years ago, which was responsible for cases of serious diarrhoea. "The *E. coli* O104:H4 outbreak strain has gained the ability to make a toxin from a bacterial virus source which has made it more dangerous," explained Dr Crossman.

The unprecedented global crowd-sourcing effort meant that in the very immediate term, doctors were able to distinguish this strain from others, said Dr Crossman. "Knowing which antibiotic resistance genes are

carried by the strain, for example, can provide us with more insight into the source of the outbreak and help us avoid similar outbreaks occurring in the future," she said.

Institutions around the world have now isolated ten different variants of *E. coli* O104:H4. "These variants represent a tremendous resource to examine this bug in a new, rapid and exciting way. By studying the genetic factors involved in the survival of this [bacterium](#) on surfaces, we hope to get an angle on how this organism has been able to get a foothold in the global food chain," suggested Dr Crossman.

Provided by Society for General Microbiology

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