

# DNA Sequence Yields Clues to Germany's 'Super Toxic' *E. coli* Outbreak

by Martin Enserink on 2 June 2011, 5:50 PM |

Just from the high number of deaths and severe cases, scientists and public health experts battling Germany's massive *E. coli* outbreak knew they were up against something unusual. Now, early results from sequencing projects of the enterohemorrhagic *Escherichia coli* (EHEC) strain appear to confirm that a never-before-seen hybrid, combining the worst of several bacterial strains, is causing the havoc.

The Beijing Genomics Institute (BGI), in Shenzhen, China—which [today announced](#) that it has sequenced the microbe's entire 5.2-million-base-pair genome—says that its acquisition of several virulence genes make this EHEC strain "supertoxic."

The outbreak, which has caused mayhem in European trade relations, is still growing; so far, more than 16 patients have died. The origin of the microbe remains a riddle; cucumbers from Spain, originally [fingered as the potential source](#), were acquitted on Tuesday and have not been replaced by other suspects. All researchers know is that raw vegetables are the most likely carrier.

Scientific results announced in two press releases today—both also intended to tout the extraordinary speed of today's sequencing technology—suggest that within the microbe's DNA lie clues to its aggressive nature.

The second came from Life Technologies Corporation, which manufactures so-called third-generation sequencing machines. Today, the company [announced](#) that sequencing at its lab in Darmstadt, Germany, in collaboration with the nearby University of Münster, "strongly suggests that the bacterium ... is a new hybrid type of pathogenic *E. coli* strains." Spokespeople for the company in the United States and Germany could not provide details today. "Further analyses on Ion PGM-T"—the company's flagship sequencing machine—"will confirm [the] data," the press release promised.

BGI, meanwhile, says that the microbe's genome—which it says took just 3 days to sequence, also using Life Technologies equipment—reveals that it shares 93% of its sequence with EAEC 55989 *E. coli*, a strain isolated in the Central African Republic and known to cause serious diarrhea. It appears to have acquired several genes that make it more pathogenic, however, probably in a process called horizontal gene transfer, by which microbes exchange bits of genetic information.

In an e-mail to *ScienceInsider*, Yang Bicheng, director of BGI's marketing department, wrote that one gene fragment appears to have come from another food-borne pathogen, *Salmonella enterica*, while other genes are highly homologous to those found in other, phylogenetically distinct *E. coli* strains, including a strain called O25:H4-ST131.

BGI, which has made the sequence [available](#) for researchers to download, says the analysis also confirmed that the microbe is resistant to many antibiotics. These include aminoglycoside, the macrolides, and the beta-lactams—"all of which makes antibiotic treatment extremely difficult," according to the press release. However, German EHEC patients aren't treated with antibiotics; most scientists believe they make matters worse, because killing EHEC results in the release of more toxin.

Yang acknowledged that finding the resistance genes may not be clinically relevant, but says they may help understand how the strain arose. "The evolutionary process ... of this very strange hybrid strain may be a very interesting scientific story," Yang wrote in his e-mail.

Microbial genomicist Frederick Blattner of the University of Wisconsin, Madison—who worked for almost 15 years to [sequence the first \*E. coli\* strain](#) and finished in 1997—says the results have to be considered preliminary; it's not clear whether BGI assembled the entire genome from its sequenced pieces, he notes, and usually in such efforts, a number of stretches need to be resequenced. Still, "they did this at an amazing speed, and it looks like they found some very intriguing information," Blattner says.

Source: <http://news.sciencemag.org/scienceinsider/2011/06/sequence-yields-clues-to-germany.html>