

BGI sequences genome of the deadly *E. coli* in Germany and reveals new super-toxic strain

June 2 2011

The recent outbreak of an *E. coli* infection in Germany has resulted in serious concerns about the potential appearance of a new deadly strain of bacteria. In response to this situation, and immediately after the reports of deaths, the University Medical Centre Hamburg-Eppendorf and BGI-Shenzhen began working together to sequence the bacterium and assess its human health risk. BGI-Shenzhen has just completed the sequence and carried out a preliminary analysis that shows the current infection is caused by an entirely new super-toxic *E. coli* strain.

According to the latest announcement from German health officials, the death toll in Europe from the epidemic has risen to at least 17. Over 1,000 new cases of infection have also been reported in other parts of Europe, including Sweden, Denmark, the Netherlands, the UK, and others. The University Medical Center Hamburg-Eppendorf received the majority of the infected patients from northern Germany and found that antibiotic treatment was ineffective.

BGI was informed of the dangerous situation and, in collaboration with the University Medical Center Hamburg-Eppendorf researchers, used their [genomic technology](#) to determine the infectious strain, reveal the mechanisms of infection, and facilitate the development of measures to control the spread of this epidemic.

Upon receiving the [bacterial DNA](#) samples, BGI finished sequencing the

genome of the bacterium within three days using their third-generation sequencing platform — Ion Torrent by Life Technologies.

Bioinformatics analysis revealed that this *E. coli* is a new [strain of bacteria](#) that is highly infectious and toxic.

According to the results of the current draft assembly, the estimated genome size of this new *E. coli* strain is about 5.2 Mb. Sequence analysis indicated this bacterium is an EHEC serotype O104 *E. coli* strain; however, this is a new serotype — not previously involved in any *E. coli* outbreaks. Comparative analysis showed that this bacterium has 93% sequence similarity with the EAEC 55989 *E. coli* strain, which was isolated in the Central African Republic and known to cause serious diarrhea. This new strain of *E. coli*, however, has also acquired specific sequences that appear to be similar to those involved in the pathogenicity of hemorrhagic colitis and hemolytic-uremic syndrome. The acquisition of these genes may have occurred through horizontal gene transfer. The analysis further showed that this deadly [bacterium](#) carries several antibiotic resistance genes, including resistance to aminoglycoside, macrolides and Beta-lactam antibiotics: all of which makes [antibiotic treatment](#) extremely difficult.

The research team will further analyze the integrity of the virulence genes, their expression profiles, drug resistance, and gene transfer mechanisms followed by validation of these genes in other strains. In addition BGI and collaborators are developing diagnostic kits to aid in curtailing this epidemic. New results will be continuously updated.

More information: The sequences of this new *E. coli* strain have been uploaded to NCBI (SRA No: SRA037315.1) and are also available for immediate download at ftp://ftp.genomics.org.cn/pub/Ecoli_TY-2482

Provided by Beijing Genomics Institute at Shenzhen

Citation: BGI sequences genome of the deadly E. coli in Germany and reveals new super-toxic strain (2011, June 2) retrieved 18 April 2024 from <https://medicalxpress.com/news/2011-06-bgi-sequences-genome-deadly-coli.html>

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