

## Two isolates from *E. coli* outbreak available

June 11 2011

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An outbreak of *Escherichia coli* causing a severe illness called hemolytic-uremic syndrome (HUS) began in Germany on May 2, 2011 and has killed more than 20 people and sickened more than 2,000. The organism causing the outbreak has been identified as a strain of *E. coli* O104:H4 that produces a Shiga toxin and causes an illness similar to infection with *E. coli* O157:H7. Two isolates from this outbreak have been sequenced. Both strains, TY-2482 and LB226692, have been annotated and are now available from Virginia Bioinformatics Institute's (VBI's) Pathosystems Resource Integration Center (PATRIC, [patricbrc.org](http://patricbrc.org)), which is funded by the National Institute of Allergy and Infectious Diseases.

In the rush to save lives, many laboratories are analyzing these genomes and providing data to the research community. Bruno Sobral, PATRIC's principal investigator, commented, "The PATRIC team is working around the clock to help the scientific community address this emergency. Analyses such as these provide insights into the origin of highly pathogenic strains and potential response strategies."

The two genomes have been annotated with Rapid Annotation using Subsystem Technology (RAST), making them consistent with the 184 *E. coli* genomes and the total 2,865 bacterial genomes available at PATRIC. The proteins conserved across all *E. coli* have been used to generate a preliminary [phylogenetic tree](#) that is based on 166640 characters across 527 genes in 354 taxa. This tree shows that the two new strains are most closely related to the pathogenic, enteroaggregative strain 559899, which may give additional insight into its origin. The tree is available in interactive form on the PATRIC website

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<http://patricbrc.org/portal/portal/patric/Phylogeny?cType=taxon&cId=561>). For a comparison of the RAST annotations with the other publicized annotations, visit [theseed.org/ecoli/](http://theseed.org/ecoli/).

As can be seen in the PATRIC Protein Family Sorter

(  
<http://patricbrc.org/portal/portal/patric/FIGfamSorterB?cType=taxon&cId=561&dm=result>), the proteins from these two new pathogenic strains have several unique islands as compared to other *E. coli* genomes. Further investigation of these islands and unique proteins may yield clues as to virulence or intervention strategies for the new strains. The "heatmap" tab of the Protein Family Sorter presents a graphical view presence and absence of the proteins across the *E. coli* genomes.

Much of the information in PATRIC is updated on an ongoing basis including:

- An interactive Disease Map with outbreak information. Visit <http://patricbrc.org/portal/portal/patric/DiseaseOverview?cType=taxon&cId=562> and then select the Disease Map tab.
- The PATRIC Google news search for countermeasures and other information  
(  
<http://patricbrc.org/portal/portal/patric/GSearch?dm=countermeasure&kw=Escherichia+coli+TY-2482>).

PATRIC is performing additional analyses, including collecting a list of the important genes identified, and will be providing gene trees and multiple sequence alignments of the genes with their closest homologs. Updates will be posted at <http://enews.patricbrc.org/>

Provided by Virginia Tech

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