EHEC 2011 outbreak: Scientists publish their prospective genomic characterization

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Scientists of the Medical Faculty of the University Munster and the University Hospital Munster in collaboration with scientists of the enterprise 'Life Technologies Corporation' were the first to release a draft genome sequence of a German enterohemorrhagic E. coli (EHEC) 2011 outbreak strain on June 3rd. Their in-depth genomic characterization of this outbreak was published on July 20th in the online open access journal *PLoS ONE*.

Microbiologist Prof. Dr. Dag Harmsen from the Department of Periodontology in Münster – the corresponding author of this publication - is leading a team responsible for sequencing and conducting the bioinformatics analysis in Münster. "Thanks to the Ion Torrent PGM™ next generation sequencing (NGS) platform we were very quick. In essence this is the first demonstration where NGS was used in real-time for genomic outbreak analysis. There have already been some publications using NGS to retrospectively analyze outbreaks, but analysis during an ongoing outbreak had not yet been performed (figure). Basically a new discipline is born, i.e. prospective genomics epidemiology," he explains.

Such rapid sequencing is to be considered a "technical masterpiece, which will have immediate impact on surveillance and diagnostics and most probably in the future also on therapeutics", says Prof. Dr. Wilhelm Schmitz, Dean of the Medical Faculty of the University Münster.

"By comparing the EHEC O104:H4 outbreak genome with a simultaneously sequenced genome of an EHEC O104:H4 isolate from an HUS patient (isolated in Germany in 2001; the HUSEC041 reference strain), we were able to demonstrate that the current outbreak strain was not– as initially suggested - derived from the very similar enteroaggregative E. coli (EAEC) O104:H4 55989 strain but from a yet unknown Shiga toxin-producing O104:H4 progenitor strain", said Dr. Alexander Mellmann of the `National Consulting Laboratory for Hemolytic Uremic Syndrome (HUS) at the Institute of Hygiene, Münster.

The senior author of the PLoS ONE study and head of the Institute of Hygiene, Prof. Dr. h.c. Helge Karch, added, "This study underlined the great importance of the long-term storage of historical HUS isolates that were collected by us since 1996 to understand the evolution of highly-pathogenic EHEC strains."

More information: Mellmann A*, Harmsen D*, Cummings CA*, Zentz EB, Leopold SR, et al. (2011) Prospective Genomic Characterization of the German Enterohemorrhagic Escherichia coli O104:H4 Outbreak by Rapid Next Generation Sequencing Technology. PLoS ONE 6(7): e22751. doi:10.1371/journal.pone.0022751

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