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Open-source genomic analysis of Shiga-toxin–producing *E. coli* O104:H4

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Abstract: An outbreak caused by Shiga-toxin–producing *Escherichia coli* O104:H4 occurred in Germany in May and June of 2011, with more than 3000 persons infected. Hamburg was in the centre of the outbreak and the University Medical Centre Hamburg-Eppendorf treated more infected patients which developed HUS than any other individual hospital in the country. Here, we report a cluster of cases associated with a single family and describe an open-source genomic analysis of an isolate from one member of the family. This analysis involved the use of rapid, bench-top DNA sequencing technology, open-source data release, and prompt crowd-sourced analyses. In less than a week, these studies revealed that the outbreak strain belonged to an enteroaggregative *E. coli* lineage that had acquired genes for Shiga toxin 2 and for antibiotic resistance.

Statement: Our report is of major significance in that we show that the German *E. coli* outbreak strain carries unusual genetic traits that could contribute to the evident exceptional clinical course. Even more importantly, it is the first example demonstrating the power of combined table top next generation sequencing technologies, unrestricted open source data release and world wide crowd sourcing efforts allowing for almost real time genome analysis and epidemiology within days.

This work was performed in the Institute of Medical Microbiology, Virology and Hygiene by Holger Rohde, Liang Yang, Moritz Hentschke, Martin Christner, and Martin Aepfelbacher. Apart from having a strong interest in nosocomial infections and infectious diarrhoea their special focus lies on the rapid identification of bacterial pathogens from clinical specimens using molecular and proteomic approaches. Liang Yang joined the Institute during a Humboldt-Foundation fellowship.