Social networking and crowdsourcing aid swift characterisation of deadly E. coli strain

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An international scientific effort, including scientists from the University of Birmingham, facilitated by social networking, has enabled the characterisation of the deadly strain of E. coli from the recent German outbreak within days, according to research published today (27 July) in the New England Journal of Medicine.

More than 3,000 people across Germany were infected with an unusual strain of Shiga-toxin-producing E. coli in May and June this year. The outbreak caught the public and health officials by surprise and resulted in over 40 deaths. Cases of infection were also reported in travellers returning from Germany to other countries, including the UK.

Professor Mark Pallen and Dr Nick Loman, in the School of Biosciences at the University of Birmingham, in collaboration with groups from Germany and China, facilitated and participated in an 'open source genomics' analysis that combined a liberal approach to data release and crowdsourced analyses, drawing on social networking services.

Researchers at the BGI-Shenzhen Institute, China, sequenced the genome from an E. coli isolate from a northern German family within three days, using a new bench-top sequencing technology, the Ion Torrent Personal Genome Machine. The sequence data was immediately released into the public domain under a Creative Commons License, which set in motion a burst of crowdsourced analyses carried out by bioinformaticians on four continents, rapidly providing information on the strain's virulence and resistance genes.

Professor Mark Pallen explains:

"This exciting project illustrates how improvements in sequencing technologies twinned with the adoption of social networking tools and a more open attitude among scientists are augmenting and even challenging traditional approaches to public health microbiology and academic scholarship.

"This research drew on the curiosity-driven efforts of researchers from around the world, communicating via Twitter, blogs and a wiki. This community effort led to the rapid design of new strain-specific diagnostic reagents and revealed that this was not an entirely new strain – close relatives had been isolated in Germany, Korea and Africa over more than a decade."

Dr Nick Loman, a bioinfromatician working in Pallen's group in the School of Biosciences at the University of Birmingham, adds:

"I was able to assemble the BGI data into a usable draft genome within just a few hours of its release and released my results back into the public domain. It was thrilling to see the deluge of analyses that quickly followed."

Within 24 hours of the release of Loman's genome assembly, the sequence had been annotated and detailed comparisons with other E. coli genomes soon revealed that the outbreak strain had emerged from a previously recognised variety of the bacterium (enteroaggregative E. coli), by acquiring genes for toxin production and antibiotic resistance.

The success of the 'open-source genomics' approach offers hope for future public health emergencies, where rapid data sharing and community efforts could leader to quicker recognition and characterisation of novel pathogens, potentially shortening outbreaks and saving lives.

For more information, please contact Amy Cory, University of Birmingham Press Office via 0121 414 6029, 07789 921165 or **a.cory@bham.ac.uk (mailto:a.cory@bham.ac.uk)** .

Notes to Editors

• Professor Pallen and Dr Loman are available for interview. Please contact the Press Office for details.

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