

C. difficile hypervirulence genes identified

September 25 2009

Five genetic regions have been identified that are unique to the most virulent strain of *Clostridium difficile* (*C. difficile*), the hospital superbug. Researchers writing in BioMed Central's open access journal *Genome Biology* studied the genome of the bacterium, looking for genes relating to motility, antibiotic resistance and toxicity.

Brendan Wren from the London School of Hygiene & Tropical Medicine worked with a team of researchers at The Wellcome Trust Sanger Institute to compare the genomes of three strains of the [bacterium](#), the hypervirulent '027' strain, an historic, non-epidemic 027 strain and one less related and also non-epidemic '630' strain.

He said, "*C. difficile* is the most frequent cause of nosocomial diarrhoea worldwide. In the past five years a new group of highly virulent *C. difficile* strains has emerged to cause outbreaks of increased severity in North America and Europe. Several studies have shown that patients infected with these '027' strains have more severe diarrhoea, higher mortality and more recurrences. This study provides genetic markers for the identification of 027 strains and offers a unique opportunity to explain their emergence".

The researchers found that the 027 strains had considerable genetic differences compared to the non-epidemic 630 strain, which may relate to the observed phenotypic difference in virulence. Additionally, five genetic regions appear to have accumulated over the last 20 years in the modern day epidemic 027 strain, compared to its historic counterpart. According to Wren, "The observed gene differences between these

strains might individually or collectively explain why modern 027 strains are more likely to be epidemic and could explain the higher case-fatality ratio and persistence associated with infection by these strains".

More information: Comparative [genome](#) and phenotypic analysis of Clostridium difficile 027 strains provides insight into the evolution of a hypervirulent bacterium; Richard A Stabler, Miao He, Lisa Dawson, Melissa Martin, Esmeralda Valiente, Craig Corton, Trevor D Lawley, Mohammed Sebahia, Michael A Quail, Graham Rose, Dale N Gerding, Maryse Gibert, Michel R Popoff, Julian Parkhill, Gordon Dougan and Brendan W Wren; [Genome Biology](#) (in press); genomebiology.com/

Source: BioMed Central ([news](#) : [web](#))

Citation: C. difficile hypervirulence genes identified (2009, September 25) retrieved 23 April 2024 from <https://phys.org/news/2009-09-difficile-hypervirulence-genes.html>

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