

This manuscript has been published online, prior to printing. Once the issue is complete and page numbers have been assigned, the citation will change accordingly.

In-depth genetic analysis of *Clostridium difficile* PCR-ribotype 027 strains reveals high genome fluidity including point mutations and inversions

Richard A. Stabler,¹ Esmeralda Valiente,¹ Lisa F. Dawson,¹ Miao He,² Julian Parkhill² and Brendan W. Wren^{1,*}

¹London School of Hygiene and Tropical Medicine; London, UK; ²Wellcome Trust Sanger Institute; Cambridge, UK

Supplementary Material

Key words: *Clostridium difficile*, 027 ribotype, point mutations, inversions, hypervirulence

Submitted: 01/28/10

Revised: 03/09/10

Accepted: 03/16/10

Previously published online:
www.landesbioscience.com/journals/gut-microbes/article/11870

*Correspondence to: Brendan W. Wren;
Email: Brendan.Wren@lshtm.ac.uk

Addendum to: Stabler RA, He M, Dawson L, Martin M, Valiente E, Corton C, et al. Comparative genome and phenotypic analysis of *Clostridium difficile* 027 strains provides insight into the evolution of a hypervirulent bacterium. *Genome Biol* 2009; 10:102; PMID: 19781061; DOI: 10.1186/gb-2009-10-9-r102.

CDR20291_1234 ATGCTAGGTGAAAAGATGAGAAATATAAGAAAAAGCAAGAAAAAACATTAAGTGATGTT 60
 CD196_1256 ATGCTAGGTGAAAAGATGAGAAATATAAGAAAAAGCAAGAAAAACATTAAGTGATGTT 60
 630_CD1388 ATGCTAGGTGAAAAGATGAGAAATATAAGAAAAAGCAAGAAAAA-CATTAAGTGATGTT 59

 CDR20291_1234 TCCAATTGACAGATTATCTATAAGTTATCTCTCAAATAGAAAGAGATGCTATTGAA 120
 CD196_1256 TCCAATTGACAGATTATCTATAAGTTATCTCTCAAATAGAAAGAGATGCTATTGAA 120
 630_CD1388 TCCAATTGACAGATTATCTATAAGTTATCTCTCAAATAGAAAGAGATGCTATTGAA 119

 CDR20291_1234 CCATCCTGCTTCATTGAGAAAAATCGCTGAAGTTTAGACACTCCTTATATATGTTT 180
 CD196_1256 CCATCCTGCTTCATTGAGAAAAATCGCTGAAGTTTAGACACTCCTTATATATGTTT 180
 630_CD1388 CCATCCTGCTTCATTGAGAAAAATCGCTGAAGTTTAGACACTCCTTATATATGTTT 179

 CDR20291_1234 ATGGATGACAATAAACTGATGATTTAGTAATTAGAAAAGAAGATAGAGTTATGATGAAA 240
 CD196_1256 ATGGATGACAATAAACTGATGATTTAGTAATTAGAAAAGAAGATAGAGTTATGATGAAA 240
 630_CD1388 ATGGATGACAATAAACTGATGATTTAGTCATTAGAAAAGAAGATAGAGTTATGATGAAA 239

 CDR20291_1234 TTTCCAAAGAGTGAATGTTTACGAGATAGTATCTCAAATGCCTACAACTGAATTTACA 300
 CD196_1256 TTTCCAAAGAGTGAATGTTTACGAGATAGTATCTCAAATGCCTACAACTGAATTTACA 300
 630_CD1388 TTTCCAAAGAGTGAATGTTTACGAGATAGTATCTCAAATGCCTACAACTGAGTTTACA 299

 CDR20291_1234 CCTTCAATTATTGAGTTGAACTTAAACCAGAAAAGTGAGGATGCTAAAGATTAT 360
 CD196_1256 CCTTCAATTATTGAGTTGAACTTAAACCAGAAAAGTGAGGATGCTAAAGATTAT 360
 630_CD1388 CCTTCAATTATTGAGTTGAACTTAAACCAGAAAAGTGAGGATGCCAAAGATTAT 359

 CDR20291_1234 ATCTATCATGCATCAGAAGAAATTATGGTGTAAACGAGTGGTGTGGTTGATATTGTATG 420
 CD196_1256 ATCTATCATGCATCAGAAGAAATTATGGTGTAAACGAGTGGTGTGGTTGATATTGTATG 420
 630_CD1388 ATATATCATGCATCAGAAGAAATTATGGTGTAAACGAGTGGTGTGGTTGATATTGTACG 419
 *** ****

 CDR20291_1234 GGTGAAAAGGTAGTTAGATTAATCCAGGTGACTCAACATTATAAAAGCTAATGTACCA 480
 CD196_1256 GGTGAAAAGGTAGTTAGATTAATCCAGGTGACTCAACATTATAAAAGCTAATGTACCA 480
 630_CD1388 GGTGAAAAGGTAGTTAGATTAATCCAGGTGACTCAACATTATAAAAGCTAATGTACCA 479

 CDR20291_1234 CATAAAATCATCAATCCAAGTAAAGATAACAATAGCTCGTGGATATGGAGTTATATCACCT 540
 CD196_1256 CATAAAATCATCAATCCAAGTAAAGATAACAATAGCTCGTGGATATGGAGTTATATCACCT 540
 630_CD1388 CATAAAATCATCAATCCAAGTAAAGATAACAATAGCTCGTGGATATGGAGTTATATCACCT 539

 CDR20291_1234 CCAATTGGCCAATAAAATCTAAATAA 567
 CD196_1256 CCAATTGGCCAATAAAATCTAAATAA 567
 630_CD1388 CCAATTGGCCAATAAAATCTAAATAA 566

CDR20291_1656 MEYYIVDSFATKLFKGNPAGVCVLDRIIIPLELMQKIAEENNLPETAFVVKGKGNYELRWF 60
CD196_1681 MEYYIVDSFATKLFKGNPAGVCVLDRIIIPLELMQKIAEENNLPETAFVVKGKGNYELRWF 60
630_CD1761 MEYYIVDSFATKLFKGNPAGVCVLDRIIIPLELMQKIAEENNLPETAFVVKGKGNYELRWF 60

CDR20291_1656 TPKAEIDLDCGHATLAAAYVISNFIDVNVRIDFFTQSGKLEVTRNGNLYEMIFPEIMPIE 120
CD196_1681 TPKAEIDLDCGHATLAAAYVISNFIDVNVRIDFFTQSGKLEVTRNGNLYEMIFPEIMPIE 120
630_CD1761 TPKAEIDLDCGHATLAAAYVISNFIDVNKKIDFFTQSGKLEVTRNGNLYEMIFPEIMPIE 120

CDR20291_1656 IELSP#QANLIGCVPSAVYSSRDLILLNLSEQEVINYKPNYAQLRKLTDWLGIIITPQGS 179
CD196_1681 IELSP#QANLIGCVPSAVYSSRDLILLNLSEQEVINYKPNYAQLRKLTDWLGIIITPQGS 179
630_CD1761 IELSPQQANLIGCVPSDVYSSRDLILLNLSEQEVINYKPNYAQLRKLTDWLGIIITAQGS 180

CDR20291_1656 NTDFVSRYFCPELDSEDPVTGSSHCHNFIPYWSEKLGHKHMVAAPLSNRGGIIQCEVLKDN 239
CD196_1681 NTDFVSRYFCPELDSEDPVTGSSHCHNFIPYWSEKLGHKHMVAAPLSNRGGIIQCEVLKDN 239
630_CD1761 NTDFVSRYFCPELDSEDPVTGSSHCHNLIPYWSEKLGHKHMVAAPLSNRGGIIQCEVLKDN 240

CDR20291_1656 TVKISGEAVLFMQGTTIKIDI 259
CD196_1681 TVKISGEAVLFMQGTTIKIDI 259
630_CD1761 TVKISGEAVLFMQGTTIKIDI 260
