

Genome sequencing used to assess a novel form of *Clostridium botulinum*

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Scientists on the Norwich Research Park have sequenced the genome of a novel strain of *Clostridium botulinum*, one of the most dangerous pathogens known to man. The strain produces an unusual botulinum neurotoxin, known as type A5 neurotoxin, which was isolated by the Health Protection Agency (HPA), following a case of wound botulism.

Professor Mike Peck and his research group at the Institute of Food Research (IFR) study *Clostridium botulinum*. Their expertise is crucial for preventing food poisoning outbreaks in the UK and internationally and to understanding the threat that these neurotoxin-producing bacteria pose to biosecurity. Outbreaks of foodborne [botulism](#) are extremely rare, due to the diligent way in which research scientists and the food industry collaborate to minimise the risks.

"Our analysis of the [genome sequence](#) indicates that while the type of neurotoxin formed is unusual, the organism itself appears closely related to other strains of *Clostridium botulinum*, and is likely to pose a similar threat to [food safety](#) and biosecurity" said Professor Peck.

The novel A5 neurotoxin and its gene sequence were first discovered by Professor Peck's research team, and other laboratories are now analysing this specific neurotoxin and assessing the implications for food safety and biosecurity.

Having the complete genome sequence is crucial to managing the potential threat that the new strain poses. The complete genome

sequence of the strain was generated by The Genome Analysis Centre (TGAC), and will help in the study of *Clostridium botulinum* and botulism in general.

High throughput sequencing was performed at TGAC using the Roche 454 and Illumina GAI next generation sequencing platforms with the longer 454 reads assembled first and followed by Illumina reads to correct ambiguities. Remaining gaps in the assembly were closed by Prof Peck's group at IFR using other sequencing methods.

"Having TGAC on our doorstep was extremely useful for this project, and will be a boon for IFR science," said Professor Peck. "It has enabled us to evaluate the threat that this new strain may pose to food safety and biosecurity by rapidly delivering a complete genome, finished genome sequence."

IFR and TGAC are institutes of the Biotechnology and Biological Sciences Research Council (BBSRC), which funded this research.

The genome was annotated at TGAC by Dr Lisa Crossman. Annotating the genome involves looking at the genomic sequence, and working out where the genes themselves are, and what they may do. This is done by comparison with genes of known function from other bacteria.

"We first annotated the genome automatically, but because of the importance in obtaining a high quality set of genes, we manually curated the most interesting parts of the genome," said Dr Crossman.

The 3.9 Mb [genome](#) is structurally similar to other strains of *C. botulinum*. The scientists identified the gene that produces the neurotoxin, which is in the same location as in many other *C. botulinum* strains, and confirmed that no other neurotoxin genes were present. The genes needed for spore germination are similar to those in related strains.

More information: This work was carried out in collaboration with the Health Protection Agency (HPA) and was published in the *Journal of Bacteriology*. The complete genome sequence has been deposited in EMBL/Genbank under accession number FR773526 for use by the wider research community.

More information on botulism: [www.hpa.org.uk/Topics/Infectio... fectionsAZ/Botulism/](http://www.hpa.org.uk/Topics/InfectiousDiseases/InfectionsAZ/Botulism/)

IFR's work on Clostridium botulinum: [www.ifr.ac.uk/info/science/foo... ogens/Cbotulinum.htm](http://www.ifr.ac.uk/info/science/food-safety/ogens/Cbotulinum.htm)

Botulism and food safety [www.foodsecurity.ac.uk/researc... ism-food-safety.html](http://www.foodsecurity.ac.uk/research/food-safety/ism-food-safety.html)

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