

Genome Sequence of the Neurotoxicogenic *Clostridium butyricum* Strain 5521

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***Clostridium* strains from six phylogenetic groups, *C. botulinum* groups I to IV, *C. baratii*, and *C. butyricum*, display the capacity to produce botulinum neurotoxin. Here, we present the genome sequence of a *C. butyricum* isolate, the neurotoxicogenic strain 5521, which encodes the type E botulinum neurotoxin.**

Received 4 June 2014 Accepted 6 June 2014 Published 26 June 2014

Citation Hassan KA, Elbourne LDH, Tetu SG, Johnson EA, Paulsen IT. 2014. Genome sequence of the neurotoxicogenic *Clostridium butyricum* strain 5521. *Genome Announc.* 2(3): e00632-14. doi:10.1128/genomeA.00632-14.

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Clostridium butyricum is a Gram-positive bacillus named for its capacity to produce butyric acid. *C. butyricum* strains are found in a variety of environments and are common human and animal gut commensals. However, some *C. butyricum* strains have been found to cause the paralytic condition botulism (1–4). These neurotoxicogenic *C. butyricum* strains harbor an operon encoding the type E botulinum neurotoxin (BoNT/E) likely to have been horizontally acquired (5). Neurotoxicogenic *C. butyricum* strains were originally identified as the cause of botulism in infants in Italy (1, 2) and have since been identified in other countries. Here, we present the genome sequence of a neurotoxicogenic *C. butyricum* strain, 5521, isolated from a case of botulism. The genome sequence of *C. butyricum* 5521 was determined to 8-fold coverage using Sanger shotgun sequencing. The sequence reads were assembled and annotated as previously described (6). The sequence is organized into 123 scaffolds and includes 3,827 putative protein-coding genes and 259 predicted pseudogenes.

The predicted protein-coding potential of *C. butyricum* 5521 is similar to that of *C. butyricum* BL 5262 (5); tblastx 2.2.5+ searches demonstrated that >96% of the 4,086 genes or pseudogenes of *C. butyricum* 5521 are shared between these two strains (E value $\leq 1e^{-30}$). Of the clostridial species for which complete genome sequences are available, 16S rRNA analyses have suggested that *C. butyricum* is most closely related to group II *Clostridium botulinum*, *Clostridium acetobutylicum*, and *Clostridium beijerinckii* (3). tblastx comparisons indicate that 2,352, 1,809, and 2,568 genes or pseudogenes of *C. butyricum* 5521 have orthologs within the genomes of *C. botulinum* E3 strain Alaska E43 (5) (Genbank accession no CP001078), *C. acetobutylicum* ATCC 824 (7), and *C. beijerinckii* NCIMB 8052 (8), respectively.

A defining characteristic of *C. butyricum* strains is their production of butyric acid. The enzymes involved in butyric acid production from acetyl-coenzyme A (CoA) in *C. butyricum* 5521 are encoded primarily within two gene clusters, CBY_2919-20 and CBY_3041-45 (both on scaffold ABDT01000094 in the current

assembly). However, acetyl-CoA acetyltransferase, CBY_1290, which mediates the first step in this pathway (9), is encoded elsewhere (scaffold ABDT01000114).

The gene encoding the BoNT/E toxin within *C. butyricum* 5521 is present in a gene cluster localized within the chromosomal *rarA* resolvase locus. This gene cluster is identical to that carried by the neurotoxicogenic *C. butyricum* strain BL 5262, which is also localized within the *rarA* locus (5). A detailed analysis of this gene cluster demonstrated that it shows an organization that is highly similar or identical to that of the BoNT/E gene clusters carried by group II type E toxin-producing *C. botulinum* strains (5).

The genome sequence of *C. butyricum* 5521 will prove useful for comparative studies and for future investigations of type E botulism.

Nucleotide sequence accession numbers. The draft genome sequence for *C. butyricum* 5521 has been added to the GenBank database under the accession no. [ABDT00000000](https://www.ncbi.nlm.nih.gov/nuccore/ABDT00000000). The version described here is [ABDT00000000.1](https://www.ncbi.nlm.nih.gov/nuccore/ABDT00000000.1).

ACKNOWLEDGMENTS

This work was supported by the National Institute of Allergy and Infectious Diseases (NIAID), National Institutes of Health, Department of Health and Human Services, under NIAID contract N01-AI-30071, and a Life Science Award to I.T.P. from the Office of Science and Medical Research, NSW government, Australia.

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