Molecular Characterization of a Novel Botulinum Neurotoxin Type H Gene

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METHODS

Bacterial Strains and Culture Conditions

DNA Sequencing

The generact C. bentlimen strain IEA/co-7640 was experiently opinioning Surger experiencing of short PCI product an often syneration sequenting. The type Hand type Bentlim grave for their wave inhall they send with the Sanger method. Polymerace child reservation (PCI) was performed with The Fail SD KINA Applicant (PCI allocation of the Sanger method. Polymerace child reservation (PCI) was performed with The Fail SD KINA Applicant (PCI allocation of the Sanger Sanger

Phylogenetic and Similarity Analyses

The gene sequences used in this study were aligned with ClustalW and then hand edited and analyzed using Mega 5 software [1:1]. Pairwise sequence identities were computed with the Mega 5 software and the Embora pairwise sequence alignment algorithm. Possible recombination events were explored using SimPlot [2:1]. The SimPlot analyses were generated with a sliding window of 2000 plut was moved on by between each data going reported with a sliding window from 2000 plut was moved on the between each data going and the simple states of the simple states

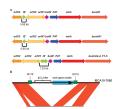
BOXT/II was found by pairwise sequence alignment analysis to differ substantially from all other tentes types and subspect Table 1). The nearest sequence felling was with BoXT/II (7.6.4) and 6.5.5 in indicated and amino and fellingth, respectively). The other boXT/II subspectioned more than 6.0 of in and 5.3.5 in monotode and amino and fellingth, respectively). BoXT/II was only \$5.7% - 6.0 of in and \$2.3% -5.0.7% it felling the other fellingth of the othe

	Nucleotides	Amino Acids
Al	66.0	50.9
A2	65.2	49.9
A3	65.7	49.1
A4	65.0	49.7
AS	65.5	50.3
81	59.9	40.6
82	60.5	41.3
83	60.2	41.3
84	59.4	41.7
05	60.4	41.4
06	60.2	41.2
87	60.6	41.5
c	53.7	32.6
C/D	56.1	32.3
0	56.9	33.0
D/C	54.6	33.3
E1	65.6	40.7
E2	65.8	40.7
E3	65.5	40.5
E4	65.5	40.4
ES	65.6	40.4
EG	65.6	40.0
E7	65.3	48.7
ES	65.6	40.7
E9 02	66.2	40.9
F1	69.0	52.8
F2	67.1	50.5
F3	67.7	50.3
F4	67.9	51.7
FS	35.4	63.5
FG	67.7	50.8
FT	67.6	52.5
6	10.0	40.6

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2 of 4 12/28/2017, 3:34 AM



3 of 4 12/28/2017, 3:34 AM

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4 of 4