Molecular Cloning of the Gene Encoding the Mosaic Neurotoxin, Composed of Parts of Botulinum Neurotoxin Types C1 and D, and PCR Detection of This Gene from *Clostridium botulinum* Type C Organisms

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The DNA fragment common to the genes encoding botulinum neurotoxin types C1 (BN/C1) and D (BN/D) was amplified by PCR from the culture supernatant of *Clostridium botulinum* type C strain 6813 (C6813) that was treated with either DNase I or proteinase K but not from the supernatant that was treated with both DNase I and proteinase K, suggesting the neurotoxin gene is located on a certain bacteriophage DNA. Thus, to isolate the neurotoxin gene, we performed PCR with the culture supernatant of C6813 and seven primer pairs designed from the genes encoding BN/C1 and BN/D. The coding region in the connected sequence encodes a neurotoxin composed of 1,280 amino acids with a molecular weight of 147,817. The neurotoxin from C6813 has 95% amino acid identity to BN/C1, except for its C-terminal one-third, which is quite similar to the C-terminal one-third of BN/D (95% identity). When we performed PCRs with four primer pairs designed from the S'-terminal two-thirds of the BN/C1 gene and two primers from the 3'-terminal one-third of the BN/D gene, DNA fragments of the expected sizes (0.5 to 1.3 kbp) could be amplified from *C. botulinum* type C strains 6812 and 6814. These results suggest that some strains of *C. botulinum* type C contain the gene encoding the mosaic neurotoxin composed of parts of BN/C1 and BN/D.

One strain of *Clostridium botulinum* produces one of seven potent but serologically distinct neurotoxins (types A, B, C1, D, E, F, and G), which have been implicated in both human and animal botulism (25). Each of the seven neurotoxins is synthesized as a single-chain molecule with a molecular mass of about 150 kDa, which is subsequently cleaved and becomes the dichain form. The dichain-form toxin is composed of a light chain (about 50 kDa) and a heavy chain (about 100 kDa) located on the N-terminal and the C-terminal sides, respectively, of a whole toxin (25).

These seven types of neurotoxins, which all have common zinc-binding motifs in their light chains, belong to zinc-dependent proteases (9, 14). These reduced toxins, or their light chains, degrade with high specificity the synaptic proteins that are involved in the fusion of synaptic vesicles with the plasma membranes, thus inhibiting release of several neurotransmitters (26). Types A and E degrade with SNAP-25 (1); types B, D, F, and G degrade with VAMP/synaptobrevin (21–23, 31); and type C1 degrades with HPC-1/syntaxin (4). Although the proteolytic activity is located on their light chains, the channelforming and the receptor-binding activities are located on the N-terminal and C-terminal halves, respectively, of their heavy chains (5, 13, 24).

Recent studies have elucidated the entire sequences of seven botulinum neurotoxin genes (2, 3, 6, 8, 10, 12, 27, 29, 30). The neurotoxin genes isolated from *C. botulinum* type C strains 468 and Stockholm are quite similar (99.9% identity) and have been reported to be the gene encoding botulinum neurotoxin type C1 (BN/C1) (10, 12). On the other hand, the neurotoxin genes isolated from C. botulinum type D strains 1873 and CB-16 are quite similar (99.9% identity) and have been reported to be the gene encoding botulinum neurotoxin type D (BN/D) (2, 27). However, some strains of C. botulinum types C and D have been known to produce neurotoxins that are not completely consistent with BN/C1 and BN/D on the basis of antigenicity (18, 28). The neurotoxin purified from strain 6813 of C. botulinum type C (BN/C6813) has antigenic structures for the BN/C1 light chain and the BN/D heavy chain, suggesting that the neurotoxins from C. botulinum type C strains could be separated into at least two isoforms. However, the difference between the primary structures of both isoforms has not yet been clarified in detail, because the entire amino acid sequence of BN/C6813 has been not determined.

In this report, we determined the entire nucleotide sequence of the gene encoding BN/C6813 and compared its deduced amino acid sequence with that of BN/C1 or BN/D. In addition, we detected the gene encoding the neurotoxin-like BN/C6813 from two other strains.

MATERIALS AND METHODS

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Organisms. *C. botulinum* type C strains 6812 (C6812), 6813 (C6813), and 6814 (C6814), and type D strains South African (Dsa) and 4947 (D4947) were grown at 30°C for 4 days in cooked meat medium (18). The culture media of those organisms were centrifuged at $10,000 \times g$. The resulting supernatants were kept at -20° C until use.

Treatment of culture supernatant with DNase I and proteinase K. Culture medium was centrifuged at 15,000 rpm for 5 min. The resulting supernatant was filtered through a 0.22-µm-pore-diameter cellulose nitrate filter. Twenty micro-

TABLE 1. Primers for PCR

Primer	<u></u>	Nucleotide position ^a		
	Sequence	BN/C1	BN/D	
C-1 ^b	5'tactgatttatttagacctg3'	-167146		
$C0^c$	3'attgacctggatctcttttg5'	492-473		
$C1^b$	5'gaaagttaggagatgttagt3'	-234		
$C2^{c}$	3'ccgtgttcttcctaaaccac5'	544-563		
$C3^b$	5'tggtagcataaatcctagtg3'	447-466		
$C4^{c}$	3'ccacttcaatgtcatttagc5'	1031-1012		
$C5^b$	5'agattcgtagtagaatcttc3'	991-1010		
$C6^c$	3'atggtcccctcttagttcag5'	1596-1577		
$C8^c$	3'agtccttcactatttcttt5'	2266-2247	2255-2236	
$C9^b$	5'cttgttcagtatccagatag3'		3358-3377	
$C10^{c}$	3'agcatattttacaacttaag5'		3906-3887	
YQA^b	5'tatcaggcagatgcaatcaaagcta3'	2197-2221	2185-2209	
LDV^{c}	3'gtagtcctatattacgtcttcactc5'	2681-2657	2669-2645	
$LDV2^{b}$	5'caggatataatgcagaagtg3'	2660-2679	2648-2667	
SVS ^c	3'agtcatagactattcttagg5'		3434-3415	
RGN ^c	3'ttactatgatctcatgctcc5'	3491–3479		

^{*a*} Nucleotide numbering is from A of the initiation codon (2, 12).

^b Sense.

^c Antisense.

liters of the filtered supernatant was mixed with 1 μ l of chloroform, and then the mixture was centrifuged at 15,000 rpm for 5 min. Either 7 U of DNase I or 10 μ g of proteinase K was added to the centrifuged supernatant. The mixture was incubated at 37°C for 1 h. After treatment with chloroform, the mixture was centrifuged at 15,000 rpm for 5 min. The resulting supernatant was used as a template for PCR. When the supernatant was treated with DNase I and proteinase K, DNase I was added to the supernatant after treatment with proteinase K and chloroform.

PCR. The degenerate oligonucleotide primers for PCR were synthesized on an Applied Biosystems, Inc., model 380B synthesizer. The nucleotide sequences of primers (designated C1, C2, C3, C4, C5, C6, C7, C8, C9, C10, YQA, LDV, LDV2, SVS, and RGN) were derived from BN/C1 and BN/D genes (Table 1). The PCR amplifications were carried out in a reaction mixture (50 µl) containing 0.5 µl of culture supernatant, 100 pmol (each) of the two primers, 2.5 U of *Taq* DNA polymerase (Boehringer Mannheim, Tokyo, Japan) in Tris-HCl (pH 8.0), 0.2 mM (each) the deoxynucleoside triphosphates, 50 mM KCl, 2.0 mM MgCl₂, and 0.01% bovine serum albumin. Twenty-five PCR cycles (at 92°C for 1 min, 45°C for 1 min, and then 74°C for 2 min) were performed. The amplified fragments were purified with SUPREC-01 (Takara, Otsu, Japan) and subcloned into the "T-vector" constructed from pBluescript SK+ (16). The sequences of three clones from different DNA amplification method with [α -³⁵S]dATP and Sequenase version 2.0 DNA polymerase (Amersham, Tokyo, Japan). Nucleotide numbers in BN/C1 and BN/D genes indicate numbering from A of the initiation codon ATG.

DNA-DNA hybridization. Amplified DNA fragments were transferred from agarose gels to Hybond N+ membranes (Amersham) (15). The amplified DNA products were labeled with $[\alpha^{-3^5}S]$ dATP with the random primer DNA labeling kit, version 2 (Takara). Hybridizations were performed at 65°C. Autoradiograms were analyzed with a Bio-Image analyzer, model BAS2000 (Fuji Film, Tokyo, Japan).

Nucleotide sequence accession number. The nucleotide sequence data reported in this article will appear in the GSDB, DDBJ, EMBL, and NCBI nucleotide sequence databases under accession number D49440.

RESULTS AND DISCUSSION

The BN/C1 gene has been shown to exist in toxigenic bacteriophage DNA from type C strains 468 (10) and Stockholm (12), whereas a toxigenic bacteriophage has not been isolated from type C strain 6813 (C6813). PCR with the primer pair YQA/LDV could amplify the DNA fragment of the expected size of 0.5 kbp from culture supernatant of C6813 that was treated with either DNase I or proteinase K (Fig. 1). However, PCR with the primer pair YQA/LDV could not amplify any DNA fragment from the culture supernatant of C6813 that was treated with both DNase I and proteinase K (Fig. 1). These

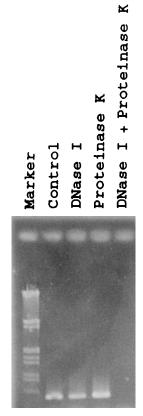


FIG. 1. Amplification of the part of the BN/C1 gene from the culture supernatant of C6813. Lamda phage genomic DNA digested with *Hind*III and *Eco*RI was used as a molecular weight marker.

results suggest that the BN/C6813 gene is located on a certain bacteriophage.

The sequencing strategy used in this study is shown in Fig. 2. The DNA fragments of the expected sizes of 0.7, 0.6, 0.6, 0.6, 1.3, and 0.5 kbp were amplified with the primer pairs C-1/C0, C1/C2, C3/C4, C5/C6, C5/C8, and YQA/LDV, respectively, which were designed from the 5'-terminal two-thirds of the BN/C1 gene and its upstream region. However, no DNA fragment could be amplified from C6813 by the primer pair LDV2/ RGN, which targets the region extending from C-2660 to G-3491 in the BN/C1 gene. On the other hand, the DNA fragment of the expected size of 0.8 kbp was amplified by the primer pair LDV2/SVS, which targets the region extending from G-2648 to C-3434 in the BN/D gene (Fig. 3A and B), suggesting that the 3'-terminal one-third of the BN/C6813 gene is similar to that of the BN/D gene rather than that of the

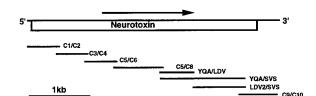


FIG. 2. Strategy for cloning the BN/C6813 gene. The open box and arrow indicate the coding region of BN/C6813 and the transcription orientation, respectively. Lines indicate PCR products created by amplification with primer pairs C1/C2, C3/C4/, C5/C6, C5/C8, YQA/LDV, YQA/SVS, LDV2/SVS, and C9/C10.

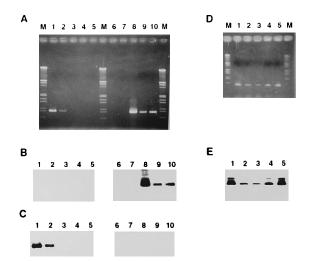


FIG. 3. Amplification of DNA fragments from *C. botulinum* type C and D strains. PCR was performed with the culture supernatants of Dsa (lanes 1 and 6), D4947 (lanes 2 and 7), C6812 (lanes 3 and 8), C6813 (lanes 4 and 9), and C6814 (lanes 5 and 10) and the primer pairs LDV2/RGN (lanes 1 to 5 in panels A, B, and C), LDV2/SVS (lanes 6 to 10 in panels A, B, and C), and YQA/LDV (lanes 1 to 5 in panels D and E). The reaction mixtures were subjected to agarose electrophoresis. The resulting gels were stained with ethidium bromide (A and D). PCR products in gels were transferred to sheets of nylon membrane and subjected to DNA-DNA hybridization. The PCR product from Dsa amplified by LDV2/RGN (C) or YQA/LDV (E) was used as a probe. The PCR product from C6813 amplified by primer pair LDV2/SVS (B) was also used as a probe. Autoradiograms are shown in panels B, C, and E.

BN/C1 gene. The DNA fragment of the expected size of 0.5 kbp was amplified from C6813 by the primer pair C9/C10, which targets the region extending from C-3358 to C-3906 in the BN/D gene. Amplified fragments were ligated to the T-vector and then sequenced.

The coding region in the connected sequence encodes a neurotoxin composed of 1,280 amino acids and with a molecular weight of 147,813 (Fig. 4). The deduced amino acid sequence has 77 and 71% identity to BN/C1 and BN/D, respectively (Fig. 5). The putative nicking site is located at the C terminus of Lys-449, as expected from the amino acid homology to BN/C1. The light chain (Met-1 to Lys-449) of the deduced neurotoxin has 97 and 48% identity to those of BN/C1 and BN/D, respectively, whereas the heavy chain (Thr-450 to Glu-1280) of the deduced protein has 66 and 85% identity to those of BN/C1 and BN/D, respectively. These comparative analyses are consistent with the finding reported by Terajima et al. (28) that the light and heavy chains of the purified BN/C6813 are similar to the BN/C1 light chain and the BN/D heavy chain, respectively.

The comparative analyses of BN/C6813, BN/C1, and BN/D (Fig. 5) indicate that BN/C6813, BN/C1, and BN/D are each composed of three regions: N-terminal (Met-1 to Leu-526 in BN/C6813 or BN/C1, Met-1 to Asn-521 in BN/D), core (Pro-527 to Val-901 in BN/C6813, Pro-527 to Leu-901 in BN/C1, Pro-522 to Leu-897 in BN/D), and C-terminal (Asn-902 to Glu-1280 in BN/C6813, Asn-902 to Glu-1291 in BN/C1, Asn-902 to Glu-1276 in BN/D) regions. The N-terminal region of BN/C6813 has 96 and 45% identity to those of BN/C1 and BN/D, respectively. The core region is conserved among three toxins (81 to 93% identity). The C-terminal region of BN/C6813 has 36 and 95% identity to those of BN/C1 and BN/D, respectively. Thus, BN/C6813 is the mosaic molecule composed of parts of BN/C1 and BN/D.

The neurotoxin from C6812 has antigenic structures similar

to those of the BN/C1 light chain and the BN/D heavy chain, because antibody to the BN/C1 light chain or BN/D heavy chain could neutralize the toxicity of the neurotoxin from C6812 (20). The DNA fragments of the expected size of 0.8 kbp that were amplified from C6812, C6814, and C6813 with the primer pair LDV2/SVS but not with LDV2/RGN could hybridize with the labeled product from C6813 (Fig. 3A, B, and C), suggesting their nucleotide sequences are quite similar. On the other hand, the DNA fragments of the expected size of 0.5 kbp that were amplified from C6812, C6813, C6814, Dsa, and D4947 by the primer pair YQA/LVD could hybridize with the labeled product from Dsa (Fig. 3D and E). In addition, the DNA fragments of the expected sizes were amplified from the strains of C. botulinum type C, but not from Dsa, by the primer pairs C1/C2, C3/C4, C5/C6, and C9/C10 (Table 2). These results suggest that some strains of C. botulinum type C contain the gene encoding the mosaic neurotoxin-like BN/C6813.

The DNA fragment of the expected size of 0.8 kbp that was amplified from Dsa or D4947 by primer pair LDV2/RGN could not hybridize with the product from C6813 amplified by primer pair LDV2/SVS (Fig. 3B and C). The nucleotide sequence of the product from Dsa amplified by primer pair LDV2/RGN has 99 and 65% identity to corresponding regions of BN/C1 and BN/D, respectively (data not shown). However, the DNA fragment of the expected size of 0.5 kbp that was amplified from Dsa by primer pair YQA/LDV could hybridize with the product from C6813 or D4947 amplified by primer pair YQA/LDV. The nucleotide sequence of the product from Dsa amplified by primer pair YQA/LDV was conserved in BN/C1 (99% identity) and BN/D (98% identity). Our previous study (18) has suggested that the neurotoxin from Dsa (BN/ Dsa) has similar antigenic structures for the BN/D light chain and for the BN/C1 heavy chain. Oguma et al. (20) reported that the antibody to the BN/D light chain or the BN/C1 heavy chain neutralized the toxicity of the neurotoxin from D4947 (BN/D4947). Thus, BN/Dsa or BN/D4947 might be composed of an N-terminal region that is quite similar to that of BN/D, the core region that is conserved between BN/C1 and BN/D, and a C-terminal region that is quite similar to that of BN/C1.

All types of botulinum neurotoxin are zinc-dependent endopeptidases, the intracellular substrates of which play an important role in the fusion of synaptic vesicles to plasma membrane (1, 4, 21–23, 31). Light chains of neurotoxins from strains 468, Stockholm, and 6813 of *C. botulinum* type C are composed of same sequence, suggesting their functions are quite similar. Thus, BN/C1 and BN/C6813 should act specifically on the same substrate, HPC-1/syntaxin.

The N-terminal halves of the heavy chains of BN/C6813, BN/C1, and BN/D may exhibit similar properties related to a specific function, because the N-terminal halves of their heavy chains correspond to the core regions that are conserved in BN/C6813, BN/C1, and BN/D. Botulinum neurotoxins have been known to form channels in lipid membranes and vesicles (5, 7, 17). The N-terminal half of the heavy chain of botulinum neurotoxin type A could form channels in lipid membrane (5). The hydrophobic amino acid sequences that exist within core regions of BN/C6813, BN/C1, and BN/D (Gly-655 to Glu-682 in BN/C1, or BN/C6813, Gly-651 to Glu-678 in BN/D) have 91% similarity (50 to 51% identity) to the ion channel-forming motif of botulinum neurotoxin type A, Gly-Ala-Val-Ile-Leu-Leu-Glu-Phe-Ile-Pro-Glu-Ile-Ala-Ile-Pro-Val-Leu-Gly-Thr-Phe-Ala-Leu-Val (17). The N-terminal half of the heavy chain of BN/Dsa might also be quite similar to those of BN/C1, BN/D, and BN/C6813, because the nucleotide sequence of the PCR product from Dsa amplified by primer pair YQA/LDV has 99% identity to that of the product from C6813 amplified

10 20 30 40 atgccaataacaattaacaactttaattattcagatcctgttgataataaaaatatttta M P I T I N N F N Y S D P V D N K N I L 70 80 90 100 110 120 tatttagatactcatttaaatacattagctaatgagcctgaaaaagcctttcgcattata Y L D T H L N T L A N E P E K A F R I I 130 140 150 160 170 180 gggaatatatgggtaatacccgatagatttcaaggagattctaatccaatttaaataa G N I W V I P D R F S R D S N P N L N K 190 200 210 220 230 240 ctcctcgagttacaagccctaaaagtggttattatgatcctaattatttgagtactgat P P R V T S P K S G Y Y D P N Y L S T D 250 260 270 280 290 3 300 tctgaaaaagatacatttttaaaagaaattataaagttatttaaaagaattaactctaga S E K D T F L K E I I K L F K R I N S 310 320 330 340 350 360
 Gaaataggagaagaattaatatatagactigcaacagacataccctttcctgggaataac

 E I G E E L I Y R L A T D I P F P G N N

 370
 380

 390
 400
 410
aatactccaattaatacttttgattttgatgtagattttaacagtgttgatgttaaaact N T P I N T F D F D V D F N S V D V K T 430 440 450 460 470 4 agacaaggtaacaactgggttaaaactggtagtataaatcctagtgttataataactgga R Q G N N W V K T G S I N P S V I I T G 490 500 510 520 530 540 600 gcggcacaagaaggatttggtgctttatcaataatttcaatatcacctagatttatgcta A A Q E G F G A L S I I S I S P R F M 610 620 630 640 650 acatatagtaatgcaactaataatgtaggaggggggaggtagattttctaagtctgaatttgc T Y S N A T N N V G E G R F S K S E F C 670 680 690 700 710 720 atggatccaatactaatttaatgcatgaatctaatcaatgcataatttaatgga M D P I L I L M H E L N H T M H N L Y G 730 740 750 760 770 780 780 atagetataceaaatgateaaagaattteatetgtaactagtaatatttttatteteaa I A I P N D Q R I S S V T S N I F Y S Q 790 800 810 820 830 84 tataaggtgaaattagagtatgcagaaatatatgcatttggaggtccaactatagacctt Y K V K L E Y A E I Y A F G G P T I D L 850 860 870 880 890 900 attectaaaagtggaaggaaatattttgaggaaaaggcattggattattatagatecata I P K S G R K Y F E E K A L D Y Y R S I 910 920 930 940 950 94 960 AKRLNSITTANPSSFNKYIG 970 980 990 1000 1010 10 gaatataaacagaaacttattagaaagtatagattcgtagtagaatcttcaggtgaagtt E Y K Q K L I R K Y R F V V E S S G E V 1030 1040 1050 1060 1070 1080 gcagtagatcgtaataagtttgctgagttatataaagaactttaccagaa A V D R N K F A E L Y K E L T Q I F T E 1090 1100 1110 1120 1130 1140 tttaactacgctaaaatatatatatgtacaaataggaaaatatatctttcaaatgtatat FNYAKIYN V QNRKIYL SNVY 1150 1160 1170 1180 1190 12 actccggttacggcaaatatattagacgataatgtttatgatatacaaaatggatttaac T P V T A N I L D D N V Y D I Q N G F N 1210 1220 1230 1240 1250 1260 atacctaaaagtaatttaaatgtactatttatgggtcaaatttatctcgaaatccaaca I P K S N L N V L F M G Q N L S R N P A 1270 1280 1290 1300 1310 1320 K V N P E N M L Y L F T K F C H K A 1330 1340 1350 1360 1370 13 LRK atagatggtagatcattatataataaaacattagattgtagagagcttttagttaaaaat G R S L Y N K T L D C R E L L V K 1390 1400 1410 1420 1430 1440 actgacttaccctttataggtgatattagtgatatcaaaactgatatatttttaagcaaa T D L P F I G D I S D I K T D I P L S K 1450 1460 1470 1480 1490 1500 gatattaatgttgaaactgaagttatagactatccggacaatgtttcagtggatcaagtt D I N V E T E V I D Y P D N V S V 1510 1520 1530 1540 1550 DQV atteteagtaagaataceteagaacatggacaaetagattattataaceetattattgaa I L S K N T S E H G Q L D L L Y P I I E 1570 1580 1590 1600 1610 1620 ggtgaggtcaagtattaccgggaggaatcaagtcttttatgatatagaatcaag G E S Q V L P G E N Q V F Y D N R T Q N 1630 1640 1650 1660 1670 1680 gttgattatttgaattcttattattacctagaatctcaaaaactaagtgataatgttgaaV D Y L N S Y Y Y L E S Q K L S D N V 1690 1700 1710 1720 1730 gattttacttttacgacatcaattgaggaagctttggataatagtggaaaagtatatact D F T F T T S I E E A L D N S G K V Y T 1750 1760 1770 1780 1790 1800 tactttcctaaactagctgataaagtaaatacgggtgttcaaggtggttttaattttaatg Y F P K L A D K V N T G V Q G G L F L M 1810 1820 1830 1840 1850 1860 tgggcaaatgatgtagttgaagattttactacaaatattctaagaaaagatacattagat
 WANDVVEDFTTNILRKDTLD

 1870
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 aaaatatcagatgtatcagctattattccctatataggacctgcattaaatataagtaat K I S D V S A I I P Y I G P A L N I S N 1930 1940 1950 1960 1970 1980

(-145) attgtataacattttcatataatga

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taacaaggtgcctaaaggcgcacatttgtggatattagaaagttaggagatgttagtatt

1990 2000 2010 2020 2030 2040 gaagcgtttcaagaatttacaatacctgcacttggtgcatttgtgatttatagtaaggtt E A F Q E F T I P A L G A F V I Y S K V 2050 2060 2070 2080 2090 2100 caagaaagaaacgagattattaaaactatagataattgtttagaacaaaggattaaaaga ...аа _ к I К 2150 ан Q E R N E I I K T I D N C L E Q 2110 2120 2130 2140 2 2160 tggaaagattcatatgaatggatgataggaacgtggttatccaggattactactcatt W K D S Y E W M I G T W L S R I T T Q F 2170 2180 2190 2200 2210 2220 aataatataagttatcaaatgtatgattctttaaattatcaggcagatgcaatcaaagat N N I S Y Q M Y D S L N Y Q A D A I K D 2230 2240 2250 2260 2270 226 aaaatagatttagaatataaaaaatactcaggaagtgataaagaaaatataaaaaggccaa K I D L E Y K K Y S G S D K E N I K S Q 2290 2300 2310 2320 2330 2340 gttgaaaatttaaaaatagtttagatataaaatctcggaagcaatgaataatataaat V E N L K N S L D I K I S E A M N N I N 2350 2360 2370 2380 2390 2400 aatttatacgagaatgttctgtaacatacttatttaaaaatatgctccctaaagtaatt K F I R E C S V T Y L F K N M L P K V 2410 2420 2430 2440 2450 2460 DELNKFDLKTKTELINLI 2470 2480 2490 2500 2510 2520
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 <thL gaaaatacaataccetttaatattttttcatatactaataattetttattaaaagatata ENTIPFNIFSYTNNSLLKD 2590 2600 2610 2620 2630 attaatgaatatttcaatagtattaatgattcaaaaattttgagcttacaaaacaaaaa I N E Y F N S I N D S K I L S L Q N K K 2650 2660 2670 2680 2690 2700 aatgotttagtggatacatcaggatataatgcaggaggtagggtgaggtgatgtcaa N A L V D T S G Y N A E V R L E G D V Q 2710 2720 2730 2740 2750 2760 gttaatacgatatatacaaatgattttaaattaagtagttcaggagataaaattatagta N T TIYTNDFKLSSSGDKII 2770 2780 2790 2800 2810 2820 aatttaaataataatatttatatagegetatttatgagaaetetagtgttagtttttgg N 1. N N N T I. Y S B T V F N C C V C F M N L N N N I L Y S A I Y E N S S V S F 2830 2840 2850 2860 2870 2880 aaacaaaattctgggtggaaattatgtattaggaatggcaatatagaatggattttacaa K Q N S G W K L C I R N G N I E W I L 2950 2960 2970 2980 2990 gatattaatagaaagtataaaagtttaattttgattatagtgaatcattaagtcataca D I N R K Y K S L I F D Y S E S L S H T 3010 3020 3030 3040 3050 3060 tttatataaatggagaattaaagcagagtgaaagaattgaagatttaaatgaggttaag LYINGELKQSERIEDLNEV 3130 3140 3150 3160 3170 3180 ttagataaaaccatagtatttggaatagatgagaatatagatgagaatcagatgctttgg L D K T I V F G I D E N I D E N Q M L W 3190 3200 3210 3220 3230 3240 attagagatttaatattttttctaaagattaagcaatgaagatattaatattgtatat I R D F N I F S K E L S N E D I N I V Y 3250 3260 3270 3280 3290 3300 gagggacaaatattaagaaatgttattaaagattattggggaaatcctttgaagtttgat E G Q I L R N V I K D Y W G N P L K F 3310 3320 3330 3340 3350 3360 acagaatattatattattatgataattatatagataggtatataggcactaaaagtaat T E Y Y I I N D N Y I D R Y I A P K S N 3370 3380 3390 3400 3410 3420 atacttgtacttgttcagtatccagatagatctaaattatatatggaaatcctattact I L V L V Q Y P D R S K L Y T G N P I T 3430 3440 3450 3460 3470 3480 attaaatcagtatctgataagaatccttatagtagaattttaaatggagataatataatg S V S D K N P Y S R I L N G D N I M 3490 3500 3510 3520 3530 35 IKS tttcatatgttatataatagtgggaaatatatgataataagagatactgatacaatatat F H M L Y N S G K Y M I I R D T D T I 3550 3560 3570 3580 3590 3600 gcaatagaaggaaggagtgttcaaaaattgtgtgtatagcattaaaattacagagtaat A I E G R E C S K N C V Y A L K L Q S N 3610 3620 3630 3640 3650 3660 3660 L G N Y G I G I F S I K N I V S Q N K Y 3670 3680 3690 3700 3710 3720 tgtagtcaaattttctctagttttatgaaaaatacaatgcttctagcagatatataaaa C S Q I F S S F M K N T M L L A D I Y K 3730 3740 3750 3760 3770 3780 ccttggagatttctttgaaaatgcatacacgccagttgcagtaactaattatgagaca P W R F S F E N A Y T P V A V T N Y E T 3790 3800 3810 3820 3830 3840 ctattatcaacttcatctttttggaaatttatttctagggatccaggatgggtagag KLLSTSSFWKFISRDPGW 3850 3860 3870 3880 3890 taatacaataaaaatttaatataaactattaaattatattacaagttttggaaattta

FIG. 4. Nucleotide sequence and deduced amino acid sequence of the BN/C6813 gene. The deduced amino acid sequence is shown under the nucleotide sequence. The dot underline (aggaga near the top, left column) and asterisks indicate a ribosome binding site and the termination codon, respectively.

C68 1'	MPITINNFNYSDPVDNKNILYLDTHLNTLANEPEKAFRIIGNIWVIPDRFSRDSNPNLNK	660'	LEAFQEFTIPALGAFVIYSKVQERNEIIKTIDNCLEQRIKRWKDSYEWMIGTWLSRITTQ
C1 1	**************************************	660	****p*********************************
D 1	*TWPVKD******NDND****RIPQ*K*ITT*V***M*TQ*****E***S*T**S*S*	556	**G*P*******V*TF**SI***EK****E****V*****Q**VSN*******
61'	PPRVTSPKSGYYDPNYLSTDSEKDTFLKEIIKLFKRINSREIGEELIYRLATDIPFPGNN	720'	FNNISYQMYDSLNYQADAIKDKIDLEYKKYSGSDKENIKSQVENLKNSLDIKISEAMNNI
61	**************************************	720	***************G***A******************
61	***P**KYQS****S****EQ*****G******E*D**KK**NY*VVGS**M*DS		**H*N******S*****A***A******************
121'	NTPINTFDFDVDFNSVDVKTRQGNNWVKTGSINPSVIITGPRENIIDPETSTFKLTNNTF	780'	NKFIRECSVTYLFKNMLPKVIDELNKFDLKTKTELINLIDSHNIILVGEVDRLKAKVNES
121	***************************************	780	**************************************
121	S**ED****TRHTTNIA*EKFENGS*KV*NI*T***L*F**LP**L*YTA*LTLQGQQSN	776	**************************************
181'	AAQEGFGALSIISISPRFMLTYSNATNNVGEGRFSKSEFCMDPILILMHELNHTMHNLYG	840'	FENTIPFNIFSYTNNSLLKDIINEYFNSINDSKILSLONKKNALVDTSGYNAEVRLEGDV
181	****************************D*********	840	*Q************************************
181	PSF****T***LKVA*E*L**F*DV*S*QSSAVLG**I*****VIA*****T*SL*Q***	836	****M*********************************
241'	IAIPNDQRISSVTSNIFYSQYKVKLEYAEIYAFGGPTIDLIPKSGRKYFEEKALDYYRSI	900'	QVNTIYTNDFKLSSSGDKIIVNLNNNILYSAIYENSSVSFWIKISKDLTNSHNEYTI
241	******T************N******************	900	*L*P*FPF****G***EDRG*V**TQ*E**V*NSM**SF*I****R*N*-WVSNLPG***
241	*N**S*K**RPQV*EG*F**DGPNVQFE*L*T***LDVEI**QIE*SQLR****GH*KD*	896	*L*************************************
301'	AKRLNSITTANPSSFNKYIGEYKQKLIRKYRFVVESSGEVAVDRNKFAELYKELTQIFTE	957'	
301	**************************************	958	*D*V*N****SIG*ISNFLVFT*KQNEDSEQ*IN*S*DI*NNAP**-******V***M*
301	*****N*NKTI***WISN*DK**KIFSE**N*DKDNT*NFV*NID**NS**SD**NVMS*	953	****E*********************************
361'	FNYAKIYNVQNRKIYLSNVYTPVTANILDDNVYDIQNGFNIPKSNLNVLFMGQNLSRNPA	1017'	GYMKLYINGELKQSERIEDLNEVKLDKTIVFGIDENIDENQMLWIRDFNIFS
361	***************************************	1018	*N**I****K*IDTIKVKE*TGINFS***T*EINKIPDT*LITSDSD*INM*****Y**A
361	VV*SSQ***K**TH*F*RH*L**F******I*T*RD***LTNKGF*IENS***IE****	1013	**************************************
	LRKVNPENMLYLFTKFCHKAIDGRSLYNKTLDCRELLVKNTDLPFIGDISDIKTDIFLSK	1068'	
421	**************************************	1078	***DGK****LFNSLQYT**V****D*RYNK***MV*ID*LN**MYAN*RQI*FNTRR
421	*Q*LSS*SVVD****V*LRLTKNSRDDS-T*IK***NR**YVA*KDS*SQE**EN*	1065	**************************************
481'	DINVETEVIDYPDNVSVDQVILSKNTSEHGQLDLLYPIIEGESQVLPGENQVFYDNRTQN	1129'	DRSKLYTGNPITIKSVSDKNPYSRILNGDNIMFHMLYNSGKYMIIRDTDTIYAIEGRECS
481	***E****Y*****************************	1138	NNNDFNE*YK*I**RIRGNTNDT*VRG**ILY*D*TI*NKA*NLFMKNE*M**-DNHSTE
476	I*TD**N*QN*S*KF*L*ES**DGQVPINPEIV*P*L*NVNM*PLN****EI****DI*K	1125	**************************************
541'		1189'	KNCVYALKLQSNLGNYGIGIFSIKNIVSQNKYCSQIF-SSFMKNTML-LADIYKPWRFSF
541	-*************************************	1137	DIYAIG*RE*TKDI*DN*-**Q*QPMNNTYY*A****K*N*NGENISGICS*-GTY**RL
536	Y******************N***NI*L***V****GY*N*I**FL*S**E***K***A****	1185	Q*************************************
600'	MWANDVVEDFTTNILRKDTLDKISDVSAIIPYIGPALNISNSVRRENFTEAFAVTGVTIL	1247'	ENAYTPVAVTNYETKLLSTSSFWKFISRDPGWVE
600	**********G*****************	1255	GGDWYRHN*LVPT*KQG**ASL*E***TH*G*VPVSE
596	N***E********MK************V*****G**AL*G**NQ***TA**AF*	1243	K*******************************

FIG. 5. Comparison of the amino acid sequence of BN/C6813 with that of BN/C1 or BN/D. Dashes and asterisks denote gaps and homologous residues, respectively. The sequences of BN/C1 and BN/D are as cited in reports by Kimura et al. (12) and Binz et al. (2), respectively.

by primer pair YQA/LDV (data not shown). The core regions of neurotoxins from strains of *C. botulinum* types C and D may exhibit similar channel-forming abilities.

BN/C1 could bind to a receptor different from the receptor for BN/D on the target cells (32). A monoclonal antibody recognizing the sequence within the C-terminal 50 amino acids of the BN/C1 heavy chain could inhibit the binding of the whole toxin to neuroblastoma cells, suggesting that the binding domain of the target cell is located on the C-terminal 50 amino acids of the heavy chain (13). BN/C6813 might not bind to the receptor for BN/C1, because the C-terminal 50 amino acids of BN/C6813 were quite different from those of BN/C1 but were the same as those of BN/D. Thus, BN/C6813 might bind to the receptor for BN/D.

A *C. botulinum* type C organism has been known to produce either of two types of ADP-ribosyltransferase C3: the D1873 type or the Dsa type (19). both isoforms have 66% amino acid homology. Although type C strains 468 and Stockholm could produce BN/C1 and D1873-type C3, type C strains 6812, 6813,

TABLE 2. Detection of PCR products from C. botulinumtype C and D organisms

Tem- plate	Detection of PCR product after amplification with primer pair ^a						
	C1/C2	C3/C4	C5/C6	YQA/LDV	LVD2/RGN	LDV2/SVS	C9/C10
C6812	+	+	+	+	_	+	+
C6813	+	+	+	+	_	+	+
C6814	+	+	+	+	-	+	+
Dsa	-	-	-	+	+	-	_

 a +, a DNA fragment of the expected size in the reaction mixture after the PCR could be detected on an agarose gel stained with ethidium bromide; –, no DNA fragment of the expected size in the PCR mixture could be detected on an agarose gel stained with ethidium bromide, even if the PCR cycle was repeated after addition of *Taq* DNA polymerase to the mixture.

and 6814 could produce BN/C6813 and Dsa-type C3. A C3 gene and a neurotoxin gene from a type C organism have been shown to be located on a toxigenic bacteriophage (19). Hauser et al. (11) suggested that a 21.5-kbp DNA fragment carrying the C3 gene in C468, Cst, and D1873 phage might be a putative transposable element. However, the mechanisms of the construction of mosaic neurotoxin genes from type C and D organisms have not been clarified. Further analyses of several genetic events involved in the evolution and construction of the botulinum neurotoxin gene are necessary for exact diagnosis and effective treatment of botulism.

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