(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
23 August 2007 (23.08.2007)

PCT

(10) International Publication Number
WO 2007/094754 A2

(51) International Patent Classification: Not classified

(21) International Application Number: PCT/US2006/003070

(22) International Filing Date: 26 January 2006 (26.01.2006)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/648,256 27 January 2005 (27.01.2005) US

(71) Applicant *(for all designated States except US)*: **THE REGENTS OF THE UNIVERSITY OF CALIFORDNIA** [US/US]; 1111 Franklin Street, 12th Floor, Oakland, CA 94607-5200 (US).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: **MARKS, James, D.** [US/US]; 107 Ardmore Road, Kensington, CA 94707 (US). **AMERSDORFER, Peter** [US/US]; 3802 Nykonos Lane, #23, San Diego, CA 92130 (US). **GEREN, Isin** [US/US]; 560 Alabama Street #303, San Francisco, CA 94110 (US). **LOU, Jianlong** [US/US]; 5127 Shelter Creek Lane, San Bruno, CA 94066 (US). **RAZAI, Ali** [US/US]; 1366 Turk Stret #3A, San Francisco, CA 94115 (US). **GARCIA, Maria, Consuelos** [US/US]; 2515 24th Street #4, San Francisco, CA 94110 (US).

(74) Agent: **HUNTER, Tom**; Beyer Weaver LLP, P.O. Box 70250, Oakland, CA 94612-0250 (US).

(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, LY, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NG, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SM, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LT, LU, LV, MC, NL, PL, PT, RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

— *without international search report and to be republished upon receipt of that report*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 2007/094754 A2

(54) **Title:** THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM NEUROTOXINS

(57) **Abstract:** This invention provides antibodies that specifically bind to and neutralize botulinum neurotoxin type A (BoNT/ A) and the epitopes bound by those antibodies. The antibodies and derivatives thereof and/or other antibodies that specifically bind to the neutralizing epitopes provided herein can be used to neutralize botulinum neurotoxin and are therefore also useful in the treatment of botulism.

THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM NEUROTOXINS

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims priority to and benefit of USSN 60/648,256, filed January 27, 2005, which is incorporated herein by reference in its entirety for all purposes.

STATEMENT AS TO RIGHTS TO INVENTIONS MADE UNDER FEDERALLY SPONSORED RESEARCH AND DEVELOPMENT

[0002] This invention was made with Government support by Grant No: AI53389 and AI56493, awarded by the National Institutes of Health, and by Department of Defense Grants DAMD17-03-C-0076 and DAMD17-98-C-8030. The Government has certain rights in this invention.

FIELD OF THE INVENTION

[0003] This invention relates antibodies that neutralize botulinum neurotoxins (*e.g.*, BoNT/A) and their use in the treatment of botulism.

BACKGROUND OF THE INVENTION

[0004] Botulism is caused by botulinum neurotoxin secreted by members of the genus *Clostridium* and is characterized by flaccid paralysis, which if not immediately fatal requires prolonged hospitalization in an intensive care unit and mechanical ventilation. Naturally occurring botulism is found in infants or adults whose gastrointestinal tracts become colonized by Clostridial bacteria (infant or intestinal botulism), after ingestion of contaminated food products (food botulism), or in anaerobic wound infections (wound botulism) (Center for Disease Control (1998) Botulism in the United States, 1899-1998. Handbook for epidemiologists, clinicians,and laboratory workers. Atlanta, Georgia U.S. Department of Health and Human Services, Public Health Service: downloadable at "www.bt.cdc.gov/agent/botulism/index.asp"). Botulism neurotoxins (BoNTs) are also classified by the Centers for Disease Control (CDC) as one of the six highest-risk threat agents for bioterrorism (the "Category A agents"), due to their extreme potency and lethality, ease of production and transport, and need for prolonged intensive care (Arnon *et al.* (2001) *JAMA* 285: 1059-1070). Both Iraq and the former Soviet Union produced BoNT for use as weapons (United Nations Security Council (1995) Tenth report of the executive committee of the special commission established by the secretary-general pursuant to paragraph 9(b)(I) of security council resolution 687 (1991), and paragraph 3 of resolution 699 (1991) on the activities of the Special Commision; Bozheyeva *et al.* (1999) Former soviet biological weapons facilities in Kazakhstan: past, present, and future. Center for Nonproliferation Studies, Monterey Institute of International Studies), and the Japanese cult Aum Shinrikyo attempted to use BoNT for bioterrorism (Arnon *et al.* (2001) *supra*). As a result of these threats, specific pharmaceutical agents are needed for prevention and treatment of intoxication.

[0005] No specific small molecule drugs exist for prevention or treatment of botulism, but an investigational pentavalent toxoid vaccine is available from the CDC (Siegel (1988) *J. Clin. Microbiol.* 26: 2351-2356) and a recombinant vaccine is under development (Smith (1998) *Toxicon* 36: 1539-1548). Regardless, mass civilian or military vaccination is unlikely due to the rarity of disease or exposure and the fact that vaccination would prevent subsequent medicinal use of BoNT. Post-exposure vaccination is useless, due to the rapid onset of disease. Toxin neutralizing antibody (Ab) can be used for pre- or post-exposure prophylaxis or for treatment (Franz *et al.* (1993) Pp. 473-476 In B. R. DasGupta (ed.), Botulinum and Tetanus Neurotoxins: Neurotransmission and Biomedical Aspects. Plenum Press, New York). Small quantities of both equine antitoxin and human botulinum immune globulin exist and are currently used to treat adult (Black and Gunn. (1980) *Am. J. Med.*, 69: 567-570; Hibbs *et al.* (1996) *Clin. Infect. Dis.*, 23: 337-340) and infant botulism (Arnon (1993). Clinical trial of human botulism immune globulin., p. 477-482. In B. R. DasGupta (ed.), Botulinum and Tetanus Neurotoxins: Neurotransmission and Biomedical Aspects. Plenum Press, New York) respectively.

[0006] Recombinant monoclonal antibody (mAb) could provide an unlimited supply of antitoxin free of infectious disease risk and not requiring human donors for plasmapheresis. Given the extreme lethality of the BoNTs, mAbs must be of high potency in order to provide an adequate number of doses at reasonable cost. The development of such mAbs has become a high priority research aim of the National Institute of Allergy and Infectious Diseases. While to date no single highly potent mAbs have been described, we recently reported that combining two to three mAbs could yield highly potent BoNT neutralization (Nowakowski *et al.* (2002) *Proc. Natl. Acad. Sci. U S A*, 99: 11346-50).

[0007] The development of mAb therapy for botulism is complicated by the fact that there are at least seven BoNT serotypes (A-G) (Hatheway (1995) *Curr. Top. Microbio. Immunol*, 195: 55-75.) that show little, if any, antibody cross-reactivity. While only four of the BoNT serotypes routinely cause human disease (A, B, E, and F), there has been one reported case of infant botulism caused by BoNT C (Oguma *et al.* (1990) *Lancet* 336: 1449-1450), one outbreak of foodborne botulism linked to BoNT D (Demarchi, *et al.* (1958) *Bull. Acad. Nat. Med.*, 142: 580-582), and several cases of suspicious deaths where BoNT G was isolated (Sonnabend *et al.* (1981) *J. Infect. Dis.*, 143: 22-27). Aerosolized BoNT/C, D, and G have also been shown to produce botulism in primates by the inhalation route (Middlebrook and Franz (1997) Botulinum Toxins, chapter 33. In F.R. Sidell, E.T. Takafuji, D.R. Franz (eds.), Medical Aspects of Chemical and Biological Warfare. TMM publications, Washington, D.C.), and would most likely also affect humans. Thus it is likely that any one of the seven BoNT serotypes can be used as a biothreat agent.

[0008] Variability of the BoNT gene and protein sequence within serotypes has also been reported and there is evidence that such variability can affect the binding of monoclonal antibodies to BoNT/A (Kozaki et al. (1998) *Infect. Immun.*, 66: 4811-4816; Kozaki et al. (1995) *Microbiol. Immunol.*, 39: 767-774). It is currently not clear the extent of such toxin variability within the different serotypes, nor its impact on the binding and neutralization capacity of monoclonal antibody panels.

SUMMARY OF THE INVENTION

[0009] This invention pertains to antibodies that bind to and neutralize botulinum neurotoxin(s). We have discovered that particularly effective neutralization of a Botulism neurotoxin (BoNT) serotype can be achieved by the use of neutralizing antibodies that bind two or more subtypes of the particular neurotoxin serotype with high affinity. While this can be accomplished by using two or more different antibodies directed against each of the subtypes, in certain embodiments even more efficient neutralization is achieved by the use of one or more antibodies where each antibody is cross-reactive with at least two BoNT subtypes. In certain embodiments this invention provides for compositions comprising neutralizing antibodies that bind two or more BoNT subtypes (*e.g.*, BoNT/A1, BoNT/A2, BoNT/A3, *etc.*) with high affinity.

[0010] Thus, in one embodiment, this invention provides a method of neutralizing botulinum neurotoxin in a mammal (*e.g.*, a human). The method typically involves administering to the mammal at least two different neutralizing antibodies for a BoNT serotype, wherein at least one of the two antibodies binds at least two different subtypes of said BoNT serotype (*e.g.*, BoNT/A, BoNT/B, BoNT/C, BoNT/D, BoNT/E, BoNT/F, *etc.*) with an affinity greater than about 10 nM. In certain embodiments at least one of the antibodies binds at least two different subtypes selected from the group consisting of BoNT/A1, BoNT/A2, BoNT/A3, and BoNT/A4, each with an affinity greater than about 10 nM. In certain embodiments at least one of the antibodies binds BoNT/A1 and BoNT/A2 each with an affinity greater than about 10 nM. In certain embodiments both antibodies simultaneously bind at least one, preferably at least two of the subtypes. In certain embodiments the antibodies each comprise at least one, at least two, at least three, at least 4, at least five, or at least six CDRs selected from the group consisting of RAZ1 VL CDR1, RAZ1 VL CDR2, RAZ1 VL CDR3, RAZ1 VH CDR1, RAZ1 VH CDR2, RAZ1 VH CDR3, 1D11 VL CDR1, 1D11 VL CDR2, 1D11 VL CDR3, 1D11 VH CDR1, 1D11 VH CDR2, 1D11 VH CDR3, 2G11 VL CDR1, 2G11 VL CDR2, 2G11 VL CDR3, 2G11 VH CDR1, 2G11 VH CDR2, 2G11 VH CDR3, 5G4 VL CDR1, 5G4 VL CDR2, 5G4 VL CDR3, 5G4 VH CDR1, 5G4 VH CDR2, 5G4 VH CDR3, 3D12 VL CDR1, 3D12 VL CDR2, 3D12 VL CDR3, 3D12 VH CDR1, 3D12 VH CDR2, 3D12 VH CDR3, CR1 VL CDR1, CR1 VL CDR2, CR1 VL CDR3, CR1 VH CDR1, CR1 VH CDR2, CR1 VH CDR3, CR2 VL CDR1, CR2 VL CDR2, CR2 VL CDR3, CR2 VH CDR1, CR2 VH CDR2, CR2 VH CDR3, ING1 VL CDR1, ING1 VL CDR2, ING1 VL CDR3, ING1 VH CDR1, ING1 VH CDR2, ING1 VH CDR3, ING2 VL CDR1, ING2 VL CDR2, ING2 VL CDR3, ING2 VH CDR1, ING2 VH CDR2, and ING2 VH CDR3 (*see, e.g.*, Figures 18, and 26, Tables 2 and/or Table 13, *etc.*). In various embodiments the antibodies each comprise a VH CDR1, CDR2, and CDR3 all selected from a VH domain selected from the group consisting of a RAZ1 VH domain, a CR1 VH domain, an ING1 VH domain, an ING2 VH domain, a 1D11 VH domain, a 2G11 VH domain, a 3D12 VH domain, and a 5G4 VH domain. In various embodiments the antibodies each comprise a VL CDR1, CDR2, and CDR3 all selected from a VL domain selected from the group consisting of a RAZ1 VL domain, a CR1 VL domain, a CR2 VL domain, an ING1 VL domain, an ING2 VL domain, a 1D11 VL domain, a 2G11 VL domain, a 3D12 VL domain, and a 5G4 VL domain. In certain embodiments the antibodies each comprise: a VH CDR1, CDR2, and CDR3 all selected from a VH domain selected from the group consisting of a RAZ1 VH domain, a CR1 VH domain, a CR2 VH domain, an ING1 VH domain, an ING2 VH domain, a 1D11 VH domain, a 2G11 VH domain, a 3D12 VH domain, and a 5G4 VH domain; and a VL CDR1, CDR2, and CDR3 all selected from a VL domain selected from the group consisting of a RAZ1 VL domain, a CR1 VL domain, a CR2 VL domain, an ING1 VL domain, an ING2 VL domain, a 1D11 VL domain, a 2G11 VL domain, a 3D12 VL domain, and a 5G4 VL domain. In certain embodiments at least one of said antibodies comprises a VH CDR1, VH CDR2, VH CDR3, VL CDR1, VL CDR2, and VL CDR3 selected from an antibody selected from the group consisting of RAZ1, CR1, ING1, and ING2. In various embodiments at least one of the antibodies is a single chain Fv (scFv), an IgG, an IgA, an IgM, an Fab, an $(Fab')_2$, or an $(scFv')_2$. In certain embodiments at least one of said antibodies is selected from the group consisting of RAZ1, CR1, CR2, ING1, ING2, 2G11, 3D12, and 5G4.

[0011] In various embodiments, this invention provides an isolated antibody that specifically binds to an epitope specifically bound by an antibody selected from the group consisting of C25, 1C6, 3D12, B4, 1F3, HuC25, AR1, AR2, AR3, AR4, WR1(V), WR1(T), 3-1, 3-8, 3-10, ING1, CR1, CR2, RAZ1, and/or ING2. In certain embodiments, the antibody binds to and neutralizes one or preferably two or more botulinum neurotoxin subtypes (*e.g.*, BoNT/A1, BoNT/A2, BoNT/A3, *etc.*). The antibody can be of virtually any mammalian animal type (*e.g.* mouse, human, goat, rabbit) or chimeric (*e.g.* humanized), but is most preferably human, or humanized.

[0012] In one embodiment, the antibody comprises at least one (more preferably at least two and most preferably at least three) of the variable heavy (V_H) complementarity determining regions (CDRs) listed in Table 2, and/or Table 6, and/or Table 9 and/or Table 13 and/or Figure 26, or conservative substitutions thereof. In another embodiment, the antibody comprises at least one (more preferably at least two and most preferably at least three) of the variable light (V_L) complementarity determining regions (CDRs) listed in Table 2, and/or Table 6, and/or Table 9 and/or Table 13, and/or Figure 26, or conservative substitutions thereof. In still another embodiment, the antibody comprises at least one (more preferably at least two and most preferably at least three) of the variable heavy (V_H) complementarity determining regions (CDRs) listed in Table 2, and/or Table 6, and/or Table 9 and/or Table 13, and/or Figure 26, or conservative substitutions thereof and at least one (more preferably at least two and most preferably at least three) of the variable light (V_L) complementarity determining regions (CDRs) listed in able 2, and/or Table 6, and/or Table 9 and/or Table 13 and/or Figure 26, or conservative substitutions thereof and/or one, two, or three of the VL or VH framework regions listed in Table 2, and/or Table 6, and/or Table 9 and/or Table 13, and/or Figure 26. Certain preferred antibodies include, but are not limited to C25, 1C6, 3D12, B4, 1F3, HuC25, AR1, AR2, AR3, AR4, WR1(V), WR1(T), 3-1, 3-8, 3-10, ING1, CR1, RAZ1, ING2, 1D11, 2G11, 3D12, and/or 5G4. Certain preferred antibodies include an IgG, a single chain Fv (scFv), while other preferred antibodies include, but are not limited to an IgG, an IgA, an IgM, a Fab, a $(Fab')_2$, a $(scFv')_2$, and the like. In certain embodiments, the antibodies can be multi-valent. The antibodies can include fusion proteins comprising of two scFv fragments.

[0013] This invention also provides for compositions comprising one or more of the botulinum neurotoxin-neutralizing antibodies described herein in a pharamcological excipient.

[0014] This invention also provides BoNT-neutralizing epitopes. Certain preferred epitopes include BoNT/A H_C epitopes specifically bound by C25, 1C6, 3D12, B4, 1F3, HuC25, AR1, AR2, AR3, AR4, WR1(V), WR1(T), 3-1, 3-8, 3-10, ING1, CR1, CR2, RAZ1, ING2, 1D11, 2G11, 3D12, and/or 5G4. Certain preferred polypeptides are not a full-length BoNT and more particularly preferred polypeptides are not a full-length BoNT H_c fragment. Thus, most preferred epitopes are a BoNT/A H_C subsequence or fragment with preferred subsequences having a length of at least 4, preferably at least 6, more preferably at least 8 and most preferably at least 10, 12, 14, or even 15 amino acids. In this regard, it is noted that HuC25 and its derivatives (AR1, 2, 3, 4, and CR1) bind an HC domain that is N-terminal, while 3D12/RAZ1 bind a HC domain that is C-terminal. Neither of these epitopes are linear.

<u>Definitions.</u>

[0015] A "BoNT polypeptide" refers to a Botulinum neurotoxin polypeptide (*e.g.,* a BoNT/A polypeptide, a BoNT/B polypeptide, a BoNT/C polypeptide, and so forth). The BoNT polypeptide can refer to a full-length polypeptide or to a fragment thereof. Thus, for example, the term "BoNT/A polypeptide" refers to either a full-length BoNT/A (a neurotoxin produced by *Clostridium botulinum* of the type A serotype) or a fragment thereof (*e.g.* the Hc fragment). The H_C fragment approximately a 50 Da C-terminal fragment (residues 873-1296) of BoNT/A (Lacy and Stevens (1999) *J. Mol. Biol.*, 291: 1091-1104).

[0016] A "BoNT" serotype refers one of the standard known BoNT serotypes (*e.g.* BoNT/A, BoNT/C, BoNT/D, BoNT/E, BoNT/F, *etc.*). BoNT serotypes differ from each other by as little as about 35% at the amino acid level (*e.g.*, between BoNT/E and BoNT/F) up to about 66% at the amino acid level, (*e.g.*, for BoNT/A vs BoNT/C or D). Thus, BoNT serotypes differ from each other by about 35-66% at the amino acid level.

[0017] The term "BoNT subtype" (*e.g.*, a BoNT/A1A subtype) refers to botulinum neurotoxin gene sequences of a particular serotype (*e.g.*, A, C, D, F, *etc.*) that differ from each other sufficiently to produce differential antibody binding. In certain embodiments, the subtypes differ from each other by at least 2.5%, preferably by at least 5%, or 10%, more preferably by at least 15% or 20% at the amino acid level. In certain embodiments, the subtypes differ from each other by nor more than 35%, preferably by no more than 31.6%, still more preferably by no more than 30%, or 25%, more preferably by less than about 20% or 16% at the amino acid level.. In certain embodiments, BoNT subtypes differ from each other by at least 2.6%, more preferably by at least 3%, and most preferably by at least 3.6% at the amino acid level. BoNT subtypes typically differ from each other by less than about 31.6%, more preferally by less than about 16%, at the amino acid level.

[0018] "Neutralization" refers to a measurable decrease in the toxicity of a Botulinum neurotoxin (*e.g.*, BoNT/A).

[0019] The term "high affinity" when used with respect to an antibody refers to an antibody that specifically binds to its target(s) with an affinity (K_D) of at least about 10^{-8} M, preferably at least about 10^{-9}M, more preferably at least about 10^{-10}M, and most preferably at last about 10^{-11} M. In certain embodiments "high affinity" antibodies have a K_D that ranges from about 1 nM to about 5 pM.

[0020] The following abbreviations are used herein: AMP, ampicillin; BIG, botulinum immune globulin; BoNT, botulinum neurotoxin; BoNT/A, BoNT type A; CDR, omplementarity determining region; ELISA, enzyme-linked immunosorbent assay; GLU, glucose; HBS, HEPES-buffered saline (10 mM HEPES, 150 mM NaCl [pH 7.4]); H_c, c-terminal domain of BoNT heavy chain (binding domain); H_N, N-terminal domain of BoNT heavy chain (translocation domain); IgG, immunoglobutin G; IMAC, immobilized-metal affinity chromatography; IPTG, isopropyl-β-D-thiogalactopyranoside; KAN, kanamycin; K_d, equilibrium constant; k_{off}, dissociation rate constant; k_{on}, association rate constant; MPBS, skim milk powder in PBS; NTA, nitrilotriacetic acid; PBS, phosphate-buffered saline (25 mM NaH_2PO_4, 125 mM NaCl [pH 7.0]; RU, resonance units; scFv, single-chain Fv antibody fragments; TPBS, 0.05% (vol/vol) Tween 20 in PBS; TMPBS, 0.05% (vol/vol) Tween 20 in MPBS; TU, transducing units; V_H, immunoglobulin heavy-chain variable region; V_K, immunoglobulin kappa light-chain variable region; V_L immunoglobulin light-chain variable region; wt, wild type.

[0021] The terms "polypeptide", "peptide", or "protein" are used interchangeably herein to designate a linear series of amino acid residues connected one to the other by peptide bonds between the alpha-amino and carboxy groups of adjacent residues. The amino acid residues are preferably in the natural "L" isomeric form. However, residues in the "D" isomeric form can be substituted for any L-amino acid residue, as long as the desired functional property is retained by the polypeptide. In addition, the amino acids, in addition to the 20 "standard" amino acids, include modified and unusual amino acids, which include, but are not limited to those listed in 37 CFR (1.822(b)(4). Furthermore, it should be noted that a dash at the beginning or end of an amino acid residue sequence indicates either a peptide bond to a further sequence of one or more amino acid residues or a covalent bond to a carboxyl or hydroxyl end group.

[0022] As used herein, an "antibody" refers to a protein consisting of one or more polypeptides substantially encoded by immunoglobulin genes or fragments of immunoglobulin genes. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon and mu constant region genes, as well as myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD and IgE, respectively.

[0023] A typical immunoglobulin (antibody) structural unit is known to comprise a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

[0024] Antibodies exist as intact immunoglobulins or as a number of well characterized fragments produced by digestion with various peptidases. Thus, for example, pepsin digests an antibody below the disulfide linkages in the hinge region to produce $F(ab)'_2$, a dimer of Fab which itself is a light chain joined to V_H-C_H1 by a disulfide bond. The $F(ab)'_2$ may be reduced under mild conditions to break the disulfide linkage in the hinge region thereby converting the $(Fab')_2$ dimer into an Fab' monomer. The Fab' monomer is essentially an Fab with part of the hinge region (*see*, *Fundamental Immunology*, W.E. Paul, ed., Raven Press, N.Y. (1993), for a more detailed description of other antibody fragments). While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such Fab' fragments may be synthesized *de novo* either chemically or by utilizing recombinant DNA methodology. Thus, the term antibody, as used herein also includes antibody fragments either produced by the modification of whole antibodies or synthesized *de novo* using recombinant DNA methodologies. Preferred antibodies include Fab'_2, IgG, IgM, IgA, and single chain antibodies, more preferably single chain Fv (scFv) antibodies in which a variable heavy and a variable light chain are joined together (directly or through a peptide linker) to form a continuous polypeptide.

[0025] An "antigen-binding site" or "binding portion" refers to the part of an immunoglobulin molecule that participates in antigen binding. The antigen binding site is formed by amino acid residues of the N-terminal variable ("V") regions of the heavy ("H") and light ("L") chains. Three highly divergent stretches within the V regions of the heavy and light chains are referred to as "hypervariable regions" which are interposed between more conserved flanking stretches known as "framework regions" or "FRs". Thus, the term "FR" refers to amino acid sequences that are naturally found between and adjacent to hypervariable regions in immunoglobulins. In an antibody molecule, the three hypervariable regions of a light chain and the three hypervariable regions of a heavy chain are disposed relative to each other in three dimensional space to form an antigen binding "surface". This surface mediates recognition and binding of the target antigen. The three hypervariable regions of each of the heavy and light chains are referred to as "complementarity determining regions" or "CDRs" and are characterized, for example by Kabat *et al. Sequences of proteins of immunological interest*, 4th ed. U.S. Dept. Health and Human Services, Public Health Services, Bethesda, MD (1987).

[0026] An S25 antibody refers to an antibody expressed by clone S25 or to an antibody synthesized in other manners, but having the same CDRs and preferably, but not necessarily, the same framework regions as the antibody expressed by clone s25. Similarly, antibodies C25, 1C6, 3D12, B4, 1F3, HuC25, AR1, AR2, AR3, AR4, WR1(V), WR1(T), 3-1, 3-8, 3-10, ING1, CR1, RAZ1, or ING2 refer to antibodies expressed by the corresponding clone(s) and/or to antibodies synthesized in other manners, but having the same CDRs and preferably, but not necessarily, the same framework regions as the referenced antibodies.

[0027] As used herein, the terms "immunological binding" and "immunological binding properties" refer to the non-covalent interactions of the type which occur between an immunoglobulin molecule and an antigen for which the immunoglobulin is specific. The strength or affinity of immunological binding interactions can be expressed in terms of the dissociation constant (K_d) of the interaction, wherein a smaller K_d represents a greater affinity. Immunological binding properties of selected polypeptides can be quantified using methods well known in the art. One such method entails measuring the rates of antigen-binding site/antigen complex formation and dissociation, wherein those rates depend on the concentrations of the complex partners, the affinity of the interaction, and on geometric parameters that equally influence the rate in both directions. Thus, both the "on rate constant" (K_{on}) and the "off rate constant" (K_{off}) can be determined by calculation of the concentrations and the actual rates of association and dissociation. The ratio of K_{off}/K_{on} enables cancellation of all parameters not related to affinity and is thus equal to the dissociation constant K_d. *See, generally*, Davies *et al. Ann. Rev. Biochem.*, 59: 439-473 (1990).

[0028] A "BoNT-neutralizing antibody" refers to an antibody that binds to one or more Botulinum neurotoxin(s) (e.g., BoNT/A1, BoNT/A2, *etc.*) and that by so-binding reduces the toxicity of that BoNT neurotoxin. Thus, for example the term "BoNT/A-neutralizing antibody", as used herein refers to an antibody that specifically binds to a BoNT/A polypeptide (*e.g.* a BoNT/A1 polypeptide), in certain embodiments, to an H_C domain of a BoNT/A polypeptide and that by so-binding reduces the toxicity of the BoNT/A polypeptide. Reduced toxicity can be measured as an increase in the time that paralysis developed and/or as a lethal dosage (*e.g.* LD_{50}) as described herein. Antibodies derived from BoNT-neutralizing antibodies include, but are not limited to, the antibodies whose sequence is expressly provided herein.

[0029] Antibodies derived from BoNT-neutralizing antibodies preferably have a binding affinity of about 1.6 x 10^{-8} or better and can be derived by screening libraries of single chain Fv fragments displayed on phage or yeast constructed from heavy (VH) and light (VL) chain variable region genes obtained from mammals, including mice and humans, immunized with botulinum toxoid, toxin, or BoNT fragments. Antibodies can also be derived by screening phage or yeast display libraries in which a known BoNT-neutralizing variable heavy (V_H) chain is expressed in combination with a multiplicity of variable light (V_L) chains or conversely a known BoNT-neutralizing variable light chain is expressed in combination with a multiplicity of variable heavy (V_H) chains. BoNT-neutralizing antibodies also include those antibodies produced by the introduction of mutations into the variable heavy or variable light complementarity determining regions (CDR1, CDR2 or CDR3) as described herein. Finally BoNT-neutralizing antibodies include those antibodies produced by any combination of these modification methods as applied to the BoNT-neutralizing antibodies described herein and their derivatives.

[0030] A neutralizing epitope refers to the epitope specifically bound by a neutralizing antibody.

[0031] A single chain Fv ("scFv" or "scFv") polypeptide is a covalently linked V_H::V_L heterodimer which may be expressed from a nucleic acid including V_H- and V_L- encoding sequences either joined directly or joined by a peptide-encoding linker. Huston, *et al.* (1988) *Proc. Nat. Acad. Sci. USA*, 85: 5879-5883. A number of structures for converting the naturally aggregated-- but chemically separated light and heavy polypeptide chains from an antibody V region into an scFv molecule which will fold into a three dimensional structure substantially similar to the structure of an antigen-binding site. *See, e.g.* U.S. Patent Nos. 5, 091,513 and 5,132,405 and 4,956,778.

[0032] In one class of embodiments, recombinant design methods can be used to develop suitable chemical structures (linkers) for converting two naturally associated--but chemically separate--heavy and light polypeptide chains from an antibody variable region into a scFv molecule which will fold into a three-dimensional structure that is substantially similar to native antibody structure.

[0033] Design criteria include determination of the appropriate length to span the distance between the C-terminal of one chain and the N-terminal of the other, wherein the linker is generally formed from small hydrophilic amino acid residues that do not tend to coil or form secondary structures. Such methods have been described in the art. *See, e.g.*, U.S. Patent Nos. 5,091,513 and 5,132,405 to Huston *et al.*; and U.S. Patent No. 4,946,778 to Ladner *et al.*

[0034] In this regard, the first general step of linker design involves identification of plausible sites to be linked. Appropriate linkage sites on each of the V_H and V_L polypeptide domains include those which will result in the minimum loss of residues from the polypeptide domains, and which will necessitate a linker comprising a minimum number of residues consistent with the need for molecule stability. A pair of sites defines a "gap" to be linked. Linkers connecting the C-terminus of one domain to the N-terminus of the next generally comprise hydrophilic amino acids which assume an unstructured configuration in physiological solutions and preferably are free of residues having large side groups which might interfere with proper folding of the V_H and V_L chains. Thus, suitable linkers under the invention generally comprise polypeptide chains of alternating sets of glycine and serine residues, and may include glutamic acid and lysine residues inserted to enhance solubility. One particular linker under the invention has the amino acid sequence $[(Gly)_4Ser]_3$ (SEQ ID NO:1). Another particularly preferred linker has the amino acid sequence comprising 2 or 3 repeats of $[(Ser)_4Gly]$ (SEQ ID NO:2), such as $[(Ser)_4Gly]_3$ (SEQ ID NO:3), and the like. Nucleotide sequences encoding such linker moieties can be readily provided using various oligonucleotide synthesis techniques known in the art. *See, e.g.,* Sambrook, *supra.*

[0035] The phrase "specifically binds to a protein" or "specifically immunoreactive with", when referring to an antibody refers to a binding reaction which is determinative of the presence of the protein in the presence of a heterogeneous population of proteins and other biologics. Thus, under designated immunoassay conditions, the specified antibodies bind to a particular protein and do not bind in a significant amount to other proteins present in the sample. Specific binding to a protein under such conditions may require an antibody that is selected for its specificity for a particular protein. For example, BoNT/A-neutralizing antibodies can be raised to BoNT/A protein)s that specifically bind to BoNT/A protein(s), and not to other proteins present in a tissue sample. A variety of immunoassay formats may be used to select antibodies specifically immunoreactive with a particular protein. For example, solid-phase ELISA immunoassays are routinely used to select monoclonal antibodies specifically immunoreactive with a protein. See Harlow and Lane (1988) Antibodies, A Laboratory Manual, Cold Spring Harbor Publications, New York, for a description of immunoassay formats and conditions that can be used to determine specific immunoreactivity.

[0036] The term "conservative substitution" is used in reference to proteins or peptides to reflect amino acid substitutions that do not substantially alter the activity (specificity or binding affinity) of the molecule. Typically conservative amino acid substitutions involve substitution one amino acid for another amino acid with similar chemical properties (*e.g.* charge or hydrophobicity). The following six groups each contain amino acids that are typical conservative substitutions for one another: 1) Alanine (A), Serine (S), Threonine (T); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); and 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W).

BRIEF DESCRIPTION OF THE DRAWINGS

[0037] Figure 1 illustrates the strategy for *in vitro antibody* production using phage libraries. mRNA is prepared from splenocytes, first-strand cDNA is prepared, and antibody V_H and V_L genes are amplified by PCR. V_H and V_L genes are spliced together randomly using PCR to create a repertoire of scFv genes. The scFv gene repertoire is cloned into a phagemid vector in frame with a gene (gIII) encoding a phagemid minor coat protein (pIII). Each phage in the resulting phage antibody library expresses and scFv-pIII fusion protein on its surface and contains the gene encoding the scFv inside. Phage antibodies binding a specific antigen can be separated from nonbinding phage antibodies by affinity chromatography on immobilized antigen. A single round of selection increases the number of antigen-binding phage antibodies by a factor ranging from 20 to 10,000 depending on the affinity of the antibody. Eluted phage antibodies are used to infect *E. coli*, which then produce more phage antibodies for the next round of selection. Repeated rounds of selection make it possible to isolate antigen-binding phage antibodies that were originally present at frequencies of less than one in a billion.

[0038] Figure 2 panel A and panel B show sensor grams illustrating the technique used to epitope map scFv binding to BoNT/A H_C. Epitope mapping was performed by using surface plasmon resonance in a BIAcore, with scFv studied in pairs. Each scFv was injected into the BIAcore and allowed to bind to BoNT/A H_C coupled to the sensor chip surface until saturation was achieved. The amount (in RU) bound for each scFv alone was compared to the amount bound when the two scFv were mixed and injected together. Point a shows the baseline, followed by the beginning of injection. Points b_1 and b_2 show the initial association phase. Points c_1 and c_2 show the beginning of dissociation. The differences in RU between points a and c equal the amount of scFv bound to BoNT/A H_C. Panel A shows two scFv recognizing different epitopes (C25 and C9). The amount bound of the two scFv injected together (C9/C25, point c_2) is the sum of the two scFv injected alone (c_1). Panel B shows two scFv recognizing the same epitope (C39 and C25). The amount bound for the two scFv injected together (C25/C39; point c) is the same as that for the two scFv injected alone (c). The large differences in RU between points b_1 and c_1, b_2 and c_2, and b_1 and c are due to differences in refractive index between scFv and running buffer.

[0039] Figure 3 shows the evaluation of scFv neutralization of BoNT/A in a mouse hemidiaphragm model. The twitch tension developed after electrical stimulation of a mouse hemidiaphragm was measured below (-30 to 0 min) and after the addition of 20 pM BoNT/A (control), 20 pM BoNT/A plus 20 nM scFv S25, C25, 1C6, or 1F3 (representing epitopes 1 to 4 respectively), or a combination of S25 and C25 at a final concentration of 20 nM each. Results are expressed as the fraction of steady-state twitch tension (at 0 min) versus time. scFv 1C6 and 1F3 do not alter the time to 50% twitch reduction, whereas scFv C25 and S25 significantly prolong it. The combination of S25 and C25 significantly prolonged the time to neuroparalysis compared to C25 or S25 alone.

[0040] Figure 4 shows *in vitro* toxin neutralization by mAb, pairs of mAbs, and oligoclonal Ab. Time to 50% twitch reduction was measured in isolated mouse hemidiaphragms and reported for toxin only control, single mAb (C25, S25, or 3D12), pairs of mAbs (C25 S25, C25 + 3D12, or 3D12 + S25), and oligoclonal Ab (C25 + 3D12 + S25). Single mAb significantly prolonged time to neuroparalysis compared with toxin only. Pairs of mAbs significantly prolonged time to neuroparalysis compared with single mAbs.

[0041] Figures 5A and 5B show *in vivo* toxin neutralization by mAbs (Fig. 5A) and pairs (Fig. 5B) of mAbs. Fifty micrograms total Ab was mixed with 20 or 100 mouse LD_{50}s of toxin and injected i.p. Time to death and number of surviving mice was determined. No single mAb showed significant protection against 20 LD_{50}s. All mice survived challenge with 100 LD_{50}s when given any pair of mAbs.

[0042] Figure 6 shows *in vivo* toxin neutralization by mAbs, pairs of mAbs, and oligoclonal Ab. *In vivo* toxin neutralization was determined for mAbs, pairs of mAbs, and oligoclonal Ab at increasing toxin challenge doses. No single mAb showed significant protection. In contrast all mAb pairs neutralized at least 100 LD_{50}s, with approximately 50% of mice surviving challenge with 1,500 LD_{50}s of toxin for the most potent pair (C25 + 3D12). Oligoclonal Ab was even more potent with approximately 50% of mice surviving challenge with 20,000 LD_{50}s of toxin.

[0043] Figure 7 shows solution equilibrium dissociation constants (K_d) of antibodies. The solution K_d of single mAb C25 and 3D12 were determined in a flow fluorimeter by measuring the amount of free Ab present as a function of increasing BoNT H_C toxin. Combining C25 and 3D12 mAb in equimolar amounts decreased the C25 K_d more than 100-fold. Adding a third Ab (S25) decreased the Kd another 4-fold to 18 pM.

[0044] Figures 8A and 8B show ELISA characterization of soluble scFv antibodies. Assays were performed by immobilizing each indicated BoNT serotype, BoNT/A HC and BoNT/A HN coated onto a polystyrene plate. Fig. 8A: Bacterially expressed scFv antibodies derived from the immune library, reactive with the coated antigen was detected with the peroxidase-conjugated mAb anti-E antibody (1:2500). Fig. 8B: Bacterially expressed scFv antibodies derived from the non-immune library, reactive with the coated antigen were detected with 9E10 antibody (1:500) followed by peroxidase-conjugated anti-mouse-Fc antibody. The results of the assay are shown as absorbance at 405 nm which have not been normalized for protein concentrations.

[0045] Figures 9A and 9B show sensorgrams of epitope mapping of scFv binding to BoNT/A H_C. Point 'a': beginning of injection, point 'b': end of injection, and point 'c': amount of scFv bound. The difference in RU between points b and c is due to differences in refractive index between scFv and running buffer. Fig. 9A: The scFv 3A6 and 3D12 recognize the same epitope, as indicated by no increase in the RU bound when the two scFv are mixed. Fig. 9B: scFv 2A9 and 2A1 recognize different epitopes, as indicated by an almost additive increase in the RU bound when the two scFv are mixed.

[0046] Figures 10A and 10B show the individual and combined effects of scFv antibodies targeting BoNT/A HC domain. Fig. 10A: The twitch tension developed after electrical stimulation of a mouse hemidiaphragm was measured before (−30 to 0 min) and after the addition of 20pM BoNT/A (control), 20pM BoNT/A plus 20nM of members of cluster I (3D12), cluster II (3F10), C25 or S25. The scFv 3F10 did not alter the time to 50% twitch reduction, whereas scFv C25, S25 or 3D12 significantly prolong the time to 50% twitch reduction. Fig. 10B: The combination of C25 with S25 or 3D12 (cluster I) prolong significantly the time to 50% twitch reduction.

[0047] Figure 11 shows a phylogenetic tree of published botulinum neurotoxin genes. The phylogenetic tree was constructed from the DNA sequences of published Clostridial neurotoxin genes using Vector NTI software.

[0048] Figures 12A and 12B show an analysis of BoNT/A gene sequences. Figure 12A: Phylogenetic tree of BoNT/A genes reveals two clusters, A1 and A2. Figure 12B: Model of the amino acid side chain differences between BoNT/A1 and BoNT/A2. The BoNT/A heavy chain binding domain is in white at the top of the figure, with the putative ganglioside binding residues in blue and the ganglioside in red. The heavy chain translocation domain is in orange and the light chain in white at the bottom of the figure. Side chain differences between BoNT A1 and A2 toxins are shown in green.

[0049] Figure 13 shows an analysis of BoNT/B gene sequences. A phylogenetic tree of BoNT/B genes reveals four clusters: BoNT/B1, BoNT/B2, nonproteolytic BoNT/B, and bivalent BoNT/B. Percent differences between clusters range from 3.6 to 7.7%. As with BoNT/A, the greatest differences are seen in the heavy chain.

[0050] Figure 14 shows binding of BoNT/A H_C monoclonal antibodies (C25, B4, S25, and 3D12) to BoNT/A1 and BoNT/A2 toxins as determined by capture ELISA. Wells were coated with the indicated mAb followed by varying concentrations of pure or complex BoNT/A1 or BoNT/A2. Toxin binding was detected using polyclonal equine BoNT/A antisera. A1 toxins are indicated by solid squares; A2 toxins by open circles. Pure toxins are solid lines; toxin complexes are dashed lines.

[0051] Figure 15 shows binding of BoNT/A translocation domain and light chain monoclonal antibodies to BoNT/A1 and BoNT/A2 toxins as determined by capture ELISA. Methods were as described for Figure 14.

[0052] Figure 16 illustrates the ability of mAb pairs to protect mice challenged with BoNT/A1 toxin. A range of mouse LD_{50}s of BoNT/A1 toxin complex was mixed with 50 ug of an equimolar ratio of the indicated mAbs and the mixture was injected intraperitoneally. The number of mice surviving vs challenge dose is indicated.

[0053] Figures 17A and 17B illustrate the ability of mAb triplets to protect mice challenged with BoNT/A1 or BoNT/A2 toxins. A range of mouse LD_{50}s of BoNT/A1 toxin complex (Figure 17A) or BoNT/A2 toxin complex (Figure 17B) was mixed with 50 ug of an equimolar ratio of the indicated mAbs and the mixture was injected intraperitoneally. The number of mice surviving versus challenge dose is indicated.

[0054] Figure 18. Sequences for mutated and selected antibodies (HU-C25 (SEQ ID NO:4), AR1 (SEQ ID NO:5), AR2 (SEQ ID NO:6), AR3 (SEQ ID NO:7), AR4 (SEQ ID NO:8), CR1 (SEQ ID NO:9)). Dashes indicate conserved residues. Letters indicate mutated residues.

[0055] Figures 19A and 19B. Sequences for mutated and selected antibodies. Figure 19A: 3D12 (SEQ ID NO:10), and RAZ1 (SEQ ID NO:11)). Figure 19B: ING1 (SEQ ID NO:12), 1D11 (SEQ ID NO:13), 2G11 (SEQ ID NO:14), 5G4 (SEQ ID NO:15), ING2 (SEQ ID NO:16). Dashes indicate conserved residues. Letters indicate mutated residues.

[0056] Figures 20A and 20B show a scheme used for affinity maturation of HuC25 (Figure 20A) and 3D12 (Figure 20B) scFv using yeast display.

[0057] Figures 21A through 21D show affinities of wild type and affinity matured yeast displayed scFv. Figure 21A: Hu C25 and AR1; Figure 21B: AR1 and AR2; Figure 21C: AR2 and AR4; Figure 21D: 3D12 and RAZ1.

[0058] Figure 22 illustrates detection of BoNT/A by flow cytometry using wild type and affinity matured antibodies.

[0059] Figures 23A and 23B show the potency of neutralization of BoNT/A by wild type and affinity matured antibodies. Figure 23A: 100 mouse LD50 challenge. Figure 23B: 200 mouse LD50 challenge.

[0060] Figures 24A 24B show potency of neutralization of BoNT/A by pairs of wild type and affinity matured antibodies. Figure 24A: 500 mouse LD_{50} challenge. Figure 24B: 5000 mouse LD_{50} challenge.

[0061] Figure 25 illustrates neutralization of BoNT/A2 by antibody combinations.

[0062] Figure 26 shows alignment of Hu-C25 lineage antibodies (HU-C25 (SEQ ID NO:17), AR1 (SEQ ID NO:18), AR2 (SEQ ID NO:19), AR3 (SEQ ID NO:20), AR4 (SEQ ID NO:21), CR1 (SEQ ID NO:22), and CR2 (SEQ ID NO:23)).

DETAILED DESCRIPTION

[0063] This invention provides novel antibodies that specifically bind to and neutralize botulinum neurotoxin type A and, in certain embodiments, other botulinum neurotoxin serotypes (*e.g.*, B, C, D, E, F, *etc.*). Botulinum neurotoxin is produced by the anaerobic bacterium *Clostridium botulinum.* Botulinum neurotoxin poisoning (botulism) arises in a number of contexts including, but not limited to food poisoning (food borne botulism), infected wounds (wound botulism), and "infant botulism" from ingestion of spores and production of toxin in the intestine of infants. Botulism is a paralytic disease that typically begins with cranial nerve involvement and progresses caudally to involve the extremities. In acute cases, botulism can prove fatal.

[0064] Botulism neurotoxins (BoNTs) are also classified by the Centers for Disease Control (CDC) as one of the six highest-risk threat agents for bioterrorism (the "Category A agents"), due to their extreme potency and lethality, ease of production and transport, and the need for prolonged intensive care (Arnon *et al.* (2001) *JAMA* 285: 1059-1070). Both Iraq and the former Soviet Union produced BoNT for use as weapons (UN Security Council (1995) *supra*; Bozheyeva (1999) *supra.*) and the Japanese cult Aum Shinrikyo attempted to use BoNT for bioterrorism (Arnon (2001) *supra.*). As a result of these threats, specific pharmaceutical agents are needed for prevention and treatment of intoxication.

[0065] It has recently been discovered that there are multiple subtypes of various BoNT serotypes. Moreover, we have further discovered that many antibodies that bind, for example the BoNT/A1 subtype will not bind the BoNT/A2 subtype, and so forth

[0066] We have discovered that particularly efficient neutralization of a botulism neurotoxin (BoNT) subtype is achieved by the use of neutralizing antibodies that bind two or more subtypes of the particular BoNT serotype with high affinity. While this can be accomplished by using two or more different antibodies directed against each of the subtypes, this is less effective, inefficient and not practical. A BoNT therapeutic is desirably highly potent, given the high toxicity of BoNT. Since it is already necessary to use multiple antibodies to neutralize a given BoNT serotype with the desired potency (see below and Figures 5, 6, 16, and 17), the number of antibodies required would be prohibitive from a manufacturing standpoint if it were necessary to use different antibodies for each subtype. Increasing the number of antibodies in the mixture also reduces the potency. Thus, for example, if in a mixture of four antibodies, two neutralize A1 and two neutralize A2 toxin, then only 50% of the antibody will neutralize a given toxin. In contrast a mixture of two antibodies both of which neutralize A1 and A2 toxins will have 100% activity against either toxin and will be simpler to manufacture. For example for two BoNT/A subtypes (A1, A2) potent neutralization can be achieved with two to three antibodies. If different antibodies were required for BoNT/A1 and BoNT/A2 neutralization, then four to six antibodies would be required. The complexity increases further for additional subtypes. Thus, in certain embodiments this invention provides for neutralizing antibodies that bind two or more BoNT subtypes (*e.g.*, BoNT/A1, BoNT/A2, *etc.*) with high affinity.

[0067] Examples of antibodies that bind both BoNT/A1 and BoNT/A2 with high affinity include, but are not limited to, CR1, RAZ1, ING1, and ING2 described herein.

[0068] It was also a surprising discovery that when one starts combining neutralizing antibodies that the potency of the antibody combination increases dramatically. This increase makes it possible to generate a botulinum antibody of the required potency for therapeutic use. It was also surprising that as one begins combining two and three monoclonal antibodies, the particular BoNT epitope that is recognized becomes less important. Thus for example, as indicated in Example 5, antibodies that bind to the translocation domain and/or catalytic domains of BoNT had neutralizing activity, either when combined with each other or when combined with a mAb recognizing the BoNT receptor binding domain (HC) were effective in neutralizing BoNT activity. Thus, in certain embodiments, this invention contemplates compositions comprising at least two, more preferably at least three high affinity antibodies that bind non-overlapping epitopes on the BoNT.

[0069] Thus, in certain embodiments, this invention contemplates compositions comprising two or more, preferably three or more different antibodies selected from the group consisting of 3D12, RAZ1, CR1, ING1, ING2, an/or antibodies comprising one or more CDRs from these antibodies, and/or one or more antibodies comprising mutants of these antibodies, such as the 1D11, 2G11, or 5G4 mutants of ING1 (*see, e.g.*, Figure 19B).

[0070] As indicated above, in certain embodiments, the antibodies provided by this invention bind to and neutralize one or more botulinum neurotoxin type A (BoNT/A) subtypes. Neutralization, in this context, refers to a measurable decrease in the toxicity of BoNT/A. Such a decrease in toxicity can be measured *in vitro* by a number of methods well known to those of skill in the art. One such assay involves measuring the time to a given percentage (*e.g.* 50%) twitch tension reduction in a hemidiaphragm preparation. Toxicity can be determined *in vivo*, *e.g.* as an LD_{50} in a test animal (*e.g.* mouse) botulinum neurotoxin type A in the presence of one or more putative neutralizing antibodies. The neutralizing antibody can be combined with the botulinum neurotoxin prior to administration, or the animal can be administered the antibody prior to, simultaneous with, or after administration of the neurotoxin.

[0071] As the antibodies of this invention act to neutralize botulinum neurotoxin type A, they are useful in the treatment of pathologies associated with botulinum neurotoxin poisoning. The treatments essentially comprise administering to the poisoned organism (*e.g.* human or non-human mammal) a quantity of one or more neutralizing antibodies sufficient to neutralize (*e.g.* mitigate or eliminate) symptoms of BoNT poisoning.

[0072] Such treatments are most desired and efficacious in acute cases (*e.g.* where vital capacity is less than 30-40 percent of predicted and/or paralysis is progressing rapidly and/or hypoxemia with absolute or relative hypercarbia is present. These antibodies can also be used to treat early cases with symptoms milder than indicated (to prevent prgression) or even prophylactically (a use the military envisions for soldiers going in harms way). Treatment with the neutralizing antibody can be provided as an adjunct to other therapies (*e.g.* antibiotic treatment).

[0073] The antibodies provided by this invention can also be used for the rapid detection/diagnosis of botulism (type A toxin(s)) and thereby supplement and/or replace previous laboratory diagnostics.

[0074] In another embodiment this invention provides the epitopes specifically bound by botulinum neurotoxin type A neutralizing antibodies. These epitopes can be used to isolate, and/or identify and/or screen for other antibodies BoNT/A neutralizing antibodies as described herein.

I. Potency of Botulinum neurotoxin (BoNT)-neutralizing antibodies.

[0075] Without being bound to a particular theory, it is believed that the current antitoxins used to treat botulism (horse and human) have a potency of about 5000 mouse LD50s/mg (human) and 55,000 mouse LD50s mg (horse).

[0076] Based on our calculations, we believe a commercially desirable antitoxin will have a have a potency greater than about 10,000 to 100,000 LD50s/mg. Combinations of the antibodies described herein (*e.g.*, two or three antibodies) meet this potency. Thus, in certain embodiments, this invention pvoides antibodies and/or antibody combtinations that neutralize at least about 10,000 mouse LD50s/mg of antibody, preferably at least about 15,000 mouse LD50s/mg of antibody, more preferably at least about 20,000 mouse LD50s/mg of antibody, and most preferably at least about 25,000 mouse LD50s/mg of antibody.

II. Botulinum neurotoxin (BoNT)-neutralizing antibodies.

[0077] In certain preferred embodiments, BoNT neutralizing antibodies are selected that bind to one, but more preferably, to at least two or BoNT subtypes. A number of subtypes are known for each BoNT serotype. Thus, for example, BoNT/A subtypes include, but are not limited to, BoNT/A1, BoNT/A2, BoNT/A3, and the like (*see, e.g.*, Figure 11). It is also noted, for example, that the BoNT/A1 subtype includes, but is not limited to 62A, NCTC 2916, ATCC 3502, and Hall hyper (Hall Allergan) and are identical (99.9-100% identity at the amino acid level.) and have been classified as subtype A1 (Figure 12A). The BoNT/A2 sequences (Kyoto-F and FRI-A2H) (Willems, *et al.* (1993) *Res. Microbiol.* 144:547-556) are 100% identical at the amino acid level. Another BoNT/A subtype, (that we are calling A3) is produced by a strain called Loch Maree that killed a number of people in an outbreak in Scotland. We have data that three of antibodies described herein that cross react with both A1 and A2 toxins (*see* Table 1) also cross react with A3 toxin (these would be CR1, ING1, and RAZ1). Another BoNT/A toxin we have identified we refer to as A4. It is produced by a bivalent Clostridial strain that produces both B and A toxins.

[0078] Similarly, as shown in Figure 11, a number of subtypes are also known for serotypes B, C, E, and F. Using, the methods described herein, it was discovered that high-affinity antibodies that are cross-reactive with two or more subtypes within a serotype can be produced (*e.g.*, selected/engineered). Moreover, without being bound to a particular theory, it appears that these cross-reactive antibodies are substantially more efficient in neutralizing Botulinum neurotoxin, particularly when used in combination one or more different neutralizing antibodies.

[0079] The sequences of the variable heavy (VH) and variable light (VL) domains for a number of prototypically "cross-reactive" antibodies are illustrated in Table 2 and in Figures 18 and 19. As indicated above, the antibodies CR1, RAZ1, ING1, and ING2 are cross-reactive for the BoNT/A1 and BoNT/A2 subtypes, while the antibodies CR1, ING1, and RAZ1 are additionally cross-reactive for the BoNT/A3 subtype.

[0080] The antibody CR1 was produced by the mutation and selection of humanized C25 (HuC25), a derivative of AR2, *e.g.*, as described in Example 4. The antibody was mutated and selected on both the A1 and A2 subtypes. Similarly mutation of the antibody 3D12 (*see, e.g.*, Example 2) yielded RAZ1. Selection of immune scFv libraries on yeast yielded ING1 and ING2.

[0081] Table 1. Binding data for engineered antibodies.

mAb	KD BoNT/A1 (x 10^{-12}M)	KD BoNT/A2 (x 10^{-12}M)
HuC25	45	>100,000
AR2	7.2	>100,000
CR1	6.2	1700
3D12	61	152
RAZ1	1.7	3.7
B4	96	No binding
ING1	560	750
ING2	16.7	15.4

[0082] Table 2 and Figure 18 AND 19 provide amino acid sequence information for the VH and VL regions of the cross-reactive antibodies RAZ1, CR1, ING1, and ING2. Similar information is provided for the antibodies AR2 and AR3 which specifically bind to the BoNT/A1 subtype. In addition sequence information is provided herein for S25, C25, C39, 1C6, 3D12, B4, 1F3, HuC25, AR1, AR2, WR1(V), WR1(T), 3-1, 3-8, and/or 3-10 (*see, e.g.*, Table 6, and/or Table 11 and/or Table 13).

[0083] Table 2. Amino acid sequences for affinity matured, cross reactive, and/or modified antibodies.

Heavy Chains				
Clone	**Framework 1**	**CDR1**	**Framework 2**	**CDR2**
AR3	QVQLQESGGGLVQPGGSLRLSCAASGFTFG (SEQ ID NO:24)	EHYMY (SEQ ID NO:25)	WVRQAPGKGLEWVA (SEQ ID NO:26)	TISDGGSYTYYPDSVEG (SEQ ID NO:27)
AR4	QVQLQESGGGLVQPGGSLRLSCAASGFTFE (SEQ ID NO:28)	EHYMY (SEQ ID NO:29)	WVRQAPGKGLEWVA (SEQ ID NO:30)	TISDGGSYTYYPDSVEG (SEQ ID NO:31)
CR1	QVQLQESGGGLVQPGGSLRLSCAASGFTFK (SEQ ID NO:32)	YDYMY (SEQ ID NO:33)	WVRQAPGKGLEWVA (SEQ ID NO:34)	TISDGGSYTYYSDSVEG (SEQ ID NO:35)
CR2				
RAZ1	QVQLVQSGGGVVHPGRSLKLSCAGSGFTFS (SEQ ID NO:36)	DYDMH (SEQ ID NO:37)	WVRQAPGKGLEWVA (SEQ ID NO:38)	VMWFDGTEKYSAESVKG (SEQ ID NO:39)
ING1	QVQLQQSGGGLVQPGGSLRLSCAASGFTFS(SEQ ID NO:40)	NYAMT(SEQ ID NO:41)	WVRQAPGKGLEWVS(SEQ ID NO:42)	SISVGGSDTYYADSVKG(SEQ ID NO:43)
ING2	QVQLVQSGAEVKKPGSSVKVSCKASGDTFN (SEQ ID NO:44)	RNAIA (SEQ ID NO:45)	WVRQAPGQGLEWMG (SEQ ID NO:46)	RIIPNLRTTHYAQKFQG (SEQ ID NO:47)
2G11	QVQLQQSGGGLVQPGGSLRLSCAASGFTFS (SEQ ID NO:48)	NYAMT (SEQ ID NO:49)	WVRQAPGKGLEWVS (SEQ ID NO:50)	SISVGGSDTYYADSVKG (SEQ ID NO:51)
5G4	QVQLQQSGGGLVQPGGSLRLSCAASGFTFS (SEQ ID NO:52)	NYAMT (SEQ ID NO:53)	WVRQAPGKGLEWVS (SEQ ID NO:54)	SISVGGSDTYYADSVKG (SEQ ID NO:55)
Heavy Chains cont'd				
	Framework 3	**CDR3**	**Framework 4**	
AR3	RFTTSRDNSKNTLYLQMNSLRAEDTAIYYCSR (SEQ ID NO:56)	YRYDDAMDY (SEQ ID NO:57)	WGQGTLVTVSS (SEQ ID NO:58)	
AR4	RFTTSRDNSKNTLYLQMNSLRAEDTAIYYCSR (SEQ ID NO:59)	YRYDDAMDY (SEQ ID NO:60)	WGQGTLVTVSS (SEQ ID NO:61)	
CR1	RFTTSRDNSKNTLYLQMNSLRAEDTAIYYCSR (SEQ ID NO:62)	YRYDDAMDY (SEQ ID NO:63)	WGQGTRVTVSS (SEQ ID NO:64)	
CR2				
RAZ1	RFTISRDNSKNTLFLQMNSLRADDTAVYYCAR (SEQ ID NO:65)	EPDWLLWGDRGALDV (SEQ ID NO:66)	WGQGTTVTVSS (SEQ ID NO:67)	
ING1	RFTVSRDNSKNTLLLQMNSLRAEDTAVYYCAK (SEQ ID NO:68)	VRTKYCSSLSCFAGFDS (SEQ ID NO:69)	WGQGTLVTVSS (SEQ ID NO:70)	
ING2	RVAITADKHTNTVFMELSSLRSEDTAVYYCAR (SEQ ID NO:71)	DPYYYSYMDV (SEQ ID NO:72)	WGKGTTVTVSS (SEQ ID NO:73)	

2G11	RFTVSRDNSKNTLLLQMNSLRA EDTAVYYCAK (SEQ ID NO:74)	VRTKYCSSLSC FAGFDS (SEQ ID NO:75)	WGQGTRVTVSS (SEQ ID NO:76)	
5G4	RFTVSRDNSKNTLLLQMNSLRA EDTAVYYCAK (SEQ ID NO:77)	VRTKYCSSLSC FAGFDS (SEQ ID NO:78)	WGQGTRVTVSS (SEQ ID NO:79)	
Light Chains:				
Clone	**Framework 1**	**CDR1**	**Framework 2**	**CDR2**
AR3	EIVLTQSPATLSLSPGERATIS C (SEQ ID NO:80)	RASESVDSYGH SFMQ (SEQ ID NO:81)	WYQQKPGQAPRL LIY (SEQ ID NO:82)	RASNLEP (SEQ ID NO:83)
AR4	EIVLTQSPATLSLSPGERATIS C (SEQ ID NO:84)	RASESVDSYGH SFMQ (SEQ ID NO:85)	WYQQKPGQAPRL LIY (SEQ ID NO:86)	RASNLEP (SEQ ID NO:87)
CR1	EIVLTQSPATLSLSPGERATIS C (SEQ ID NO:88)	RASESVDSYGH SFMQ (SEQ ID NO:89)	WYQQKPGQAPRL LIY (SEQ ID NO:90)	RASNLEP (SEQ ID NO:91)
RAZ1	DIVMTQSPSTLSASVGDRVTIT C (SEQ ID NO:92)	WASQSISSRLA (SEQ ID NO:93)	WYQQKPGKAPKL LMY (SEQ ID NO:94)	EATSLGS (SEQ ID NO:95)
ING1	DIVMTQSPSSLSASVGDRVTIT C (SEQ ID NO:96)	RASQSISSYLN (SEQ ID NO:97)	WYQQKPGKAPKL LIY (SEQ ID NO:98)	AASSLQS (SEQ ID NO:99)
ING2	EIVLTQSPDSLAVSLGERATIN C (SEQ ID NO:100)	KSSRSVLYSSN NNNYLA (SEQ ID NO:101)	WYQQKPGQPPKL LIY (SEQ ID NO:102)	WASTRES (SEQ ID NO:103)
2G11	DVVMTQSPSSLSASVGDRVTIT C (SEQ ID NO:104)	RASQSISSYLH (SEQ ID NO:105)	WYQQKPGKAPTL LIS (SEQ ID NO:106)	DASSSQS (SEQ ID NO:107)
5G4	EIVLTQSPSSLSASVGDRVTIT C (SEQ ID NO:108)	RASQGISNYLA (SEQ ID NO:109)	WYQQKPGKVPKL LIY (SEQ ID NO:110)	AASTLQS (SEQ ID NO:111)
Light Chains cont'd.				
Clone	**Framework 3**	**CDR3**	**Framework 4**	
AR3	GIPARFSGSGSGTDFTLTISSL EPEDFAVYYC (SEQ ID NO:112)	QQGNEVPFT (SEQ ID NO:113)	FGQGTKVEIKR (SEQ ID NO:114)	
AR4	GIPARFSGSGSGTDFTLTISSL EPEDFAVYYC (SEQ ID NO:115)	QQGNEVPFT (SEQ ID NO:116)	FGQGTKVEIKR (SEQ ID NO:117)	
CR1	GIPARFSGSGSGTDFTLTISSL EPEDFAVYYC (SEQ ID NO:118)	QQGNEVPFT (SEQ ID NO:119)	FGQGTKVEIKR (SEQ ID NO:120)	
RAZ1	GVPSRFSGSGSGTEFTLTISSL QPDDFAAYYC (SEQ ID NO:121)	QHYDTYPYT (SEQ ID NO:122)	FGQGTKLEIKR (SEQ ID NO:123)	
ING1	GVPSRFSGSGSGTDFTLTISSL QPEDFATYYC (SEQ ID NO:124)	QQSYSTPRTT (SEQ ID NO:125)	FGGGTKVDIKR (SEQ ID NO:126)	
ING2	GVPDRFSGSGSGTDFTLTISSL QAEDVAVYYC (SEQ ID NO:127)	QQYYSTPFT (SEQ ID NO:128)	FGGGTKVEIKR (SEQ ID NO:129)	
2G11	GVPSRFSGSRFGTDFTLTISSL QPEDFATYYC (SEQ ID NO:130)	QQSYSTRALT (SEQ ID NO:131)	FGGGTKVEIKR (SEQ ID NO:132)	
5G4	GVPSRFSGSGSGTDFTLTISSL QPEDVATYYC (SEQ ID NO:133)	QQSYSTLMCS (SEQ ID NO:134)	FGQGTKLEIKR (SEQ ID NO:135)	

*Sequence for complete heavy chain is heavy chain framework 1+ CDR1 + framework 2 + CDR2 + framework 3 + CDR3 + framework 4.

Sequence for complete light chain is light chain framework 1+ CDR1 + framework 2 + CDR2 + framework 3 + CDR3 + framework 4.

[0084] Using the teachings and the sequence information provided herein, the variable light and variable heavy chains can be joined directly or through a linker (*e.g.* a (Gly_4Ser_3, SEQ ID NO:181) to form a single-chain Fv antibody. The various CDRs and/or framework regions can be used to form full human antibodies, chimeric antibodies, antibody fragments, polyvalent antibodies, and the like.

III. Preparation of BoNT neutralizing antibodies.

A) Recombinant expression of BoNT-neutralizing antibodies.

[0085] Using the information provided herein, the botulinum neurotoxin -neutralizing antibodies of this invention are prepared using standard techniques well known to those of skill in the art.

[0086] For example, the polypeptide sequences provided herein (*see, e.g.,* Table 2, and/or Table 6, and/or Table 9 and/or Table 13) can be used to determine appropriate nucleic acid sequences encoding the BoNT/A-neutralizing antibodies and the nucleic acids sequences then used to express one or more BoNT-neutralizing antibodies. The nucleic acid sequence may be optimized to reflect particular codon "preferences" for various expression systems according to standard methods well known to those of skill in the art.

[0087] Using the sequence information provided, the nucleic acids may be synthesized according to a number of standard methods known to those of skill in the art. Oligonucleotide synthesis, is preferably carried out on commercially available solid phase oligonucleotide synthesis machines (Needham-VanDevanter *et al.* (1984) *Nucleic Acids Res.* 12:6159-6168) or manually synthesized using the solid phase phosphoramidite triester method described by Beaucage *et. al.* (Beaucage *et. al.* (1981) *Tetrahedron Letts.* 22(20): 1859-1862).

[0088] Once a nucleic acid encoding a BoNT/A-neutralizing antibody is synthesized it may be amplified and/or cloned according to standard methods. Molecular cloning techniques to achieve these ends are known in the art. A wide variety of cloning and *in vitro* amplification methods suitable for the construction of recombinant nucleic acids are known to persons of skill. Examples of these techniques and instructions sufficient to direct persons of skill through many cloning exercises are found in Berger and Kimmel, *Guide to Molecular Cloning Techniques, Methods in Enzymology* volume 152 Academic Press, Inc., San Diego, CA (Berger); Sambrook *et al.* (1989) *Molecular Cloning - A Laboratory Manual* (2nd ed.) Vol. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor Press, NY, (Sambrook); and *Current Protocols in Molecular Biology*, F.M. Ausubel *et al.*, eds., Current Protocols, a joint venture between Greene Publishing Associates, Inc. and John Wiley & Sons, Inc., (1994 Supplement) (Ausubel). Methods of producing recombinant immunoglobulins are also known in the art. *See*, Cabilly, U.S. Patent No. 4,816,567; and Queen *et al.* (1989) *Proc. Nat'l Acad. Sci. USA* 86: 10029-10033.

[0089] Examples of techniques sufficient to direct persons of skill through *in vitro* amplification methods, including the polymerase chain reaction (PCR) the ligase chain reaction (LCR), Qβ-replicase amplification and other RNA polymerase mediated techniques are found in Berger, Sambrook, and Ausubel, as well as Mullis *et al.*, (1987) U.S. Patent No. 4,683,202; *PCR Protocols A Guide to Methods and Applications* (Innis *et al.* eds) Academic Press Inc. San Diego, CA (1990) (Innis); Arnheim & Levinson (October 1, 1990) *C&EN* 36-47; *The Journal Of NIH Research* (1991) 3, 81-94; (Kwoh *et al.* (1989) *Proc. Natl. Acad. Sci. USA* 86, 1173; Guatelli *et al.* (1990) *Proc. Natl. Acad. Sci. USA* 87, 1874; Lomell *et al.* (1989) *J. Clin. Chem* 35, 1826; Landegren *et al.*, (1988) *Science* 241, 1077-1080; Van

Brunt (1990) *Biotechnology* 8, 291-294; Wu and Wallace, (1989) *Gene* 4, 560; and Barringer *et al.* (1990) *Gene* 89, 117. Improved methods of cloning *in vitro* amplified nucleic acids are described in Wallace *et al.*, U.S. Pat. No. 5,426,039.

[0090] Once the nucleic acid for a BoNT/A-neutralizing antibody is isolated and cloned, one may express the gene in a variety of recombinantly engineered cells known to those of skill in the art. Examples of such cells include bacteria, yeast, filamentous fungi, insect (especially employing baculoviral vectors), and mammalian cells. It is expected that those of skill in the art are knowledgeable in the numerous expression systems available for expression of BoNT/A-neutralizing antibodies.

[0091] In brief summary, the expression of natural or synthetic nucleic acids encoding BoNT/A-neutralizing antibodies will typically be achieved by operably linking a nucleic acid encoding the antibody to a promoter (which is either constitutive or inducible), and incorporating the construct into an expression vector. The vectors can be suitable for replication and integration in prokaryotes, eukaryotes, or both. Typical cloning vectors contain transcription and translation terminators, initiation sequences, and promoters useful for regulation of the expression of the nucleic acid encoding the BoNT/A-neutralizing antibody. The vectors optionally comprise generic expression cassettes containing at least one independent terminator sequence, sequences permitting replication of the cassette in both eukaryotes and prokaryotes, *i.e.*, shuttle vectors, and selection markers for both prokaryotic and eukaryotic systems. *See* Sambrook.

[0092] To obtain high levels of expression of a cloned nucleic acid it is common to construct expression plasmids which typically contain a strong promoter to direct transcription, a ribosome binding site for translational initiation, and a transcription/translation terminator. Examples of regulatory regions suitable for this purpose in *E. coli* are the promoter and operator region of the *E. coli* tryptophan biosynthetic pathway as described by Yanofsky (1984) *J. Bacteriol.*, 158:1018-1024 and the leftward promoter of phage lambda (P_L) as described by Herskowitz and Hagen (1980) *Ann. Rev. Genet.*, 14:399-445. The inclusion of selection markers in DNA vectors transformed in *E. coli* is also useful. Examples of such markers include genes specifying resistance to ampicillin, tetracycline, or chloramphenicol. *See* Sambrook for details concerning selection markers, *e.g.*, for use in *E. coli.*

[0093] Expression systems for expressing BoNT/A-neutralizing antibodies are available using *E. coli*, *Bacillus sp.* (Palva, *et al.* (1983) *Gene* 22:229-235; Mosbach *et al.*, *Nature*, 302: 543-545 and *Salmonella*. *E. coli* systems are preferred.

[0094] The BoNT/A-neutralizing antibodies produced by prokaryotic cells may require exposure to chaotropic agents for proper folding. During purification from, *e.g.*, *E. coli*, the expressed protein is optionally denatured and then renatured. This is accomplished, *e.g.*, by solubilizing the bacterially produced antibodies in a chaotropic agent such as guanidine HCl. The antibody is then renatured, either by slow dialysis or by gel filtration. *See*, U.S. Patent No. 4,511,503.

[0095] Methods of transfecting and expressing genes in mammalian cells are known in the art. Transducing cells with nucleic acids can involve, for example, incubating viral vectors containing BoNT/A-neutralizing nucleic acids with cells within the host range of the vector. See, *e.g.*, Goeddel (1990) *Methods in Enzymology*, vol. 185, Academic Press, Inc., San Diego, CA or Krieger (1990) *Gene Transfer and Expression -- A Laboratory Manual*, Stockton Press, New York, N.Y. and the references cited therein.

[0096] The culture of cells used in the present invention, including cell lines and cultured cells from tissue or blood samples is well known in the art (*see, e.g.,* Freshney (1994) *Culture of Animal Cells, a Manual of Basic Technique, third edition,* Wiley-Liss, N. Y. and the references cited therein).

[0097] Techniques for using and manipulating antibodies are found in Coligan (1991) *Current Protocols in Immunology* Wiley/Greene, NY; Harlow and Lane (1989) *Antibodies: A Laboratory Manual* Cold Spring Harbor Press, NY; Stites *et al.* (eds.) *Basic and Clinical Immunology* (4th ed.) Lange Medical Publications, Los Altos, CA, and references cited therein; Goding (1986) *Monoclonal Antibodies: Principles and Practice* (2d ed.) Academic Press, New York, NY; and Kohler and Milstein (1975) Nature 256: 495-497. BoNT/A-neutralizing antibodies that are specific for botulinum neurotoxin type A have a K_D of 1 x 10^{-8} M or better, with preferred embodiments having a K_D of 1 nM or better and most preferred embodiments having a K_D of 0.1nM or better.

[0098] In one preferred embodiment the BoNT/A-neutralizing antibody gene (*e.g.* BoNT/A-neutralizing scFv gene) is subcloned into the expression vector pUC119mycHis (Tomlinson *et al.* (1996) *J. Mol. Biol.,* 256: 813-817) or pSYN3, resulting in the addition of a hexahistidine tag at the C-terminal end of the scFv to facilitate purification. Detailed protocols for the cloning and purification of BoNT/A-neutralizing antibodies are provided in Example 1.

B) Preparation of whole polyclonal or monoclonal antibodies.

[0099] The BoNT neutralizing antibodies of this invention include individual, allelic, strain, or species variants, and fragments thereof, both in their naturally occurring (full-length) forms and in recombinant forms. In certain embodiments, preferred antibodies are selected to bind one or more epitopes bound by the antibodies described herein (*e.g.,* S25, C25, C39, 1C6, 3D12, B4, 1F3, HuC25, AR1, AR2, WR1(V), WR1(T), 3-1, 3-8, 3-10, CR1, RAZ1, 1D11, 2G11, 5G4, ING1, and/or ING2). Certain preferred antibodies are cross-reactive with two or more BoNT subtypes (*e.g.* BoNT/A1, BoNT/A2, BoNT/A3, *etc.*). The antibodies can be raised in their native configurations or in non-native configurations. Anti-idiotypic antibodies can also be generated. Many methods of making antibodies that specifically bind to a particular epitope are known to persons of skill. The following discussion is presented as a general overview of the techniques available; however, one of skill will recognize that many variations upon the following methods are known.

1) Polyclonal antibody production.

[0100] Methods of producing polyclonal antibodies are known to those of skill in the art. In brief, an immunogen (*e.g.,* BoNT/A1 or A2, BoNT/A1 or A2 H_c, or BoNT/A1 or A2 subsequences including, but not limited to subsequences comprising epitopes specifically bound by antibodies expressed by clones clones S25, C25, C39, 1C6, 3D12, B4, 1F3, HuC25, AR1, AR2, WR1(V), WR1(T), 3-1, 3-8, 3-10, and/or CR1, RAZ1, 1D11, 2G11, 5G4, ING1, and/or ING2 disclosed herein), preferably a purified polypeptide, a polypeptide coupled to an appropriate carrier (*e.g.,* GST, keyhole limpet hemanocyanin, *etc.*), or a polypeptide incorporated into an immunization vector such as a recombinant vaccinia virus (*see,* U.S. Patent No. 4,722,848) is mixed with an adjuvant and animals are immunized with the mixture. The animal's immune response to the immunogen preparation is monitored by taking test bleeds and determining the titer of reactivity to the polypeptide of interest. When appropriately high titers of antibody to the immunogen are obtained, blood is collected from the animal and antisera are prepared. Further fractionation of the antisera to enrich for antibodies reactive to the BoNT/A polypeptide is performed where desired (*see, e.g.,* Coligan

(1991) *Current Protocols in Immunology* Wiley/Greene, NY; and Harlow and Lane (1989) *Antibodies: A Laboratory Manual* Cold Spring Harbor Press, NY).

[0101] Antibodies that specifically bind to the neutralizing epitopes described herein can be selected from polyclonal sera using the selection techniques described herein.

2) Monoclonal antibody production.

[0102] In some instances, it is desirable to prepare monoclonal antibodies from various mammalian hosts, such as mice, rodents, primates, humans, *etc.* Descriptions of techniques for preparing such monoclonal antibodies are found in, *e.g.*, Stites *et al.* (eds.) *Basic and Clinical Immunology* (4th ed.) Lange Medical Publications, Los Altos, CA, and references cited therein; Harlow and Lane, *supra*; Goding (1986) *Monoclonal Antibodies: Principles and Practice* (2d ed.) Academic Press, New York, NY; and Kohler and Milstein (1975) *Nature* 256: 495-497.

[0103] Summarized briefly, monoclonal antibody production proceeds by injecting an animal with an immunogen (*e.g.*, BoNT/A, BoNT/A H_c, or BoNT/A subsequences including, but not limited to subsequences comprising epitopes specifically bound by antibodies expressed by clones S25, C25, C39, 1C6, 3D12, B4, 1F3, HuC25, AR1, AR2, WR1(V), WR1(T), 3-1, 3-8, 3-10, and/or CR1, RAZ1, 1D11, 2G11, 5G4, ING1, and/or ING2 disclosed herein). The animal is then sacrificed and cells taken from its spleen, which are fused with myeloma cells. The result is a hybrid cell or "hybridoma" that is capable of reproducing *in vitro*. The population of hybridomas is then screened to isolate individual clones, each of which secrete a single antibody species to the immunogen. In this manner, the individual antibody species obtained are the products of immortalized and cloned single B cells from the immune animal generated in response to a specific site recognized on the immunogenic substance.

[0104] Alternative methods of immortalization include transformation with Epstein Barr Virus, oncogenes, or retroviruses, or other methods known in the art. Colonies arising from single immortalized cells are screened for production of antibodies of the desired specificity and affinity for the BoNT antigen, and yield of the monoclonal antibodies produced by such cells is enhanced by various techniques, including injection into the peritoneal cavity of a vertebrate (preferably mammalian) host. The antibodies of the present invention are used with or without modification, and include chimeric antibodies such as humanized murine antibodies.

IV. Modification of BoNT neutralizing antibodies.

A) Phage display can be used to increase antibody affinity.

[0105] To create higher affinity antibodies, mutant scFv gene repertories, based on the sequence of a binding scFv (*e.g.*, Table 2, and/or Table 6, and/or Table 9 and/or Table 13), can be created and expressed on the surface of phage. Display of antibody fragments on the surface of viruses which infect bacteria (bacteriophage or phage) makes it possible to produce human or other mammalian antibodies (*e.g.* scFvs) with a wide range of affinities and kinetic characteristics. To display antibody fragments on the surface of phage (phage display), an antibody fragment gene is inserted into the gene encoding a phage surface protein (*e.g.*, pIII) and the antibody fragment-pIII fusion protein is expressed on the phage surface (McCafferty *et al.* (1990) *Nature*, 348: 552-554; Hoogenboom *et al.* (1991) *Nucleic Acids Res.*, 19: 4133-4137).

[0106] Since the antibody fragments on the surface of the phage are functional, those phage bearing antigen binding antibody fragments can be separated from non-binding or lower affinity phage by antigen affinity chromatography (McCafferty *et al.* (1990) *Nature,* 348: 552-554). Mixtures of phage are allowed to bind to the affinity matrix, non-binding or lower affinity phage are removed by washing, and bound phage are eluted by treatment with acid or alkali. Depending on the affinity of the antibody fragment, enrichment factors of 20 fold-1,000,000 fold are obtained by single round of affinity selection.

[0107] By infecting bacteria with the eluted phage or modified variants of the eluted phage as described below, more phage can be grown and subjected to another round of selection. In this way, an enrichment of 1000 fold in one round becomes 1,000,000 fold in two rounds of selection (McCafferty *et al.* (1990) *Nature,* 348: 552-554). Thus, even when enrichments in each round are low, multiple rounds of affinity selection leads to the isolation of rare phage and the genetic material contained within which encodes the sequence of the binding antibody (Marks *et al.* (1991) *J. Mol. Biol.,* 222: 581-597). The physical link between genotype and phenotype provided by phage display makes it possible to test every member of an antibody fragment library for binding to antigen, even with libraries as large as 100,000,000 clones. For example, after multiple rounds of selection on antigen, a binding scFv that occurred with a frequency of only 1/30,000,000 clones was recovered (*Id.*).

1) Chain shuffling.

[0108] One approach for creating mutant scFv gene repertoires involves replacing either the V_H or V_L gene from a binding scFv with a repertoire of V_H or V_L genes (chain shuffling) (Clackson *et al.* (1991) *Nature,* 352: 624-628). Such gene repertoires contain numerous variable genes derived from the same germline gene as the binding scFv, but with point mutations (Marks *et al.* (1992) *Bio/Technology,* 10: 779-783). Using light or heavy chain shuffling and phage display, the binding avidities of, *e.g.,* BoNT/A1/BoNT/A2-neutralizing antibody fragment can be dramatically increased (*see, e.g.,* Marks *et al.* (1992) *Bio/Technology,* 10: 779-785 in which the affinity of a human scFv antibody fragment which bound the hapten phenyloxazolone (phox) was increased from 300 nM to 15 nM (20 fold)).

[0109] Thus, to alter the affinity of BoNT-neutralizing antibody a mutant scFv gene repertoire is created containing the V_H gene of a known BoNT-neutralizing antibody (*e.g.,* CR1, RAZ1, ING1, ING2) and a V_L gene repertoire (light chain shuffling). Alternatively, an scFv gene repertoire is created containing the V_L gene of a known BoNT-neutralizing antibody (*e.g.,* CR1, RAZ1, ING1, ING2) and a V_H gene repertoire (heavy chain shuffling). The scFv gene repertoire is cloned into a phage display vector (*e.g.,* pHEN-1, Hoogenboom *et al.* (1991) *Nucleic Acids Res.,* 19: 4133-4137) and after transformation a library of transformants is obtained. Phage were prepared and concentrated and selections are performed as described in the examples.

[0110] The antigen concentration is decreased in each round of selection, reaching a concentration less than the desired K_d by the final rounds of selection. This results in the selection of phage on the basis of affinity (Hawkins *et al.* (1992) *J. Mol. Biol. 226:* 889-896).

2) Increasing the affinity of BoNT-neutralizing antibodies by site directed mutagenesis.

[0111] The majority of antigen contacting amino acid side chains are located in the complementarity determining regions (CDRs), three in the V_H (CDRl, CDR2, and CDR3) and three in the V_L (CDRl, CDR2, and CDR3) (Chothia *et al.* (1987) *J. Mol. Biol.,*196: 901-917; Chothia *et al.* (1986) *Science,* 233: 755-8; Nhan *et al.* (1991) *J. Mol. Biol.,* 217: 133-151). These residues contribute the majority of binding energetics responsible for antibody affinity for antigen. In other molecules, mutating amino acids that contact ligand has been shown to be an effective means of increasing the affinity of one protein molecule for its binding partner (Lowman *et al.* (1993) *J. Mol. Biol.*, 234: 564-578; Wells (1990) *Biochemistry,* 29: 8509-8516). Thus mutation (randomization) of the CDRs and screening against BoNT/A, BoNT/A H_C or the epiotpes thereof identified herein, may be used to generate BoNT/A-neutralizing antibodies having improved binding affinity.

[0112] In certain embodiments, each CDR is randomized in a separate library, using, for example, S25 as a template ($K_d = 7.3 \times 10^{-8}$ M). To simplify affinity measurement, S25, or other lower affinity BoNT/A-neutralizing antibodies, are used as a template, rather than a higher affinity scFv. The CDR sequences of the highest affinity mutants from each CDR library are combined to obtain an additive increase in affinity. A similar approach has been used to increase the affinity of human growth hormone (hGH) for the growth hormone receptor over 1500 fold from 3.4×10^{-10} to 9.0×10^{-13} M (Lowman *et al.* (1993) *J. Mol. Biol.*, 234: 564-578).

[0113] To increase the affinity of BoNT-neutralizing antibodies, amino acid residues located in one or more CDRs (*e.g.*, 9 amino acid residues located in V_L CDR3) are partially randomized by synthesizing a "doped" oligonucleotide in which the wild type nucleotide occurred with a frequency of, *e.g.* 49%. The oligonucleotide is used to amplify the remainder of the BoNT-neutralizing scFv gene(s) using PCR.

[0114] For example in one embodiment, to create a library in which V_H CDR3 is randomized an oligonucleotide is synthesized which anneals to the BoNT-neutralizing antibody V_H framework 3 and encodes V_H CDR3 and a portion of framework 4. At the four positions to be randomized, the sequence NNS can be used, where N is any of the 4 nucleotides, and S is "C" or "T". The oligonucleotide is used to amplify the BoNT/A-neutralizing antibody V_H gene using PCR, creating a mutant BoNT-neutralizing antibody V_H gene repertoire. PCR is used to splice the V_H gene repertoire with the BoNT-neutralizing antibody light chain gene, and the resulting scFv gene repertoire cloned into a phage display vector (*e.g.*, pHEN-1 or pCANTAB5E). Ligated vector DNA is used to transform electrocompetent *E. coli* to produce a phage antibody library.

[0115] To select higher affinity mutant scFv, each round of selection of the phage antibody libraries is conducted on decreasing amounts of one or more BoNT subtypes, as described in the Examples. Typically, 96 clones from the third and fourth round of selection can screened for binding to the desired antigen(s) (*e.g.*, BoNT/A1 and/or BoNT/A2) by ELISA on 96 well plates. scFv from, *e.g.*, twenty to forty ELISA positive clones are expressed, *e.g.* in 10 ml cultures, the periplasm harvested, and the scFv k_{off} determined by BIAcore. Clones with the slowest k_{off} are sequenced, and each unique scFv subcloned into an appropriate vector (*e.g.*, pUC119 mycHis). The scFv are expressed in culture, and purified as described herein. Affinities of purified scFv are determined by BIAcore.

3) Creation of BoNT-neutralizing (scFv')2 homodimers.

[0116] To create BoNT-neutralizing $(scFv')_2$ antibodies, two BoNT-neutralizing scFvs are joined, either through a linker (*e.g.*, a carbon linker, a peptide, *etc.*) or through a disulfide bond between, for example, two cysteins. Thus, for example, to create disulfide linked BoNT/A-neutralizing scFv, a cysteine residue can be introduced by site directed mutagenesis between the myc tag and hexahistidine tag at the carboxy-terminus of the BoNT/A-neutralizing scFv. Introduction of the correct sequence is verified by DNA sequencing. In a preferred embodiment, the construct is in pUC119, so that the pelB leader directs expressed scFv to the periplasm and cloning sites (Ncol and Notl) exist to introduce BoNT/A-neutralizing mutant scFv. Expressed scFv has the myc tag at the C-terminus, followed by two glycines, a cysteine, and then 6 histidines to facilitate purification by IMAC. After disulfide bond formation between the two cysteine residues, the two scFv are separated from each other by 26 amino acids (two 11 amino acid myc tags and 4 glycines). An scFv was expressed from this construct, purified by IMAC may predominantly comprise monomeric scFv. To produce $(scFv')_2$ dimers, the cysteine is reduced by incubation with 1 MM beta-mercaptoethanol, and half of the scFv blocked by the addition of DTNB. Blocked and unblocked scFvs are incubated together to form $(scFv')_2$ and the resulting material can optionally be analyzed by gel filtration. The affinity of the BoNT-neutralizing scFv' monomer and $(scFv')_2$ dimer can optionally be determined by BIAcore as described herein.

[0117] In a particularly preferred embodiment, the $(scFv')_2$ dimer is created by joining the scFv fragments through a linker, more preferably through a peptide linker. This can be accomplished by a wide variety of means well known to those of skill in the art. For example, one preferred approach is described by Holliger *et al.* (1993) *Proc. Natl. Acad. Sci. USA*, 90: 6444-6448 (*see also* WO 94/13804).

[0118] Typically, linkers are introduced by PCR cloning. For example, synthetic oligonucleotides encoding the 5 amino acid linker (G_4S, SEQ ID NO:136) can be used to PCR amplify the BoNT/A-neutralizing antibody V_H and V_L genes which are then spliced together to create the BoNT/A-neutralizing diabody gene. The gene is then cloned into an appropriate vector, expressed, and purified according to standard methods well known to those of skill in the art.

4) Preparation of BoNT-neutralizing $(scFv)_2$, Fab, and $(Fab')_2$ molecules.

[0119] BoNT-neutralizing antibodies such as BoNT/A1-A2-neutralizing scFv, or variant(s) with higher affinity, are suitable templates for creating size and valency variants. For example, a BoNT/A1-A2-neutralizing $(scFv')_2$ can be created from the parent scFv (*e.g.* CR1, RAZ1, ING1, ING2, *etc.*) as described above. An scFv gene can be excised using appropriate restriction enzymes and cloned into another vector as described herein.

[0120] In one embodiment, expressed scFv has a myc tag at the C-terminus, followed by two glycines, a cysteine, and six histidines to facilitate purification. After disulfide bond formation between the two cystine residues, the two scFv should be separated from each other by 26 amino acids (*e.g.*, two eleven amino acid myc tags and four glycines). scFv is expressed from this construct and purified.

[0121] To produce $(scFv')_2$ dimers, the cysteine is reduced by incubation with 1 mM β-mercaptoethanol, and half of the scFv blocked by the addition of DTNB. Blocked and unblocked scFv are incubated together to form $(scFv')_2$, which is purified. As higher affinity scFv are isolated, their genes are similarly used to construct $(scFv')_2$.

[0122] BoNT/A-neutralizing Fab are expressed in *E. coli* using an expression vector similar to the one described by Better *et. al.* (1988) *Science*, 240: 1041-1043. To create a BoNT/A-neutralizing Fab, the V_H and V_L genes are amplified from the scFv using PCR. The V_H gene is cloned into an expression vector (*e.g.*, a PUC119 based bacterial expression vector) that provides an IgG C_H1 domain downstream from, and in frame with, the V_H gene. The vector also contains the lac promoter, a pelb leader sequence to direct expressed V_H-C_H1 domain into the periplasm, a gene 3 leader sequence to direct expressed light chain into the periplasm, and cloning sites for the light chain gene. Clones containing the correct VH gene are identified, *e.g.*, by PCR fingerprinting. The V_L gene is spliced to the C_L gene using PCR and cloned into the vector containing the V_H C_H1 gene.

B) Selection of neutralizing antibodies.

[0123] In preferred embodiments, selection of BoNT-neutralizing antibodies (whether produced by phage display, yeast display, immunization methods, hybridoma technology, *etc.*) involves screening the resulting antibodies for specific binding to an appropriate antigen(s). In the instant case, suitable antigens include, but are not limited to BoNT/A1, BoNT/A2, BoNT/A3 H_C, a C-terminal domain of BoNT heavy chain (binding domain), BoNT/A3 holotoxins, or recombinant BoNT domains such as HC (binding domain), HN (translocation domain), or LC (light chain). In particularly preferred embodiments the neutralizing antibodies are selected for specific binding of an epitope recognized by one or more of the antibodies described herein.

[0124] Selection can be by any of a number of methods well known to those of skill in the art. In a preferred embodiment, selection is by immunochromatography (*e.g.*, using immunotubes, Maxisorp, Nunc) against the desired target, *e.g.*, BoNT/A or BoNT/A H_C. In another embodiment, selection is against a BoNT HC in surface plasmon resonance system (*e.g.*, BIAcore, Pharmacia) either alone or in combination with an antibody that binds to an epitope specifically bound by one or more of the antibodies described herein. Selection can also be done using flow cytometry for yeast display libraries. In one preferred embodiment, yeast display libraries are sequentially selected, first on BoNT/A1, then on BoNT/A2 to obtain antibodies that bind with high affinity to both subtypes of BoNT/A. This can be repeated for other subtypes.

[0125] For phage display, analysis of binding can be simplified by including an amber codon between the antibody fragment gene and gene III. This makes it possible to easily switch between displayed and soluble antibody fragments simply by changing the host bacterial strain. When phage are grown in a supE suppresser strain of *E. coli,* the amber stop codon between the antibody gene and gene III is read as glutamine and the antibody fragment is displayed on the surface of the phage. When eluted phage are used to infect a non-suppressor strain, the amber codon is read as a stop codon and soluble antibody is secreted from the bacteria into the periplasm and culture media (Hoogenboom *et al.* (1991) *Nucleic Acids Res.,* 19: 4133-4137). Binding of soluble scFv to antigen can be detected, *e.g.*, by ELISA using a murine IgG monoclonal antibody (*e.g.*, 9ElO) which recognizes a C-terminal *myc* peptide tag on the scFv (Evan *et al.* (1985) *Mol. Cell Biol.,* 5: 3610-3616; Munro *et al.* (1986) *Cell,* 46: 291-300), *e.g.*, followed by incubation with polyclonal anti-mouse Fc conjugated to a detectable label (*e.g.*, horseradish peroxidase).

[0126] As indicated above, purification of the BoNT-neutralizing antibody can be facilitated by cloning of the scFv gene into an expression vector (*e.g.*, expression vector pUC119mycHIS) that results in the addition of the myc peptide tag followed by a hexahistidine tag at the C-terminal end of the scFv. The vector also preferably encodes the pectate lyase leader sequence that directs expression of the scFv into the bacterial periplasm where the leader sequence is cleaved. This makes it possible to harvest native properly folded scFv directly from the bacterial periplasm. The BoNT-neutralizing antibody is then expressed and purified from the bacterial supernatant using immobilized metal affinity chromatography.

C) Measurement of BoNT-neutralizing antibody affinity for one or more BoNT subtypes.

[0127] As explained above, selection for increased avidity involves measuring the affinity of a BoNT-neutralizing antibody (or a modified BoNT-neutralizing antibody) for one or more targets of interest (*e.g.* BoNT/A subtype(s) or domains thereof, *e.g.* Hc or other epitope). Methods of making such measurements are described in detail in the examples provided herein. Briefly, for example, the K_d of a BoNT/A-neutralizing antibody and the kinetics of binding to BoNT/A are determined in a BIAcore, a biosensor based on surface plasmon resonance. For this technique, antigen is coupled to a derivatized sensor chip capable of detecting changes in mass. When antibody is passed over the sensor chip, antibody binds to the antigen resulting in an increase in mass that is quantifiable. Measurement of the rate of association as a function of antibody concentration can be used to calculate the association rate constant (k_{on}). After the association phase, buffer is passed over the chip and the rate of dissociation of antibody (k_{off}) determined. K_{on} is typically measured in the range 1.0×10^2 to 5.0×10^6 and k_{off} in the range 1.0×10^{-1} to 1.0×10^{-6}. The equilibrium constant K_d is then calculated as k_{off}/k_{on} and thus is typically measured in the range 10^{-5} to 10^{-12}. Affinities measured in this manner correlate well with affinities measured in solution by fluorescence quench titration.

[0128] Phage display and selection generally results in the selection of higher affinity mutant scFvs (Marks *et al.* (1992) *Bio/Technology,* 10: 779-783; Hawkins *et al.* (1992) *J. Mol. Biol. 226:* 889-896; Riechmann *et al.* (1993) *Biochemistry,* 32: 8848-8855; Clackson *et al.* (1991) *Nature,* 352: 624-628), but probably does not result in the separation of mutants with less than a 6 fold difference in affinity (Riechmann *et al.* (1993) *Biochemistry,* 32: 8848-8855). Thus a rapid method is needed to estimate the relative affinities of mutant scFvs isolated after selection. Since increased affinity results primarily from a reduction in the k_{off}, measurement of k_{off} should identify higher affinity scFv. k_{off} can be measured in the BIAcore on unpurified scFv in bacterial periplasm, since expression levels are high enough to give an adequate binding signal and k_{off} is independent of concentration. The value of k_{off} for periplasmic and purified scFv is typically in close agreement.

V. Human or humanized (chimeric) antibody production.

[0129] As indicated above, the BoNT-neutralizing antibodies of this invention can be administered to an organism (*e.g.*, a human patient) for therapeutic purposes (*e.g.*, the treatment of botulism). Antibodies administered to an organism other than the species in which they are raised can be immunogenic. Thus, for example, murine antibodies repeatedly administered to a human often induce an immunologic response against the antibody (e.g., the human anti-mouse antibody (HAMA) response). While this is typically not a problem for the use of non-human antibodies of this invention as they are typically not utilized repeatedly, the immunogenic properties of the antibody are reduced by altering portions, or all, of the antibody into characteristically human sequences thereby producing chimeric or human antibodies, respectively.

A) Chimeric antibodies.

[0130] Chimeric) antibodies are immunoglobulin molecules comprising a human and non-human portion. More specifically, the antigen combining region (or variable region) of a chimeric antibody is derived from a non-human source (*e.g.*, murine) and the constant region of the chimeric antibody (which confers biological effector function to the immunoglobulin) is derived from a human source. The chimeric antibody should have the antigen binding specificity of the non-human antibody molecule and the effector function conferred by the human antibody molecule. A large number of methods of generating chimeric antibodies are well known to those of skill in the art (*see, e.g.*, U.S. Patent Nos: 5,502,167, 5,500,362, 5,491,088, 5,482,856, 5,472,693, 5,354,847, 5,292,867, 5,231,026, 5,204,244, 5,202,238, 5,169,939, 5,081,235, 5,075,431, and 4,975,369).

[0131] In general, the procedures used to produce chimeric antibodies consist of the following steps (the order of some steps may be interchanged): (a) identifying and cloning the correct gene segment encoding the antigen binding portion of the antibody molecule; this gene segment (known as the VDJ, variable, diversity and joining regions for heavy chains or VJ, variable, joining regions for light chains (or simply as the V or variable region) may be in either the cDNA or genomic form; (b) cloning the gene segments encoding the constant region or desired part thereof; (c) ligating the variable region to the constant region so that the complete chimeric antibody is encoded in a transcribable and translatable form; (d) ligating this construct into a vector containing a selectable marker and gene control regions such as promoters, enhancers and poly(A) addition signals; (e) amplifying this construct in a host cell (*e.g.*, bacteria); (f) introducing the DNA into eukaryotic cells (transfection) most often mammalian lymphocytes; and culturing the host cell under conditions suitable for expression of the chimeric antibody.

[0132] Antibodies of several distinct antigen binding specificities have been manipulated by these protocols to produce chimeric proteins (*e.g.*, anti-TNP: Boulianne *et al.* (1984) *Nature*, 312: 643; and anti-tumor antigens: Sahagan *et al.* (1986) *J. Immunol.*, 137: 1066). Likewise several different effector functions have been achieved by linking new sequences to those encoding the antigen binding region. Some of these include enzymes (Neuberger *et al.* (1984) *Nature* 312: 604), immunoglobulin constant regions from another species and constant regions of another immunoglobulin chain (Sharon *et al.* (1984) *Nature* 309: 364; Tan *et al.*, (1985) *J. Immunol.* 135: 3565-3567).

[0133] In one preferred embodiment, a recombinant DNA vector is used to transfect a cell line that produces a BoNT/A-neutralizing antibody. The novel recombinant DNA vector contains a "replacement gene" to replace all or a portion of the gene encoding the immunoglobulin constant region in the cell line (*e.g.*, a replacement gene may encode all or a portion of a constant region of a human immunoglobulin, a specific immunoglobulin class, or an enzyme, a toxin, a biologically active peptide, a growth factor, inhibitor, or a linker peptide to facilitate conjugation to a drug, toxin, or other molecule, *etc.*), and a "target sequence" which allows for targeted homologous recombination with immunoglobulin sequences within the antibody producing cell.

[0134] In another embodiment, a recombinant DNA vector is used to transfect a cell line that produces an antibody having a desired effector function, (*e.g.*, a constant region of a human immunoglobulin) in which case, the replacement gene contained in the recombinant vector may encode all or a portion of a region of an BoNT/A-neutralizing antibody and the target sequence contained in the recombinant vector allows for homologous recombination and targeted gene modification within the antibody producing cell. In either embodiment, when only a portion of the variable or constant region is replaced, the resulting chimeric antibody may define the same antigen and/or have the same effector function yet be altered or improved so that the chimeric antibody may demonstrate a greater antigen specificity, greater affinity binding constant, increased effector function, or increased secretion and production by the transfected antibody producing cell line, *etc.*

[0135] Regardless of the embodiment practiced, the processes of selection for integrated DNA (via a selectable marker), screening for chimeric antibody production, and cell cloning, can be used to obtain a clone of cells producing the chimeric antibody.

[0136] Thus, a piece of DNA which encodes a modification for a monoclonal antibody can be targeted directly to the site of the expressed immunoglobulin gene within a B-cell or hybridoma cell line. DNA constructs for any particular modification may be used to alter the protein product of any monoclonal cell line or hybridoma. Such a procedure circumvents the costly and time consuming task of cloning both heavy and light chain variable region genes from each B-cell clone expressing a useful antigen specificity. In addition to circumventing the process of cloning variable region genes, the level of expression of chimeric antibody should be higher when the gene is at its natural chromosomal location rather than at a random position. Detailed methods for preparation of chimeric (humanized) antibodies can be found in U.S. Patent 5,482,856.

B) Human and humanized antibodies.

[0137] In another embodiment, this invention provides for humanized or fully human anti-BoNT-neutralizing antibodies (*e.g.* HuC25, RAZ1, CR1, ING1, ING2, *etc.*). Human antibodies consist entirely of characteristically human polypeptide sequences. The human BoNT-neutralizing antibodies of this invention can be produced in using a wide variety of methods (*see, e.g.*, Larrick *et al.*, U.S. Pat. No. 5,001,065, for review).

[0138] In certain preferred embodiments, fully human scFv antibodies of this invention are obtained by modification and screening of fully human single-chain (*e.g.* scFv) libraries. Thus, in certain embodiments, fully human antibodies are produced using phage and/or yeast display methods as described herein. Methods of producing fully human gene libraries are well known to those of skill in the art (*see, e.g.*, Vaughn *et al.* (1996) *Nature Biotechnology,* 14(3): 309-314, Marks *et al.* (1991) *J. Mol. Biol.*, 222: 581-597, and PCT/US96/10287).

[0139] In another embodiment, human BoNT-neutralizing antibodies of the present invention are can be produced in trioma cells. Genes encoding the antibodies are then cloned and expressed in other cells, particularly, nonhuman mammalian cells.

[0140] The general approach for producing human antibodies by trioma technology has been described by Ostberg *et al.* (1983) *Hybridoma* 2: 361-367, Ostberg, U.S. Pat.No. 4,634,664, and Engelman *et al.*, U.S. Pat. No. 4,634,666. The antibody-producing cell lines obtained by this method are called triomas because they are descended from three cells; two human and one mouse. Triomas have been found to produce antibody more stably than ordinary hybridomas made from human cells.

[0141] Preparation of trioma cells requires an initial fusion of a mouse myeloma cell line with unimmunized human peripheral B lymphocytes. This fusion generates a xenogenic hybrid cell containing both human and mouse chromosomes (*see,* Engelman, *supra.*). Xenogenic cells that have lost the capacity to secrete antibodies are selected. Preferably, a xenogenic cell is selected that is resistant to 8-azaguanine. Such cells are unable to propagate on hypoxanthine-aminopterin-thymidine (HAT) or azaserine-hypoxanthine (AH) media.

[0142] The capacity to secrete antibodies is conferred by a further fusion between the xenogenic cell and B-lymphocytes immunized against a BoNT polypeptide (*e.g.*, BoNT/A, BoNT/A H_c, BoNT/A subsequences including, but not limited to subsequences comprising epitopes specifically bound by the antibodies described herein, *etc.*). The B-lymphocytes are obtained from the spleen, blood or lymph nodes of human donor. If antibodies against a specific antigen or epitope are desired, it is preferable to use that antigen or epitope thereof as the immunogen rather than the entire polypeptide. Alternatively, B-lymphocytes are obtained from an unimmunized individual and stimulated with a BoNT polypeptide, or a epitope thereof, *in vitro*. In a further variation, B-lymphocytes are obtained from an infected, or otherwise immunized individual, and then hyperimmunized by exposure to a BoNT polypeptide for about seven to fourteen days, *in vitro.*

[0143] The immunized B-lymphocytes prepared by one of the above procedures are fused with a xenogenic hybrid cell by well known methods. For example, the cells are treated with 40-50% polyethylene glycol of MW 1000-4000, at about 37°C for about 5-10 min. Cells are separated from the fusion mixture and propagated in media selective for the desired hybrids. When the xenogenic hybrid cell is resistant to 8-azaguanine, immortalized trioma cells are conveniently selected by successive passage of cells on HAT or AH medium. Other selective procedures are, of course, possible depending on the nature of the cells used in fusion. Clones secreting antibodies having the required binding specificity are identified by assaying the trioma culture medium for the ability to bind to the BoNT polypeptide or an epitope thereof. Triomas producing human antibodies having the desired specificity are subcloned by the limiting dilution technique and grown *in vitro* in culture medium, or are injected into selected host animals and grown *in vivo.*

[0144] The trioma cell lines obtained are then tested for the ability to bind a BoNT polypeptide or an epitope thereof. Antibodies are separated from the resulting culture medium or body fluids by conventional antibody-fractionation procedures, such as ammonium sulfate precipitation, DEAE cellulose chromatography and affinity chromatography.

[0145] Although triomas are genetically stable they do not produce antibodies at very high levels. Expression levels can be increased by cloning antibody genes from the trioma into one or more expression vectors, and transforming the vector into a cell line such as the cell lines typically used for expression of recombinant or humanized immunoglobulins. As well as increasing yield of antibody, this strategy offers the additional advantage that immunoglobulins are obtained from a cell line that does not have a human component, and does not therefore need to be subjected to the especially extensive viral screening required for human cell lines.

[0146] The genes encoding the heavy and light chains of immunoglobulins secreted by trioma cell lines are cloned according to methods, including but not limited to, the polymerase chain reaction (PCR), known in the art (*see, e.g.*, Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual,* 2nd ed., Cold Spring Harbor, N.Y., 1989; Berger & Kimmel, *Methods in Enzymology, Vol. 152: Guide to Molecular Cloning Techniques,* Academic Press, Inc., San Diego, Calif., 1987; Co *et al.* (1992) *J. Immunol.,* 148: 1149). For example, genes encoding heavy and light chains are cloned from a trioma's genomic DNA or cDNA produced by reverse transcription of the trioma's RNA. Cloning is accomplished by conventional techniques including the use of PCR primers that hybridize to the sequences flanking or overlapping the genes, or segments of genes, to be cloned.

[0147] Typically, recombinant constructs comprise DNA segments encoding a complete human immunoglobulin heavy chain and/or a complete human immunoglobulin light chain of an immunoglobulin expressed by a trioma cell line. Alternatively, DNA segments encoding only a portion of the primary antibody genes are produced, which portions possess binding and/or effector activities. Other recombinant constructs contain segments of trioma cell line immunoglobulin genes fused to segments of other immunoglobulin genes, particularly segments of other human constant region sequences (heavy and/or light chain). Human constant region sequences can be selected from various reference sources, including but not limited to those listed in Kabat *et al.* (1987) *Sequences of Proteins of Immunological Interest,* U.S. Department of Health and Human Services.

[0148] In addition to the DNA segments encoding BoNT/A-neutralizing immunoglobulins or fragments thereof, other substantially homologous modified immunoglobulins can be readily designed and manufactured utilizing various recombinant DNA techniques known to those skilled in the art such as site-directed mutagenesis (*see* Gillman & Smith (1979) *Gene,* 8: 81-97; Roberts *et al.* (1987) *Nature* 328: 731-734). Such modified segments will usually retain antigen binding capacity and/or effector function. Moreover, the modified segments are usually not so far changed from the original trioma genomic sequences to prevent hybridization to these sequences under stringent conditions. Because, like many genes, immunoglobulin genes contain separate functional regions, each having one or more distinct biological activities, the genes may be fused to functional regions from other genes to produce fusion proteins (*e.g.*, immunotoxins) having novel properties or novel combinations of properties.

[0149] The genomic sequences can be cloned and expressed according to standard methods as described herein.

[0150] Other approaches to antibody production include *in vitro* immunization of human blood. In this approach, human blood lymphocytes capable of producing human antibodies are produced. Human peripheral blood is collected from the patient and is treated to recover mononuclear cells. The suppressor T-cells then are removed and remaining cells are suspended in a tissue culture medium to which is added the antigen and autologous serum and, preferably, a nonspecific lymphocyte activator. The cells then are incubated for a period of time so that they produce the specific antibody desired. The cells then can be fused to human myeloma cells to immortalize the cell line, thereby to permit continuous production of antibody (*see* U.S. Patent 4,716,111).

[0151] In another approach, mouse-human hybridomas which produce human BoNT-neutralizing antibodies are prepared (*see, e.g.,* U.S. Patent 5,506,132). Other approaches include immunization of murines transformed to express human immunoglobulin genes, and phage display screening (Vaughan *et al. supra.*).

VI. Assaying for cross-reactivity at a neutralizing epitope.

[0152] In a preferred embodiment, the antibodies of this invention specifically bind to one or more epitopes recognized by antibodies described herein (*e.g.* S25, C25, C39, 1C6, 1F3, CR1, 3D12, RAZ1, ING1, ING2, *etc.*). In other words, particularly preferred antibodies are cross-reactive with one of more of these antibodies. Means of assaying for cross-reactivity are well known to those of skill in the art (*see, e.g.,* Dowbenko *et al.* (1988) *J. Virol.* 62: 4703-4711).

[0153] This can be ascertained by providing one or more isolated target BoNT polypeptide(s) (*e.g.* BoNT/A1 and/or BoNT/A2, or recombinant domains of said toxin, such as H_c) attached to a solid support and assaying the ability of a test antibody to compete with, *e.g.,* S25, C25, C39, 1C6, 1F3, CR1, 3D12, RAZ1, ING1, and/or ING2, *etc* for binding to the target BoNT peptide. Thus, immunoassays in a competitive binding format are preferably used for crossreactivity determinations. For example, in one embodiment, a BoNT/A1 and/or A2 H_C polypeptide is immobilized to a solid support. Antibodies to be tested (*e.g.* generated by selection from a phage-display library) added to the assay compete with S25, C25, C39, 1C6, 1F3, CR1, 3D12, RAZ1, ING1, ING2, *etc* antibodies binding to the immobilized BoNT polypeptide(s). The ability of test antibodies to compete with the binding of the S25, C25, C39, 1C6, 1F3, CR1, 3D12, RAZ1, ING1, and/or ING2, *etc* antibodies to the immobilized protein are compared. The percent crossreactivity above proteins is then calculated, using standard calculations.

[0154] If the test antibody competes with one or more of the S25, C25, C39, 1C6, 1F3, CR1, 3D12, RAZ1, ING1, and/or ING2, *etc* antibodies and has a binding affinity comparable to or greater than about 1×10^{-8} M with the same target then the test antibody is expected to be a BoNT-neutralizing antibody.

[0155] In a particularly preferred embodiment, cross-reactivity is performed by using surface plasmon resonance in a BIAcore. In a BIAcore flow cell, the BoNT polypeptide(s) (*e.g.,* BoNT/A1 and/or BoNT/A2 H_c) are coupled to a sensor chip (*e.g.* CM5) as described in the examples. With a flow rate of 5 µl/min, a titration of 100 nM to 1 µM antibody is injected over the flow cell surface for about 5 minutes to determine an antibody concentration that results in near saturation of the surface. Epitope mapping or cross-reactivity is then evaluated using pairs of antibodies at concentrations resulting in near saturation and at least 100 RU of antibody bound. The amount of antibody bound is determined for each member of a pair, and then the two antibodies are mixed together to give a final concentration equal to the concentration used for measurements of the individual antibodies. Antibodies recognizing different epitopes show an essentially additive increase in the RU bound when injected together, while antibodies recognizing identical epitopes show only a minimal increase in RU (*see the examples*). In a particularly preferred embodiment, antibodies are said to be cross-reactive if, when "injected" together they show an essentially additive increase (preferably an increase by at least a factor of about 1.4, more preferably an increase by at least a factor of about 1.6, and most preferably an increase by at least a factor of about 1.8 or 2.

[0156] Cross-reactivity at the desired epitopes can ascertained by a number of other standard techniques (*see, e.g.*, Geysen *et al* (1987) *J. Immunol. Meth.* 102, 259-274). This technique involves the synthesis of large numbers of overlapping BoNT peptides. The synthesized peptides are then screened against one or more of the prototypical antibodies (*e.g.*, CR1, RAZ1, ING1, ING2, *etc.*) and the characteristic epitopes specifically bound by these antibodies can be identified by binding specificity and affinity. The epitopes thus identified can be conveniently used for competitive assays as described herein to identify cross-reacting antibodies.

[0157] The peptides for epitope mapping can be conveniently prepared using "Multipin" peptide synthesis techniques (*see, e.g.*, Geysen *et al* (1987) *Science,* 235: 1184-1190). Using the known sequence of one or more BoNT subtypes (*see, e.g.*, Atassi *et al.* (1996) *J. Prot. Chem.,* 7: 691-700 and references cited therein), overlapping BoNT polypeptide sequences can be synthesized individually in a sequential manner on plastic pins in an array of one or more 96-well microtest plate(s).

[0158] The procedure for epitope mapping using this multipin peptide system is described in U.S. Patent 5,739,306. Briefly, the pins are first treated with a pre-coat buffer containing 2% bovine serum albumin and 0.1% Tween 20 in PBS for 1 hour at room temperature. Then the pins are then inserted into the individual wells of 96-well microtest plate containing the antibodies in the pre-coat buffer, *e.g.* at 2 μg/ml. The incubation is preferably for about 1 hour at room temperature. The pins are washed in PBST (*e.g.*, 3 rinses for every 10 minutes), and then incubated in the wells of a 96-well microtest plate containing 100 mu l of HRP-conjugated goat anti-mouse IgG (Fc) (Jackson ImmunoResearch Laboratories) at a 1:4,000 dilution for 1 hour at room temperature. After the pins are washed as before, the pins are put into wells containing peroxidase substrate solution of diammonium 2,2'-azino-bis [3-ethylbenzthiazoline-b-sulfonate] (ABTS) and H_2O_2 (Kirkegaard & Perry Laboratories Inc., Gaithersburg, Md.) for 30 minutes at room temperature for color reaction. The plate is read at 405 nm by a plate reader (*e.g.*, BioTek ELISA plate reader) against a background absorption wavelength of 492 nm. Wells showing color development indicated reactivity of the BoNT/A H_C peptides in such wells with S25, C25, C39, 1C6, or 1F3 antibodies.

VII. <u>Assaying for neutralizing activity of anti-BoNT antibodies.</u>

[0159] Preferred antibodies of this invention act, individually or in combination, to neutralize (reduce or eliminate) the toxicity of botulinum neurotoxin type A. Neutralization can be evaluated *in vivo* or *in vitro*. In vivo neutralization measurements simply involve measuring changes in the lethality (*e.g.*, LD_{50} or other standard metric) due to a BoNT neurotoxin administration due to the presence of one or more antibodies being tested for neutralizing activity. The neurotoxin can be directly administered to the test organism (*e.g.* mouse) or the organism can harbor a botulism infection (*e.g.*, be infected with *Clostridium botulinum*). The antibody can be administered before, during, or after the injection of BoNT neurotoxin or infection of the test animal. A decrease in the rate of progression, or mortality rate indicates that the antibody(s) have neutralizing activity.

[0160] One suitable *in vitro* assay for neutralizing activity uses a hemidiaphragm preparation (Deshpande *et al.* (1995) *Toxicon*, 33: 551-557). Briefly, left and right phrenic nerve hemidiaphragm preparations are suspended in physiological solution and maintained at a constant temperature (*e.g.* 36°C). The phrenic nerves are stimulated supramaximally (*e.g.* at 0.05 Hz with square waves of 0.2 ms duration). Isometric twitch tension is measured with a force displacement transducer (*e.g.*, GrassModel FT03) connected to a chart recorder.

[0161] Purified antibodies are incubated with purified BoNT (*e.g.* BoNT/A1, BoNT/A2, BoNT/B, *etc.*) for 30 min at room temperature and then added to the tissue bath, resulting in a final antibody concentration of about 2.0 x

10^{-8} M and a final BoNT concentration of about 2.0×10^{-11} M. For each antibody studied, time to 50% twitch tension reduction is determined (*e.g.*, three times for BoNT alone and three times for antibody plus BoNT).. Differences between times to a given (arbitrary) percentage (*e.g.* 50%) twitch reduction are determined by standard statistical analyses (*e.g.* two-tailed *t* test) at standard levels of significance (*e.g.*, a P value of <0.05 considered significant).

VIII. Diagnostic Assays.

[0162] As explained above, the anti-BoNT antibodies fo this invention can be used for the *in vivo* or *in vitro* detection of BoNT toxin (*e.g.* BoNT/A1 toxin) and thus, are useful in the diagnosis (*e.g.* confirmatory diagnosis) of botulism. The detection and/or quantification of BoNT in a biological sample obtained from an organism is indicative of a *Clostridium botulinum* infection of that organism.

[0163] The BoNT antigen can be quantified in a biological sample derived from a patient such as a cell, or a tissue sample derived from a patient. As used herein, a biological sample is a sample of biological tissue or fluid that contains a BoNT concentration that may be correlated with and indicative of a *Clostridium botulinum* infection. Preferred biological samples include blood, urine, saliva, and tissue biopsies.

[0164] Although the sample is typically taken from a human patient, the assays can be used to detect BoNT antigen in cells from mammals in general, such as dogs, cats, sheep, cattle and pigs, and most particularly primates such as humans, chimpanzees, gorillas, macaques, and baboons, and rodents such as mice, rats, and guinea pigs.

[0165] Tissue or fluid samples are isolated from a patient according to standard methods well known to those of skill in the art, most typically by biopsy or venipuncture. The sample is optionally pretreated as necessary by dilution in an appropriate buffer solution or concentrated, if desired. Any of a number of standard aqueous buffer solutions, employing one of a variety of buffers, such as phosphate, Tris, or the like, at physiological pH can be used.

A) Immunological Binding Assays

[0166] The BoNT polypeptide (*e.g.*, BoNT/A1, BoNT/A2, *etc.*) can be detected in an immunoassay utilizing one or more of the anti-BoNA antibodies of this invention as a capture agent that specifically binds to the BoNT polypeptide.

[0167] As used herein, an immunoassay is an assay that utilizes an antibody (*e.g.* a BoNT/A-neutralizing antibody) to specifically bind an analyte (*e.g.*, BoNT/A). The immunoassay is characterized by the binding of one or more anti-BoNT antibodies to a target (*e.g.* one or more BoNT/A subtypes) as opposed to other physical or chemical properties to isolate, target, and quantify the BoNT analyte.

[0168] The BoNT marker can be detected and quantified using any of a number of well recognized immunological binding assays (see, *e.g.*, U.S. Patents 4,366,241; 4,376,110; 4,517,288; and 4,837,168, and the like) For a review of the general immunoassays, see also *Methods in Cell Biology Volume 37: Antibodies in Cell Biology*, Asai, ed. Academic Press, Inc. New York (1993); *Basic and Clinical Immunology* 7th Edition, Stites & Terr, eds. (1991)).

[0169] The immunoassays of the present invention can be performed in any of a number of configurations (*see, e.g.,* those reviewed in Maggio (ed.) (1980) *Enzyme Immunoassay* CRC Press, Boca Raton, Florida; Tijan (1985) "Practice and Theory of Enzyme Immunoassays," *Laboratory Techniques in Biochemistry and Molecular Biology*, Elsevier Science Publishers B.V., Amsterdam; Harlow and Lane, *supra*; Chan (ed.) (1987) *Immunoassay: A Practical*

Guide Academic Press, Orlando, FL; Price and Newman (eds.) (1991) *Principles and Practice of Immunoassays* Stockton Press, NY; and Ngo (ed.) (1988) *Non isotopic Immunoassays* Plenum Press, NY).

[0170] Immunoassays often utilize a labeling agent to specifically bind to and label the binding complex formed by the capture agent and the analyte (*e.g.*, a BoNT/A-neutralizing antibody/BoNT/A complex). The labeling agent can itself be one of the moieties comprising the antibody/analyte complex. Thus, for example, the labeling agent can be a labeled BoNT/A polypeptide or a labeled anti-BoNT/A antibody. Alternatively, the labeling agent is optionally a third moiety, such as another antibody, that specifically binds to the BoNT antibody, the BoNT peptide(s), the antibody/polypeptide complex, or to a modified capture group (*e.g.*, biotin) which is covalently linked to BoNT polypepitde or to the anti- BoNT antibody.

[0171] In one embodiment, the labeling agent is an antibody that specifically binds to the anti-BoNT antibody. Such agents are well known to those of skill in the art, and most typically comprise labeled antibodies that specifically bind antibodies of the particular animal species from which the anti-BoNT antibody is derived (*e.g.*, an anti-species antibody). Thus, for example, where the capture agent is a human derived BoNT/A-neutralizing antibody, the label agent may be a mouse anti-human IgG, *i.e.*, an antibody specific to the constant region of the human antibody.

[0172] Other proteins capable of specifically binding immunoglobulin constant regions, such as streptococcal protein A or protein G are also used as the labeling agent. These proteins are normal constituents of the cell walls of streptococcal bacteria. They exhibit a strong non immunogenic reactivity with immunoglobulin constant regions from a variety of species (*see generally* Kronval, *et al.*, (1973) *J. Immunol.*, 111:1401-1406, and Akerstrom, *et al.*, (1985) *J. Immunol.*, 135:2589-2542, and the like).

[0173] Throughout the assays, incubation and/or washing steps may be required after each combination of reagents. Incubation steps can vary from about 5 seconds to several hours, preferably from about 5 minutes to about 24 hours. However, the incubation time will depend upon the assay format, analyte, volume of solution, concentrations, and the like. Usually, the assays are carried out at ambient temperature, although they can be conducted over a range of temperatures, such as 5°C to 45°C.

1) Non competitive assay formats.

[0174] Immunoassays for detecting BoNT neurotoxins (*e.g.* BoNT serotypes and/or subtypes) are, in certain embodiments, either competitive or noncompetitive. Noncompetitive immunoassays are assays in which the amount of captured analyte (in this case, BoNT polypeptide) is directly measured. In one preferred "sandwich" assay, for example, the capture agent (*e.g.*, an anti-BoNT antibody) is bound directly or indirectly to a solid substrate where it is immobilized. These immobilized anti-BoNT antibodies capture BoNT polypeptide(s) present in a test sample (*e.g.*, a blood sample). The BoNT polypeptide(s) thus immobilized are then bound by a labeling agent, *e.g.*, a BoNT/A-neutralizing antibody bearing a label. Alternatively, the second antibody may lack a label, but it may, in turn, be bound by a labeled third antibody specific to antibodies of the species from which the second antibody is derived. Free labeled antibody is washed away and the remaining bound labeled antibody is detected (*e.g.*, using a gamma detector where the label is radioactive).

2) Competitive assay formats.

[0175] In competitive assays, the amount of analyte (*e.g.*, BoNT/A) present in the sample is measured indirectly by measuring the amount of an added (exogenous) analyte displaced (or competed away) from a capture agent (*e.g.*, BoNT/A-neutralizing antibody) by the analyte present in the sample. For example, in one competitive assay, a known amount of BoNT/A is added to a test sample with an unquantified amount of BoNT/A, and the sample is contacted with a capture agent, *e.g.*, a BoNT/A-neutralizing antibody that specifically binds BoNT/A. The amount of added BoNT/A that binds to the BoNT/A-neutralizing antibody is inversely proportional to the concentration of BoNT/A present in the test sample.

[0176] The BoNT/A-neutralizing antibody can be immobilized on a solid substrate. The amount of BoNT/A bound to the BoNT/A-neutralizing antibody is determined either by measuring the amount of BoNT/A present in an BoNT/A-BoNT/A-neutralizing antibody complex, or alternatively by measuring the amount of remaining uncomplexed BoNT/A.

B) Reduction of Non Specific Binding.

[0177] One of skill will appreciate that it is often desirable to reduce non specific binding in immunoassays and during analyte purification. Where the assay involves, for example BoNT/A polypeptide(s), BoNT/A-neutralizing antibody, or other capture agent(s) immobilized on a solid substrate, it is desirable to minimize the amount of non specific binding to the substrate. Means of reducing such non specific binding are well known to those of skill in the art. Typically, this involves coating the substrate with a proteinaceous composition. In particular, protein compositions such as bovine serum albumin (BSA), nonfat powdered milk, and gelatin are widely used.

C) Substrates.

[0178] As mentioned above, depending upon the assay, various components, including the BoNT polypeptide(s), anti-BoNT antibodies, *etc.*, are optionally bound to a solid surface. Many methods for immobilizing biomolecules to a variety of solid surfaces are known in the art. For instance, the solid surface may be a membrane (*e.g.*, nitrocellulose), a microtiter dish (*e.g.*, PVC, polypropylene, or polystyrene), a test tube (glass or plastic), a dipstick (*e.g.*, glass, PVC, polypropylene, polystyrene, latex, and the like), a microcentrifuge tube, or a glass, silica, plastic, metallic or polymer bead. The desired component may be covalently bound, or noncovalently attached through nonspecific bonding.

[0179] A wide variety of organic and inorganic polymers, both natural and synthetic may be employed as the material for the solid surface. Illustrative polymers include polyethylene, polypropylene, poly(4-methylbutene), polystyrene, polymethacrylate, poly(ethylene terephthalate), rayon, nylon, poly(vinyl butyrate), polyvinylidene difluoride (PVDF), silicones, polyformaldehyde, cellulose, cellulose acetate, nitrocellulose, and the like. Other materials which may be employed, include paper, glasses, ceramics, metals, metalloids, semiconductive materials, cements or the like. In addition, substances that form gels, such as proteins (*e.g.*, gelatins), lipopolysaccharides, silicates, agarose and polyacrylamides can be used. Polymers which form several aqueous phases, such as dextrans, polyalkylene glycols or surfactants, such as phospholipids, long chain (12-24 carbon atoms) alkyl ammonium salts and the like are also suitable. Where the solid surface is porous, various pore sizes may be employed depending upon the nature of the system.

[0180] In preparing the surface, a plurality of different materials may be employed, *e.g.*, as laminates, to obtain various properties. For example, protein coatings, such as gelatin can be used to avoid non specific binding, simplify covalent conjugation, enhance signal detection or the like.

[0181] If covalent bonding between a compound and the surface is desired, the surface will usually be polyfunctional or be capable of being polyfunctionalized. Functional groups which may be present on the surface and used for linking can include carboxylic acids, aldehydes, amino groups, cyano groups, ethylenic groups, hydroxyl groups, mercapto groups and the like. The manner of linking a wide variety of compounds to various surfaces is well known and is amply illustrated in the literature. See, for example, *Immobilized Enzymes*, Ichiro Chibata, Halsted Press, New York, 1978, and Cuatrecasas, (1970) *J. Biol. Chem.* 245 3059.

[0182] In addition to covalent bonding, various methods for noncovalently binding an assay component can be used. Noncovalent binding is typically nonspecific absorption of a compound to the surface. Typically, the surface is blocked with a second compound to prevent nonspecific binding of labeled assay components. Alternatively, the surface is designed such that it nonspecifically binds one component but does not significantly bind another. For example, a surface bearing a lectin such as concanavalin A will bind a carbohydrate containing compound but not a labeled protein that lacks glycosylation. Various solid surfaces for use in noncovalent attachment of assay components are reviewed in U.S. Patent Nos. 4,447,576 and 4,254,082.

D) Other Assay Formats

[0183] BoNT polypeptides or anti-BoNT antibodies (*e.g.* BoNT/A neutralizing antibodies) can also be detected and quantified by any of a number of other means well known to those of skill in the art. These include analytic biochemical methods such as spectrophotometry, radiography, electrophoresis, capillary electrophoresis, high performance liquid chromatography (HPLC), thin layer chromatography (TLC), hyperdiffusion chromatography, and the like, and various immunological methods such as fluid or gel precipitin reactions, immunodiffusion (single or double), immunoelectrophoresis, radioimmunoassays (RIAs), enzyme-linked immunosorbent assays (ELISAs), immunofluorescent assays, and the like.

[0184] Western blot analysis and related methods can also be used to detect and quantify the presence of BoNT polypeptides in a sample. The technique generally comprises separating sample products by gel electrophoresis on the basis of molecular weight, transferring the separated products to a suitable solid support, (such as a nitrocellulose filter, a nylon filter, or derivatized nylon filter), and incubating the sample with the antibodies that specifically bind either the BoNT polypeptide. The antibodies specifically bind to the biological agent of interest on the solid support. These antibodies are directly labeled or alternatively are subsequently detected using labeled antibodies (*e.g.*, labeled sheep anti-human antibodies where the antibody to a marker gene is a human antibody) which specifically bind to the antibody which binds the BoNT polypeptide.

[0185] Other assay formats include liposome immunoassays (LIAs), which use liposomes designed to bind specific molecules (*e.g.*, antibodies) and release encapsulated reagents or markers. The released chemicals are then detected according to standard techniques (see, Monroe *et al.*, (1986) *Amer. Clin. Prod. Rev.* 5:34-41).

E) Labeling of anti-BoNT (*e.g.*, BoNT/A-neutralizing) antibodies.

[0186] Anti-BoNT antibodies can be labeled by an of a number of methods known to those of skill in the art. Thus, for example, the labeling agent can be, *e.g.*, a monoclonal antibody, a polyclonal antibody, a protein or complex such as those described herein, or a polymer such as an affinity matrix, carbohydrate or lipid. Detection proceeds by any known method, including immunoblotting, western analysis, gel-mobility shift assays, tracking of radioactive or bioluminescent markers, nuclear magnetic resonance, electron paramagnetic resonance, stopped-flow spectroscopy, column chromatography, capillary electrophoresis, or other methods which track a molecule based upon an alteration in size and/or charge. The particular label or detectable group used in the assay is not a critical aspect of the invention. The detectable group can be any material having a detectable physical or chemical property. Such detectable labels have been well-developed in the field of immunoassays and, in general, any label useful in such methods can be applied to the present invention. Thus, a label is any composition detectable by spectroscopic, photochemical, biochemical, immunochemical, electrical, optical or chemical means. Useful labels in the present invention include magnetic beads (*e.g.* Dynabeads™), fluorescent dyes (*e.g.*, fluorescein isothiocyanate, Texas red, rhodamine, and the like), radiolabels (*e.g.*, ^{3}H, ^{125}I, ^{35}S, ^{14}C, or ^{32}P), enzymes (*e.g.*, LacZ, CAT, horse radish peroxidase, alkaline phosphatase and others, commonly used as detectable enzymes, either as marker gene products or in an ELISA), and colorimetric labels such as colloidal gold or colored glass or plastic (*e.g.* polystyrene, polypropylene, latex, *etc.*) beads.

[0187] The label may be coupled directly or indirectly to the desired component of the assay according to methods well known in the art. As indicated above, a wide variety of labels may be used, with the choice of label depending on the sensitivity required, ease of conjugation of the compound, stability requirements, available instrumentation, and disposal provisions.

[0188] Non radioactive labels are often attached by indirect means. Generally, a ligand molecule (*e.g.*, biotin) is covalently bound to the molecule. The ligand then binds to an anti-ligand (*e.g.*, streptavidin) molecule which is either inherently detectable or covalently bound to a signal system, such as a detectable enzyme, a fluorescent compound, or a chemiluminescent compound. A number of ligands and anti-ligands can be used. Where a ligand has a natural anti-ligand, for example, biotin, thyroxine, and cortisol, it can be used in conjunction with the labeled, naturally occurring anti-ligands. Alternatively, any haptenic or antigenic compound can be used in combination with an antibody.

[0189] The molecules can also be conjugated directly to signal generating compounds, *e.g.*, by conjugation with an enzyme or fluorophore. Enzymes of interest as labels will primarily be hydrolases, particularly phosphatases, esterases and glycosidases, or oxidoreductases, particularly peroxidases. Fluorescent compounds include fluorescein and its derivatives, rhodamine and its derivatives, dansyl, umbelliferone, *etc.* Chemiluminescent compounds include luciferin, and 2,3-dihydrophthalazinediones, *e.g.*, luminol. For a review of various labeling or signal producing systems which may be used, see, U.S. Patent No. 4,391,904, which is incorporated herein by reference.

[0190] Means of detecting labels are well known to those of skill in the art. Thus, for example, where the label is a radioactive label, means for detection include a scintillation counter or photographic film as in autoradiography. Where the label is a fluorescent label, it may be detected by exciting the fluorochrome with the appropriate wavelength of light and detecting the resulting fluorescence, *e.g.*, by microscopy, visual inspection, via photographic film, by the use of electronic detectors such as charge coupled devices (CCDs) or photomultipliers and the like. Similarly, enzymatic labels may be detected by providing appropriate substrates for the enzyme and detecting the resulting reaction product. Finally, simple colorimetric labels may be detected simply by observing the color associated with the label. Thus, in various dipstick assays, conjugated gold often appears pink, while various conjugated beads appear the color of the bead.

[0191] Some assay formats do not require the use of labeled components. For instance, agglutination assays can be used to detect the presence of BoNT peptides. In this case, antigen-coated particles are agglutinated by samples comprising the target antibodies. In this format, none of the components need be labeled and the presence of the target antibody is detected by simple visual inspection.

IX. Pharmaceutical Compositions.

[0192] The BoNT-neutralizing antibodies of this invention are useful in mitigating the progression of botulisum produced, *e.g.*, by endogenous disease processes or by chemical/biological warfare agents. Typically compositions comprising one or preferably two or more different antibodies are administered to a mammal (*e.g.*, to a human) in need thereof.

[0193] We have discovered that particularly efficient neutralization of a botulism neurotoxin (BoNT) subtype is achieved by the use of neutralizing antibodies that bind two or more subtypes of the particular BoNT serotype with high affinity. While this can be accomplished by using two or more different antibodies directed against each of the subtypes, this is less effective, inefficient and not practical. A BoNT therapeutic is desirably highly potent, given the high toxicity of BoNT. Since it is generally necessary to use multiple antibodies to neutralize a given BoNT serotype with the required potency (see below and Figures 5, 6, 16, and 17), the number of antibodies required would be prohibitive from a manufacturing standpoint if it were necessary to use different antibodies for each subtype. Increasing the number of antibodies in the mixture also reduces the potency, thus if in a mixture of four antibodies, two neutralize A1 and two neutralize A2 toxin, then only 50% of the antibody will neutralize a given toxin. In contrast a mixture of two antibodies both of which neutralize A1 and A2 toxins will have 100% activity against either toxin and will be simpler to manufacture. For example for two BoNT/A subtypes (A1, A2) potent neutralization can be achieved with two to three antibodies. If different antibodies were required for BoNT/A1 and BoNT/A2 neutralization, then four to six antibodies would be required. The complexity increases further for additional subtypes. Thus in certain embodiments this invention provides for compositions comprising neutralizing antibodies that bind two or more BoNT subtypes (*e.g.*, BoNT/A1, BoNT/A2, BoNT/A3, *etc.*) with high affinity.

[0194] It was also a surprising discovery that when one starts combining neutralizing antibodies that the potency of the antibody combination increases dramatically. This increase makes it possible to generate a botulinum antibody of the required potency for therapeutic use. It was also surprising that as one begins combining two and three monoclonal antibodies, the particular BoNT epitope that is recognized becomes less important Thus for example, as indicated in Example 5, antibodies that bind to the translocation domain and/or catalytic domains of BoNT had neutralizing activity, either when combined with each other or when combined with a mAb recognizing the BoNT receptor binding domain (HC) were effective in neutralizing BoNT activity. Thus, in certain embodiments, this invention contemplates compositions comprising at least two, more preferably at least three high affinity antibodies that bind non-overlapping epitopes on the BoNT.

[0195] In certain embodiments, this invention contemplates compositions comprising two or more, preferably three or more different antibodies selected from the group consisting of 3D12, RAZ1, CR1, ING1, ING2, an/or antibodies comprising one or more CDRs from these antibodies, and/or one or more antibodies comprising mutants of these antibodies, such as the 1D11, 2G11, and 5G4 mutants of ING1.

[0196] The BoNT-neutralizing antibodies of this invention are useful for parenteral, topical, oral, or local administration, such as by aerosol or transdermally, for prophylactic and/or therapeutic treatment. The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include powder, tablets, pills, capsules and lozenges. The antibodies comprising the pharmaceutical compositions of this invention, when administered orally, are preferably protected from digestion. This is typically accomplished either by complexing the antibodies with a composition to render them resistant to acidic and enzymatic hydrolysis or by packaging the antibodies in an appropriately resistant carrier such as a liposome. Means of protecting proteins from digestion are well known in the art.

[0197] The pharmaceutical compositions of this invention are particularly useful for parenteral administration, such as intravenous administration or administration into a body cavity or lumen of an organ. The compositions for administration will commonly comprise a solution of one or more BoNT-neutralizing antibody dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, *e.g.*, buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents and the like, for example, sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate and the like. The concentration of BoNT/A-neutralizing antibody in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight and the like in accordance with the particular mode of administration selected and the patient's needs.

[0198] Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1 to 10 mg per patient per day. Dosages from about 1 mg up to about 200 mg per patient per day can be used. Methods for preparing parenterally administrable compositions will be known or apparent to those skilled in the art and are described in more detail in such publications as *Remington's Pharmaceutical Science*, 15th ed., Mack Publishing Company, Easton, Pennsylvania (1980).

[0199] The compositions containing the BoNT-neutralizing antibodies of this inventon or a cocktail thereof are generally administered for therapeutic treatments. Preferred pharmaceutical compositions are administered in a dosage sufficient to neutralize (mitigate or eliminate) the BoNT toxin(s) (*i.e.,* reduce or eliminate a symptom of BoNT poisoning (botulism)). An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health.

[0200] Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the antibodies of this invention to effectively treat the patient.

X. Kits For Diagnosis or Treatment.

[0201] In another embodiment, this invention provides for kits for the treatment of botulism or for the detection/confirmation of a *Clostridium botulinum* infection. Kits will typically comprise one or more anti-BoNT antibodies (*e.g.*, BoNT-neutralizing antibodies for pharmaceutical use) of this invention. For diagnostic purposes, the antibody(s) can optionally be labeled. In addition the kits will typically include instructional materials disclosing means of use BoNT-neutralizing antibodies in the treatment of symptoms of botulism. The kits may also include additional components to facilitate the particular application for which the kit is designed. Thus, for example, where a kit contains one or more anti-BoNT antibodies for detection of diagnosis of BoNT subtype, the antibody can be labeled, and the kit can additionally contain means of detecting the label (*e.g.* enzyme substrates for enzymatic labels, filter sets to detect fluorescent labels, appropriate secondary labels such as a sheep anti-human antibodies, or the like). The kits may additionally include buffers and other reagents routinely used for the practice of a particular method. Such kits and appropriate contents are well known to those of skill in the art.

[0202] In certain embodiments, kits provided for the treatment of botulisum comprise one or more BoNT neutralizing antibodies. The antibodies can be provided separately or mixed together. Typically the antibodies will be provided in a steril pharmacologically acceptoable excipient. In certain embodiments, the antibodies can be provided pre-loaded into a delivery device (*e.g.*, a disposable syringe).

[0203] The kits can optionally include instructional materials teaching the use of the antibodies, recommended dosages, conterindications, and the like.

EXAMPLES

[0204] The following examples are provided by way of illustration only and not by way of limitation. Those of skill will readily recognize a variety of noncritical parameters that can be changed or modified to yield essentially similar results.

EXAMPLE 1

Preparation of Botulinum Neurotoxin Neutralizing Antibodies.

Materials and Methods

A) Oligonucleotide design.

[0205] Family-specific murine V_H and V_K primers were designed as previously described for human V-gene primers (Marks, *et al.* (1991) *J. Mol. Biol.* 222:581-597; Marks, *et al., Eur. J. Immunol.* 21:985-991) to amplify full-length rearranged V genes. Briefly, murine V_H and V_K DNA sequences were collected from the Kabat (Kabat, *et al.* (1991) *Sequences of proteins of immunological interest*, U.S. Department of Health and Human Services, U.S. Government Printing Office, Bethesda, MD) and GenBank databases, aligned, and classified by family, and family-specific primers were designed to anneal to the first 23 nucleotides comprising framework 1. Similarly, J_H and J_K gene-segment specific primers were designed to anneal to the final 24 nucleotides comprising each of the 4 J_H and 5 J_K gene segments (Kabat, *et al. supra.*).

B) Vector construction.

[0206] To construct the vector pSYN3, a 1.5 kb stuffer fragment was amplified from pCANTAB5E (Pharmacia Biotech, Milwaukee, WI.) using PCR with the primers LMB3 (Marks, *et al.* (1991) *Eur. J. Immunol.* 21:985-991) and E-tagback (5'-ACC ACC GAA TTC TTA TTA ATG GTG ATG ATG GTG GAT GAC CAG CCG GTT CCA GCG G-3', (SEQ ID NO:137). The DNA fragment was digested with *Sfi*I *and Notf,* gel purified, and ligated into pCANTAB5E digested with *Sfi*I *and* NotI. Ligated DNA was used to transform *Escherichia coli* TGl (Gibson (1991) *Studies on the Epstein-Barr virus genome. University of Cambridge, Cambridge, U. K.*), and clones containing the correct insert were identified by DNA sequencing. The resulting vector permits subcloning of phage-displayed scFv as *SfiI-NotI or McoI-NotI* fragments for secretion into the periplasm of *E. coli* as native scFv with a C-terminal E epitope tag followed by a hexahistidine tag.

C) **Immunizations.**

[0207] For construction of library 1, BALB/c mice (16 to 22 g) were immunized at 0, 2, and 4 weeks with pure BoNT/A H_c (Ophidian Pharmaceuticals, Madison, WI.). Each animal was given subcutaneously 1 µg of material adsorbed onto alum (Pierce Chemical Co., Rockford, IL.) in a volume of 0.5 ml. Mice were challenged 2 weeks after the second immunization with 100,000 50% lethal doses of pure BoNT/A and were sacrificed 1 week later.

[0208] For construction of library 2, CD-1 mice (16 to 22 g) were immunized at 0, 2, and 4 weeks with pure BoNT/A H_c and were sacrificed two weeks after the third immunization. For both libraries, the spleens were removed immediately after sacrifice and total RNA was extracted by the method of Cathala *et al.* (1993) *DNA* 2: 329.

D) **Library construction.**

[0209] First-strand cDNA was synthesized from approximately 10 µg of total RNA as previously described in Marks, *et al.* (1991) *J. Mol. Biol.* 222:581-597, except that immunoglobulin mRNA was specifically primed with 10 pmol each of oligonucleotides MIgGl For, MIgG3 For, and MC_K For (Table 3). For construction of library 1, rearranged V_H, and V_K genes were amplified from first-strand cDNA by using commercially available V_H and V_K back primers and J_H and J_K forward primers (Recombinant Phage Antibody System; Pharmacia Biotech). For library 2, equimolar mixtures of family-specific V_H and V_K back primers were used in conjunction with equimolar mixtures of J_H or J_K gene-segment-specific forward primers in an attempt to increase library diversity (see "Oligonucleotide design" above). Re-arranged V_H and V_K genes were amplified separately in 50-µl reaction mixtures containing 5 µl of the first-strand CDNA reaction mixture, 20 pmol of an equimolar mixture of the appropriate back primers, 20 pmol of an equimolar mixture of the appropriate forward primers, 250 µm (each) deoxynucleoside triphosphate, *1.5* mm $MgCl_2$, 10 µg of bovine serum albumin/ml, and 1 µl (5 U) of *Thermus aquaticus (Taq)* DNA polymerase (Promega) in the buffer supplied by the manufacturer. The reaction mixture was overlaid with paraffin oil (Sigma) and cycled 30 times (at 95°C for 1 min, 60°C for 1 min, and 72°C for 1 min). Reaction products were gel purified, isolated from the gel by using DEAE membranes, eluted from the membranes with high-salt buffer, ethanol precipitated, and resuspended in 20 µL of water (Sambrook, *et al.* (1989) *Molecular cloning; a laboratory manual, 2nd ed. Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y.*).

[0210] Table 3. Oligonucleotide primers used for PCR of mouse immunoglobulin genes.

Primer ID	Sequence	Seq I.D. No.
A. 1st strand cDNA synthesis		
Mouse heavy chain constant region primers		
MIgG1/2 For	5′ CTG GAC AGG GAT CCA GAG TTC CA 3′	138
MIgG3 For	5′ CTG GAC AGG GCT CCA TAG TTC CA 3′	139
Mouse κ constant region primer		
MC_κFor	5′ CTC ATT CCT GTT GAA GCT CTT GAC 3′	140
B. Primary PCR		
Mouse V_H back primers		
VH1 Back	5′ GAG GTG CAG CTT CAG GAG TCA GG 3′	141
VH2 Back	5′ GAT GTG CAG CTT CAG GAG TCR GG 3′	142
VH3 Back	5′ CAG GTG CAG CTG AAG SAG TCA GG 3′	143
VH4/6 Back	5′ GAG GTY CAG CTG CAR CAR TCT GG 3′	144
VH5/9 Back	5′ CAG GTY CAR CTG CAG CAG YCT GG 3′	145
VH7 Back	5′ GAR GTG AAG CTG GTG GAR TCT GG 3′	146
VH8 Back	5′ GAG GTT CAG CTT CAG CAG TCT GG 3′	147
VH10 Back	5′ GAA GTG CAG CTG KTG GAG WCT GG 3′	148
VH11 Back	5′ CAG ATC CAG TTG CTG CAG TCT GG 3′	149
Mouse V_H back primers		
VH1 Back	5′ GAC ATT GTG ATG WCA CAG TCT CC 3′	150
VH2 Back	5′ GAT GTT KTG ATG ACC CAA ACT CC 3′	151
VH3 Back	5′ GAT ATT GTG ATR ACB CAG GCW GC 3′	152
VH4 Back	5′ GAC ATT GTG CTG ACM CAR TCT CC 3′	153
VH5 Back	5′ SAA AWT GTK CTC ACC CAG TCT CC 3′	154
VH6 Back	5′ GAY ATY VWG ATG ACM CAG WCT CC 3′	155
VH7 Back	5′ CAA ATT GTT CTC ACC CAG TCT CC 3′	156
VH8 Back	5′ TCA TTA TTG CAG GTG CTT GTG GG 3′	157
Mouse Jh forward primers		
JH1 For	5′ TGA GGA GAC GGT GAC CGT GGT CCC 3′	158
JH2 For	5′ TGA GGA GAC TGT GAG AGT GGT GCC 3′	159
JH3 For	5′ TGC AGA GAC AGT GAC CAG AGT CCC 3′	160
JH4 For	5′ TGA GGA GAC GGT GAC TGA GGT TCC 3′	161
Mouse Jκ forward primers:		
Jκ1 For	5′ TTT GAT TTC CAG CTT GGT GCC TCC 3′	162
Jκ2 For	5′ TTT TAT TTC CAG CTT GGT CCC CCC 3′	163
Jκ3 For	5′ TTT TAT TTC CAG TCT GGT CCC ATC 3′	164
Jκ4 For	5′ TTT TAT TTC CAA CTT TGT CCC CGA 3′	165
Jκ5 For	5′ TTT CAG CTC CAG CTT GGT CCC AGC 3′	166
C. Reamplification primers containing restriction sites		
Mouse VH Sfi back primers		
VH1 Sfi	5′ GTC CTC GCA ACT GCG GCC CAG CCG GCC ATG GCC GAG GTG CAG CTT CAG GAG TCA GG 3′	167
VH2 Sfi	5′ GTC CTC GCA ACT GCG GCC CAG CCG GCC ATG GCC GAT GTG CAG CTT CAG GAG TCR GG 3′	168

	VH3 Sfi 5' GTC CTC GCA ACT GCG GCC CAG CCG GCC ATG GCC CAG GTG CAG CTG AAG SAG TCA GG 3'	169
	VH4/6 Sfi 5' GTC CTC GCA ACT GCG GCC CAG CCG GCC ATG GCC GAG GTY CAG CTG CAR CAR TCT GG 3'	170
	VH5/9 Sfi 5' GTC CTC GCA ACT GCG GCC CAG CCG GCC ATG GCC CAG GTY CAR CTG CAG CAG YCT GG 3'	171
	VH7 Sfi 5' GTC CTC GCA ACT GCG GCC CAG CCG GCC ATG GCC GAR GTG AAG CTG GTG GAR TCT GG 3'	172
	VH8 Sfi 5' GTC CTC GCA ACT GCG GCC CAG CCG GCC ATG GCC GAG GTT CAG CTT CAG CAG TCT GG 3'	173
	VH10 Sfi 5' GTC CTC GCA ACT GCG GCC CAG CCG GCC ATG GCC GAA GTG CAG CTG KTG GAG WCT GG 3'	174
	VH11 Sfi 5' GTC CTC GCA ACT GCG GCC CAG CCG GCC ATG GCC CAG ATC CAG TTG CTG CAG TCT GG 3'	175
D	Mouse Jκ Not forward primers	
	Jκ1 Not 5' GAG TCA TTC TCG ACT TGC GGC CGC TTT GAT TTC CAG CTT GGT GCC TCC 3'	176
	Jκ2 Not 5' GAG TCA TTC TCG ACT TGC GGC CGC TTT TAT TTC CAG CTT GGT CCC CCC 3'	177
	Jκ3 Not 5' GAG TCA TTC TCG ACT TGC GGC CGC TTT TAT TTC CAG TCT GGT CCC ATC 3'	178
	Jκ4 Not 5' GAG TCA TTC TCG ACT TGC GGC CGC TTT TAT TTC CAA CTT TGT CCC CGA 3'	179
	Jκ5 Not 5' GAG TCA TTC TCG ACT TGC GGC CGC TTT CAG CTC CAG CTT GGT CCC AGC 3'	180
	R = A/G, Y = C/T, S = G/C, K = G/T, W = A/T, M = A/C, V = C/G/A, B = G/C/T, and H = C/A/T.	

[0211] ScFv gene repertoires were assembled from purified V_H and V_K gene repertoires and linker DNA by using splicing by overlap extension. Linker DNA encoded the peptide sequence (Gly_4Ser_3, (SEQ ID NO:181) Huston, *et al.* (1988) *Proc. Natl. Acad. Sci. USA* 85:5879-5883) and was complementary to the 3' ends of the rearranged V_H genes and the 5' ends of the rearranged V. genes. The V_H and V_K DNAs (1.5 µg of each) were combined with 500 ng of linker DNA (Recombinant Phage Antibody System; Pharmacia Biotech) in a 25 µl PCR mixture containing 250 µm (each) deoxynucteoside triphosphate, 1.5 mM MgCl, 10 µg of bovine serum albumin/ml, and 1 µl (5 U) of *Taq* DNA polymerase (Promega) in the buffer supplied by the manufacturer, and the mixture was cycled 10 times (at 94°C for 1 min, 62°C for 1 min, and 72°C for 1 min) to join the fragments. Flanking oligonucleotide primers (RS, provided in the Recombinant Phage Antibody System kit, for library I and an equimolar mixture of V_HSfi and JKNot primers [Table 3] for library 2) were added, and the reaction mixture was cycled for 33 cycles (at 94°C for 1 min, 55°C for 1 min, and 72°C for 1 min) to append restriction sites.

[0212] ScFv gene repertoires were gel purified as described above, digested with Sfif *and NotI,* and purified by electroelution, and 1 µg of each repertoire was ligated into either 1 µg of pCANTAB5E vector (Pharmacia Biotech) (library 1) or 1 µg of pHEN-1 (Hoogenboom, *et al.* (1991) *Nucleic Acids Res.* 19: 4133-4137) (library 2) digested with SfiI and *NotI.* The ligation mix was purified by extraction with phenol-chloroform, ethanol precipitated, resuspended in 20 µl of water, and 2.5 µl samples were electroporated (Dower, *et al.* (1988) *Nucleic Acids Res.* 16:6127-6145) into 50 µl of *E. coli* TGI (Gibson (1984), *Studies on the Epstein-Barr virus genome.* University of Cambridge, Cambridge, U.K.). Cells were grown in 1 ml of SOC (Sambrook, *et al.supra.*) for 30 min and then plated on TYE (Miller (1972) *Experiments in molecular genetics.,* Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y.) medium containing 100 µg of AMP/ml and 1% (wt/vol) GLU(TYE-AMP-GLU). Colonies were scraped off the plates into 5 ml of 2x TY broth (Miller (1972) *supra.*) containing 100 µg of AMP/ml, 1% GLU (2x TY-AMP-GLU), and 15% (vol/vol) glycerol for storage at -70°C. The cloning efficiency and diversity of the libraries were determined by PCR screening (Gussow, *et al.* (1989), *Nucleic Acids Res.* 17: 4000) as described by Marks *et al.* (1991) *Eur. J. Immunol.*, 21: 985-991.

E) Preparation of phage.

[0213] To rescue phagemid particles from the libraries, 10 ml of 2x. TY-AMP-GLU was inoculated with an appropriate volume of bacteria (approximately 50 to 100 µl) from the library stocks to give an A_{600} of 0.3 to 0.5 and bacteria were grown for 30 min with shaking at 37°C. About 10^{12} PFU of VCS-Ml3 (Stratagene) particles were added, and the mixture was incubated at overnight at 4°C. Tubes were blocked for 1 h at 37°C with 2% MPBS, and selection, washing, and elution were performed exactly as described in reference 35 by using phage at a concentration of 5.0 x 10^{12} TU/ml. One-third of the eluted phage was used to infect 10 ml of log-phase *E. coli* TGI, which was plated on TYE-AMP-GLU plates as described above.

[0214] The rescue-selection-plating cycle was repeated three times, after which clones were analyzed for binding by ELISA. Libraries were also selected on soluble BoNT/A H_c. For library 1, 1.0 mg of BoNT/A H_c (700 µg/ml) was biotinylated (Recombinant Phage Selection Module; Pharmacia) and purified as recommended by the manufacturer. For each round of selection, 1 ml of phage (approximately 10^{13} TU) were mixed with 1 ml of PBS containing 4% skim milk powder, 0.05% Tween 20, and 10 µg of biotinylated BoNT/A H_c/ml. After 1 h at room temperature, antigen-bound phage were captured on blocked streptavidin-coated M280 magnetic beads (Dynabeads; Dynal) as described by Schier *et al.* (1996) *J. Mol. Biol.*, 255: 28-43. Dynabeads were washed a total of 10 times (three times in TPBS, twice in TMPBS, twice in PBS, once in MPBS, and two more times in PBS). Bound phage were eluted from the Dynabeads by incubation with 100 µl of 100 mM triethylamine for 5 min and were neutralized with 1 M Tris-HCl, pH 7.5, and one-third of the eluate was used to infect log-phase *E. coli* TG1.

[0215] For library 2, affinity-driven selections (Hawkins, *et al.* (1992) *J. Mol. Biol.* 226: 889-896; Schier, *et al.* (1996) *supra.*)) were performed by decreasing the concentration of soluble BoNT/A H_c used for selection (10 µg/ml for round 1, 1 µg/ml for round 2, and 10 ng/ml for round 3). Soluble BoNT/A H_c was captured on 200 µl of Ni^{2+}-NTA (Qiagen) via a C-terminal hexahistidine tag. After capture, the Ni^{2+}-NTA resin was washed a total of 10 times (5 times in TPBS and 5 times in PBS), bound phage were eluted as described above, and the eluate was used to infect log-phase *E. coli* TGI.

F) Initial characterization of binders.

[0216] Initial analysis for binding to BoNT/A, BoNT/A H_c, and BoNT/A H_N (Chen, *et al.* (1997) *Infect. Immun.* 65: 1626-1630) was performed by ELISA using bacterial supernatant containing expressed scFv. Expression of scFv (De Bellis, *et al.*, (1990) *Nucleic Acids Res.* 18: 1311) was performed in 96-well microtiter plates as described by marks *et al.* (1991) *J. Mol. Biol.*, 222: 581-597. For ELISA, microtiter plates (Falcon 3912) were coated overnight at 4°C with either BoNT/A, BoNT/A H_c, or BoNT/A H_N (10 µg/ml) in PBS and then were blocked with 2% MPBS for 1 h at room temperature. Bacterial supernatants containing expressed scFv were added to wells and incubated at room temperature for 1.5 h. Plates were washed six times (3 times with TPBS and 3 times with PBS), and binding of scFv was detected via their C-terminal peptide tags (E epitope tag for library 1 in pCANTAB5E and myc epitope tag [Munro, *et al.* (1986) *Cell* 46: 291-300] for library 2 in pHEN-1) by using either anti-myc tag antibody (9E10; Santa Cruz Biotechnology) or anti-E antibody (Pharmacia Biotech) and peroxidase-conjugated anti-mouse Fc antibody

(Sigma), as described by Marks *et al.* (1991) *J. Mol. Biol.*, 222: 581-597 and Schier *et al.* (1996) *Gene* 169: 147-155. The number of unique binding scFv was determined by *Bst*N1 fingerprinting and DNA sequencing.

G Subcloning, expression, and purification of scFv.

[0217] To facilitate, purification, scFv genes were subcloned into the expression vector pUC119mycHis (Schier *et al.* (1995) *J. Mol. Biol.*, 263: 551-567) or pSYN3, resulting in the addition of a hexahistidine tag at the C-terminal end of the scFv. Two hundred-milliliter cultures of *E. coli* TG1 harboring one of the appropriate phagemids were grown, expression of scFv was induced with IPTG (De Bellis, *et al.* (1990), *Nucleic Acids Res.* 18:1311), and the cultures were grown at 25°C overnight. scFv was harvested from the periplasm (Breitling, *et al.* (1991) *Gene* 104:147-153), dialyzed overnight at 4°C against IMAC loading buffer (50 mM sodium phosphate [pH 7.5], 500 mM NaCl, 20 mM imidazole), and then filtered through a 0.2-μm-pore-size filter. scFv was purified by IMAC (Hochuli, *et al.* (1988) *Bio/Technology* 6: 1321-1325) as described by Schier *et al.* (1995) *supra.*

[0218] To separate monomeric scFv from dimeric and aggregated scFv, samples were concentrated to a volume of <1 ml in a centrifugal concentrator (Centricon 10; Amicon) and fractionated on a Superdex 75 column (Pharmacia) by using HBS. The purity of the final preparation was evaluated by assaying an aliquot by sodium dodecyl sulfate-polyacrylamide gel electrophoresis. Protein bands were detected by Coomassie blue staining. The concentration was determined spectrophotometrically, on the assumption that an A_{280} of 1.0 corresponds to an scFv concentration of 0.7 mg/ml.

H) Measurement of affinity and binding kinetics.

[0219] The K_ds of purified scFv were determined by using surface plasmon resonance in a BIAcore (Pharmacia Biosensor AB). In a BIAcore flow cell, approximately 600 RU of BoNT/A H_c (15 μg/ml in 10 mM sodium acetate [pH 4.5]) was coupled to a CM5 sensor chip by using N-hydroxysuccinimide-N-ethyl-*N'*-(dimethylaminopropyl) carbodimide chemistry (Johnson, *et al.* (1991) *Anal. Biochem.* 198: 268-277). This amount of coupled BoNT/A H_c resulted in a maximum RU of 100 to 175 of scFv bound. For regeneration of the surface after binding of scFv, 5 μl of 4 M $MgCl_2$ was injected, resulting in a return to baseline. The surface was reused 20 to 30 times under these regeneration conditions. Association was measured under a continuous flow of 5 μl/min with a concentration range from 50 to 1,000 nM. k_{on} was determined from a plot of ln $(dR/dt)/t$ versus concentration, where R is response and t is time (Karlsson, *et al.* (1991) *J. Immunol. Methods* 145: 229-240). k_{off} was determined from the dissociation part of the sensorgram at the highest concentration of scFv analyzed (Karlsson, *et al.* (1991) *J. Immunol. Methods* 145: 229-240) by using a flow rate of 30 μl/min. K_d was calculated as k_{off}/k_{on}.

I) Epitope mapping.

[0220] Epitope mapping was performed by using surface plasmon resonance in a BIAcore. In a BIAcore flow cell, approximately 1,200 RU of BoNT/A H_c was coupled to a CM5 sensor chip as described above. With a flow rate of 5 μl/min, a titration of 100 nM to 1 μM scFv was injected over the flow cell surface for 5 min to determine an scFv concentration which resulted in near saturation of the surface. Epitope mapping was performed with pairs of scFv at concentrations resulting in near saturation and at least 100 RU of scFv bound. The amount of scFv bound was determined for each member of a pair, and then the two scFv were mixed together to give a final concentration equal to the concentration used for measurements of the individual scFv. scFv recognizing different epitopes showed an additive increase in the RU bound when injected together (Figure 2 panel A), while scFv recognizing identical epitopes showed only a minimal increase in RU (Figure 2 panel B).

J) *In vitro* neutralization studies.

[0221] In vitro neutralization studies were performed by using a mouse hemidiaphragm preparation, as described by Deshpande *et al.* (1995) *Toxicon* 33: 551-557. Briefly, left and right phrenic nerve hemidiaphragm preparations were excised from male CD/1 mice (25 to 33 g) and suspended in physiological solution (135 mM NaCl, 5 mM KC1, 15 mM $NaHCO_3$, 1 mM Na2HPO4, 1 mM $MgCl_2$, 2 mM $CaCl_2$, and 11 mM GLU). The incubation bath was bubbled with 95% O_2-5% CO_2 and maintained at a constant temperature of 36°C. Phrenic nerves were stimulated supramaximally at 0.05 Hz with square waves of 0.2 ms duration. Isometric twitch tension was measured with a force displacement transducer (Model FT03; Grass) connected to a chart recorder. Purified scFv were incubated with purified BoNT/A for 30 min at room temperature and then added to the tissue bath, resulting in a final scFv concentration of 2.0×10^{-8} M and a final BoNT/A concentration of 2.0×10^{-11} M. For each scFv studied, time to 50% twitch tension reduction was determined three times for BoNT/A alone and three times for scFv plus BoNT/A. The combination of S25 and C25 was studied at a final concentration of 2.0×10^{-8} M each. Differences between times to 50% twitch reduction were determined by a two-tailed *t* test, with a *P* value of <0.05 considered significant.

[0222] Table 4. Frequency of binding of clones from phage antibody libraries

Antigen used for selection	Frequency of ELISA-positive clones[a] in selection round:		
	1	2	3
Library 1[b]			
BoNT/A: immunotube[c]	20/184	124/184	ND
BoNT/A H_c: immunotube	7/92	86/92	88/92
BoNT/A H_c: biotinylated[d]	7/90	90/90	90/90
	14/48	48/48	ND
Library 2[e]			
BoNT/A: immunotube	ND	81/92	*ND*
BoNT/A H_c: immunotube	ND	ND	76/92
BoNT/A H_c: Ni^{2+}-NTA[f]	ND	ND	67/92

[a]Expressed as number of positive clones/total number of clones. For selections on BoNT/A and BoNT/A H_c, ELISA was done on immobilized BoNT/A and BoNT/A H_c, respectively. ND, data not determined from selection performed.
[b]Derived from a mouse immunized twice with BoNT/A H_c and once with BoNT/A.
[c]Immunotube selections were performed with the antigen absorbed onto immunotubes.
[d]Biotinylated selections were performed in solution with capture on streptavidin magnetic beads.
[e]Derived from a mouse immunized three times with BoNT/A H_c.
[f]Ni^{2+}-NTA selections were performed in solution with capture on Ni^{2+}-NTA agarose.

Results.

A) Phage antibody library construction and characterization.

[0223] Two phage antibody libraries were constructed from the V_H and V_K genes of immunized mice (Figure 1). For library 1, a mouse was immunized twice with BoNT/A H_C and challenged 2 weeks after the second immunization with 100,000 50% lethal doses of BoNT/A. The mouse survived the BoNT/A challenge and was sacrificed 1 week later. The spleen was removed immediately after sacrifice, and total RNA was prepared. For library construction, IgG heavy-chain and kappa light-chain mRNA were specifically primed and first-strand cDNA was synthesized. V_H and V_K gene repertoires were amplified by PCR, and V_H, J_H V_K, and J_K primers were provided in the recombinant phage antibody system.

[0224] The V_H and V_K gene repertoires were randomly spliced together to create an scFv gene repertoire by using synthetic DNA encoding the 15-amino-acid peptide linker $(G_4S)_3$ (SEQ ID NO:182). Each scFv gene repertoire was separately cloned into the phage display vector pCANTAB5E (Pharmacia). After transformation, a library of 2.1 x 10^6 members was obtained. Ninety percent of the clones had an insert of the appropriate size for an scFv gene, as determined by PCR screening, and the cloned scFv genes were diverse, as determined by PCR fingerprinting. DNA sequencing of 10 unselected clones from library 1 revealed that all V_H genes were derived from the murine V_H2 family and all V_K genes were derived from the murine V_K4 and V_K6 families (Kabat, *et al.* (1991) *supra.*). Based on this observed V-gene bias, family-specific V_H and V_K primers were designed along with J_H and J_K gene-segment-specific primers (Table **3**). These primers were then used to construct a second phage antibody library.

[0225] For library 2, a mouse was immunized three times with BoNT/A H_c and sacrificed 2 weeks after the third immunization. The mouse was not challenged with BoNT/A prior to spleen harvest, as this led to the production of non-H_c-binding antibodies (see "Selection and initial characterization of phage antibodies" below). The spleen was harvested, and a phage antibody library was constructed as described above, except that V_H-, J_H-, V_K-, and J_K-specific primers were used. After transformation, a library of 1.0 x 10^6 members was obtained. Ninety-five percent of the clones had an insert of the appropriate size for an scFv gene, as determined by PCR screening, and the cloned scFv genes were diverse, as determined by PCR fingerprinting (data not shown). DNA sequencing of 10 unselected clones from library 2 revealed greater diversity than was observed in library 1; V_H genes were derived from the $V_{H1,}$ V_K2, and V_K3 families, and V_K genes were derived from the V_K2, V_K3, V_K4, and V_K6 families (Kabat, *et al.* (1991) *supra.*).

B) Selection and initial characterization of phage antibodies.

[0226] To isolate BoNT/A binding phage antibodies, phage were rescued from the library and selected on either purified BoNT/A or BoNT/A H_c. Selections were performed on the holotoxin in addition to H_c, since it was unclear to what extent the recombinant toxin H_c would mimic the conformation of the H_c in the holotoxin. Selection for BoNT/A and BoNT/A H_c binders was performed on antigen adsorbed to polystyrene. In addition, H_c binding phage were selected in solution on biotinylated H_c, with capture on streptavidin magnetic beads (for library 1) or on hexahistidine tagged H_c, with capture on Ni^{2+}-NTA agarose (for library 2). Selections in solution were utilized based on our previous observation that selection on protein adsorbed to polystyrene could yield phage antibodies that did not recognize native protein (Schier *et al.* (1995) *Immunotechnology,* 1: 73-81). Selection in solution was not performed on the holotoxin due to our inability to successfully biotinylate the toxin without destroying immunoreactivity.

[0227] After two to three rounds of selection, at least 67% of scFv analyzed bound the antigen used for selection (Table 2). The number of unique scFv was determined by DNA fingerprinting followed by DNA sequencing, and the specificity of each scFv was determined by ELISA on pure BoNT/A and recombinant BoNT/A H_c and HN scFv binding BoNT/A but not binding, H_c or HN were presumed to bind the light chain (catalytic domain). A total of 33 unique scFv were isolated from mice immunized with H_c and challenged with BoNT/A (Table 5, library 1). When library 1 was selected on holotoxin, 25 unique scFv were identified. Only 2 of these scFv, however, bound H_c, with the majority (Hathaway, *et al.* (1984) *J. Infect. Dis.* 150:407-412) binding the light chain and 2 binding H_N. The two H_c binding scFv did not express as well as other scFv recognizing similar epitopes, and they were therefore not characterized with respect to affinity or neutralization capacity (see below).

[0228] Selection of library 1 on H_c yielded an additional eight unique scFv (Tables 3 and 4). Overall, however, only 50% of scFv selected on H_c also bound holotoxin. This result suggests that a significant portion of the

H_c surface may be inaccessible in the holotoxin. Alternatively, scFv could be binding, H_c conformations that do not exist in the holotoxin. From mice immunized with H_c only (library 2), all scFv selected on holotoxin also bound H_c. As with library 1, however, only 50% of scFv selected on H_c bound holotoxin. In all, 18 unique H_c binding scFv were isolated from library 2, resulting in a total of 28 unique H_c binding scFv (Tables 5 and 6). scFv of identical or related sequences were isolated on both H_c immobilized on polystyrene and H_c in solution. Thus, in the case of H_c, the method of selection was not important.

[0229] Table 5. Specificity of BoNT binding scFv selected from phage antibody libraries.

	Number of unique scFv	
scFv Specificity	library 1	library 2
BoNT/A H_C	10	18
BoNT/A H_N	2	0
BoNT/A light chain	21	0
Total	33	18

C) Epitope mapping.

[0230] All 28 unique H_c binding scFv were epitope mapped using surface plasmon resonance in a BIAcore. Epitope mapping was performed with pairs of scFv at concentrations resulting in near saturation of the chip surface and at least 100 RU of scFv bound. The amount of scFv bound was determined for each member of a pair, and then the two scFv were mixed together to give a final concentration equal to the concentration used for measurements of the individual scFv. Those scFv recognizing different epitopes showed an additive increase in the RU bound when injected together (Figure 2, panel A), while scFv recognizing identical epitopes showed only a minimal increase in RU (Figure 2, panel B). By this technique, mapping of the 28 scFv yielded 4 nonoverlapping epitopes recognized on H_c (Table 6). scFv recognizing only epitopes 1 and 2 were obtained from library 1, whereas scFv recognizing all 4 epitopes were obtained from library 2.

[0231] Many of the scFv recognizing the same epitope (Cl and S25; C9 and C15; 1E8 and 1G7; 1B6 and 1C9; C25 and C39; 2G5, 3C3, 3F4, and 3H4; 1A1 and 1F1; 1B3 and 1C6; 1G5 and 1H6; 1F3 and 2E8) had V_H domains derived from the same V-D-J rearrangement, as evidenced by the high level of homology of the V_HCDR3 and V_H-gene segment (Table 6). These scFv differ only by substitutions introduced by somatic hypermutation or PCR error. For epitopes 1 and 2, most or all of the scFv recognizing the same epitope are derived from the same or very similar V_H-gene segments but differ significantly with respect to V_HCDR3 length and sequence (5 of 9 scFv for epitope 1;8 of 8 scFv for epitope 2) (Table 6). These include scFv derived from different mice. Given the great degree of diversity in V_HCDR2 sequences in the primary repertoire (Tomlinson *et al.* (1996) *J. Mol. biol.,* 256: 813-817), specific V_H-gene segments may have evolved for their ability to form binding sites capable of recognizing specific pathogenic antigenic shapes. In contrast, greater structural variation appears to occur in the rearranged Y_K genes. For example, three different germ line genes and CDR1 main-chain conformations (Chothia, *et al.* (1987) *J. Mol. Biol.* 196: 901-917) are observed for epitope 21 where all the V_H (genes are derived from the same germ line gene. Such "promiscuity" in chain pairings has been reported previously (Clackson, *et al.* (1991) *Nature* 352: 624-628).

D) Affinity, binding kinetics, and *in vitro* toxin neutralization.

[0232] Affinity, binding kinetics, and *in vitro* toxin neutralization were determined for one representative scFv binding to each epitope. For each epitope, the scFv chosen for further study had the best combination of high expression level and slow k_{off}, as determined during epitope mapping studies. K_d for the four scFv studied ranged between 7.3×10^{-8} and 1.1×10^{-9} M (Table 7), values comparable to those reported for monoclonal IgG produced from hybridomas (Foote, *et al.* (1991) *Nature* 352: 530-532). C25 has the highest affinity ($K_d = 1.1 \times 10^{-9}$ M) reported for an anti-botulinum toxin antibody. k_{on} differed over 84-fold, and

[0233] Table 6. Deduced protein sequences of V_H and V_L of BoNT/A H_C binding scFv, classified by epitope recognized.

TABLE. Deduced protein sequences of V_H and V_L of BoNT/A H_C binding scFv, classified by epitope recognized

Region	Epitope	Clone	Lib[a]	Sequence[b]						
				Framework 1	CDR 1	Framework 2	CDR 2	Framework 3	CDR 3	Framework 4
V_H	1	C15	1	QVKLQQSGAELVRPGASVKLSCKTSGYSFT	SYWMN	WVKQGPGQGLEWIG	MIHPSNSEIRFNQKFED	MATLTVDKSSSTAYMQLSSPTSEDSAVYYCAR	GIYYDYDGGNYYAMDY	WGQGTTVTASS
		C9	1	------------------------------	-----	--------------	----------------N	--------------------------------	----V-----------	--------V--
		1D5	2	E---VE------------N----A------	-----	----R---------	---------T-L----K-	K-------------------------------	-------E-Y--TL--	------L-V--
		C1	1	-----------------------A------	-----	----R---------	-------DT--------	K------R-----IH-----------------	-L-GYGP WYFDV	--------V--
		S25	1	-----------------------A----L-	-----	----R---------	-----D-DT--------	K------T------------------------	-L-NGF WYF-V	--------V--
		1B6	2	--Q-------------V---I---A---T-I	D-A-H	----S-AKS-----	V-SSYYGDTDY--I-KG	K---------N----E-ARL--D---I-----	RGKG ----	--------V--
		1C9	2	--Q-K-----------V---I---G---T-I	D-AVH	----SHAKS-----	V-STYYGDADY-PK-KG	K-----N---N----E-PRL------I-----	RGKG ----	-----S--V--
		1E8	2	E-Q--E--PG--K-SQ-LS-T-TVT---I-	D-AW-	-IR-F--KK---M-	Y-S YSGSTGYNPSLKS	RISI-R-T-KNQFFL--N-V-T--TGT-----	-YD ----	-----S--V--
		1G7	2	E-Q--E--PG -K-SQ-LS-T-TVT---I-	D-AWY	-IR-F--KK---M-	Y-S YSGSTGYNPSLKS	RISI-R-T-KNQFFL--N-V-T--TGT-----	-YD ----	-----S--V--
	2	1A1	2	EVKLVESGGGLVQPGGSRKLSCATSGFTFS	DYYMS	WIRQSPDKRLEWVA	TISDGGTYTYYPDSVKG	RFTISRDNAKNTLYLQMSSLKSEDTAMYYCVR	HGYGNYPSH WYFDV	WGAGTTVTVSS
		1F1	2	------------------L-----A------	N-G--	-V--T---------	M--S--S-N--S-----	-V--------S---------Q-------L-T-	--------Y -----	-----------
		C39	1	Q-Q-Q-----S-K----L-----A------	-----	-V--T-E-------	------S----------	-----------N--------------I-----	YR-DEGL -Y	--Q--------
		C25	1	Q-Q-Q-------K----L-----A------	----Y	-V--T-E-------	------S----------	-----------N-------------------S-	YR-DDAM -Y	--Q--------
		2G5	2	------------K----L-----A------	S-A--	-V--T-E-------	-----------T-N---	----------HN------H-----------A-	NLPYDHV -Y	--Q--S-----
		3C3	2	----K-------K----L-----A------	S-A--	-V--T-E-------	-----------T-N---	----------HN------H-----------A-	NLPYDHV -Y	--Q--S-----
		3F4	2	EG----------K----L-----A------	S-A--	-V--T-EH------	-------P---T-N---	----------HN------H-----------A-	NLPYDHV -Y	--Q--S-----
		3H4	2	------------K---PL-----A------	S-A--	-V--T-EH------	-------F---T-N---	----------HN------H-----------A-	NLPYDHV -Y	--Q--S-----
	3	1B3	2	EVQLQESGGGVVQPGRSLRLSCAASGFTFS	SYAMH	WVRQAPGKGLEWVA	VISYDGSNKYYADSVKG	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR	DWSEGYYYYG MDV	WGQGTTVIVSS
		1C6	2	QI--LQ------------------------	-----	--------------	-----------------	--------------------------------	---------- ---	-----------
		2B6	2	VKLVES/GP-L-KPSQSLSLTCTVTGYSIT-	D-AWN	-I--F--NK---MG	Y-N-----N-NP -L-N	-ISIT--T---QFF-KL--VTS----T-----	AGDGY-VD WYFDV	--T--------
		1G5	2	Q----Q--AEL----A-VKM--K---Y--T	--WTT	--K-R--Q----IG	D-YPGSGSTNYNEKF-S	KA-LTV-T-SS-A-N-LS--TS--S-------	ELGD A--Y	-----S-----
		1H6	2	-----Q--AEL-K--A-VKM--K---Y--T	--WTT	--K-R--Q----IG	D-YP-SGSTNYNEKF-S	KA-LTV-T-SS-A-M-LS--TS--S-------	ELGD A--Y	-----S-----
	4	1F3	2	EVQLQQSGAELVKPGASVKLSCKASGYTFT	SFWMH	WVKQRPGRGLEWIG	RLDPNSGETKYNEKFKS	KATLTVDKPSSTAYMELSSLTSEDSAVYYCAR	EAYGYWN FDV	WGTGTTVTVSS
		2E8	2	------------------------------	-----	--------------	------------K----	--------------------------------	------- ---	-----------
V_L	1	C15	1	DIELTQSPAIMSASPGEKVIMTC	SASS SVSHMY	WYQQKPGSSPRLLIY	DTSNLAS	GVPIRFSGSGSGTSYSLTISRMEAEDSATYYC	QQWSSYPFT	FGSGTKLELKR
		C9	1	--D---------S--------I--	---- ---Y-H	-F-----T--KPW--	S------	---A----------------SV----A-----	--Y-G--L-	--A-----I--
		1D5	2	------------A--------I--	----S I-S-NLH	-----SETSPKPW--	G------	---V----------------S-----A-----	---G---L-	--G-----I--
		C1	1	-----------------------	---- ---Y--	---------------	-------	---V----------------------A-----	-------L-	--A--------
		S25	1	----------L-A--------I--	-V--S I-S-NLH	-----S-T--KPW--	G------	---V----------------S-----A-----	-------L-	--A-----I--
		1B6	2	----------SLAV-L-QRA-IS-	RA-ESVDSYGN-F-H	-------QP-K----	RA---E-	-I-A-------R-DFT--INPV--D-V-----	--SNED-P-	--A--------
		1C9	2	----------SLAV-L-QRA-IS-	RA-ESVDSYGN-F-H	-------QP-K----	RA---E-	-I-A-------R-DFT---NPV--D-V-----	--SNED-Y-	--G-----I--
		1E8	2	-----------------------	---- ---Y-H	-----S-T--KRW--	---K---	---A----------------S-----A-----	-----N-L-	--A--------
		1G7	2	-----------------------	---- ---Y-H	-----S-T--KRW--	---K---	---A----------------S-----A-----	-----N-L-	--A--------
	2	1A1	2	DIELTQSPASLAVSLGQRATISC	RASESVDSYGNSFMH	WYQQKPGQPPKLLIY	LASNLES	GVPARFSGSGSRTDFTLTIDPVEADDAATYYC	QQNNEDPYT	FGGGTKLEIKR
		1F1	2	--------T--------------	---------------	---------------	-------	--------------------------------	---------	-----------
		C39	1	-----------------R-----	----------H----	---------------	-------	--------------------------------	---------	-----------
		C25	1	-----------------------	----------H---Q	---------------	R-----P	-I---------G-------N------V-----	--S----F-	--S--------
		2G5	2	---------IMSA-P-EKVTTT-	S--S SV-Y--	-F-----TS-K-W--	ST---A-	-----------G-SYS---SRM--E-------	--RSSY---	----DQAGN-S
		3C3	2	---------IMSA-P-EKVTTT-	----------H---Q	-F-----TS-K-W--	ST---A-	-----------G-SYS---SRM--E-------	--RSSY---	----DQAGN--
		3F4	2	-T-------IMSA-P-EKVTMT-	S--S SV-Y-Y	-------SS-R----	DT---A-	---V-------G-SYS---SRM--E-------	--WSSY-P-	-----------
		3H4	2	---------IMSA-P-EKVTMT-	---S- VSS-YL-	-------SS-R----	DT---A-	---V-------G-SYS---SRM--E-------	--WSSY-P-	-----------
	3	1B3	2	DSELTQSPTTMAASPGEKITTTC	SASSS ISSNYLH	WYQQRPGFSPKLLIY	RTSNLAS	GVPARFSGSGSGTSYSLTIGTMEAEDVATYYC	QQGSSIPRT	FGGGTKLEIKR
		1C6	2	-I------ASL-V-L-RRA--S-	R--E-VEYYGTSLMQ	----K--QP------	AA--VE-	-------------DF--N-HPV-E -I-M-F-	--SRKV-W-	-----------
		2B6	2	YI------ASL-V-L-QRA--S-	R--E-VDSYGNSFM-	----K--QP------	LA---E-	-----------R-DFT---DPV--D-A-----	--NNED-Y-	----------S
		1G5	2	-I------ASL-V-L-QRA--S-	R--E-VEYYGTSLMQ	----K--QP------	AA--VE-	-A-----------DF--N-HPV-ED-I-M-F-	--SRKV-Y-	-----------
		1H6	2	-I------AI-S------V----	-V--- ---SN--	----KS-T----W--	G------	---V---------------SS-----A-----	--W--Y-L-	--A---V-LR-
	4	1F3	2	DIELTQSPASMSASPGEKVTMTC	RATSS VSSSYLH	WYQQKSGASPKLWIY	SASNLAS	GVPSRFSGSGSGTSYSLTISSVEAEDAATYYC	QQYIGYPYT	FGGGTKLEIKR
		2E8	2	--------TT-A------I-I--	S-S-- IG-N---	-----P-F----L--	RT-----	---A---------------GAM----V-----	--GSSI---	-----------

[a] Lib, library.

[b] Full-length sequences were not determined for clones C12, C13, C2, and S44 (all bind epitope 1). Accession can be made through GenBank with nos. AF003702 to AF003725.

k_{off} differed over 33-fold, between scFv (Table 7). *In vitro* toxin neutralization was determined by using a mouse hemidiaphragm preparation and measuring the time to 50% twitch tension reduction for BoNT/A alone and in the presence of 2.0 x 10^{-8} M scFv. Values are reported in time to 50% twitch reduction. scFv binding to epitope 1 (S25) and epitope 2 (C25) significantly prolonged the time to neuroparalysis: 1.5-fold (152%) and 2.7-fold (270%), respectively (Table 7 and Figure 3). In contrast, scFv binding to epitopes 3 and 4 had no significant effect on the time to neuroparalysis. A mixture of S25 and C25 had a significant additive effect on the time to neuroparalysis, with the time to 50% twitch reduction increasing 3.9-fold (390%).

[0234] Table 7. Affinities, binding kinetics, and *in vitro* toxin neutralization results of scFv selected from phage antibody libraries

scFv clone	Epitope	K_d[a] (M)	k_{on} (10^4 M^{-1} s^{-1})	k_{off} (10^{-3} s^{-1})	Paralysis Time[b]
S25	1	7.3 x 10^{-8}	1.1	0.82	85 ± 10[c]
C25	2	1.1 x 10^{-9}	30	0.33	151 ± 12[c]
C39	2	2.3 x 10^{-9}	14	0.32	139 ± 8.9[c]
1C6	3	2.0 x 10^{-8}	13	2.5	63 ± 3.3
1F3	4	1.2 x 10^{-8}	92	11	52 ± 1.4
C25 + S25 Combination					218 ± 22[c, d]
BoNT/A pure toxin (control)					56 ± 3.8

[a] k_{on} and k_{off} were measured by surface plasmon resonance and K_d calculated as k_{off}/k_{on}.

[b] Time (min.) to 50% twitch reduction in mouse hemidiaphragm assay using 20 nM scFv + 20 pM BoNT/A, compared to time for BoNT/A alone. For C25 + S25 combination, 20 nM scFv each was used. Each value is the mean ± SEM of at least three observations.

[c] $p < 0.01$ compared to BoNT/A.

[d] $p < 0.05$ compared to C25

Discussion.

[0235] BoNTs consist of a heavy and a light chain linked by a single disulfide bond. The carboxy-terminal half of the toxin binds to a specific membrane receptor(s), resulting in internalization, while the amino-terminal half mediates translocation of the toxin from the endosome into the cytosol. The light chain is a zinc endopeptidase which cleaves an essential synaptosomal protein, leading to failure of synaptic transmission and paralysis. Effective immunotherapy must prevent binding of the toxin to the receptor, since the other two toxin functions occur intracellularly. Identification of epitopes on H_c which mediate binding is an essential first step, both to the design of better vaccines and to development of a high-titer neutralizing monoclonal antibody (or antibodies) for passive immunotherapy.

[0236] For this work, we attempted to direct the immune response to a neutralizing epitope(s) by immunization with recombinant BoNT/A H_c. This should lead to the production of antibodies that prevent binding of toxin to its cellular receptor(s). One limitation of this approach is the extent to which recombinant H_c mimics the conformation of H_c in the holotoxin. The fact that 50% of antibodies selected on H_c recognize holotoxin suggests significant structural homology for a large portion of the molecule. Although 50% of antibodies selected on H_c do not bind holotoxin, this could result from packing of a significant portion of the H_c surface against other toxin domains. Our results do not, however, exclude the possibility that some of these antibodies are binding H_c conformations that do not exist in the holotoxin or that conformational epitopes present in the holotoxin are absent from recombinant H_c. This could lead to failure to generate antibodies to certain conformational epitopes. Regardless, immunizing and selecting with H_c resulted in the isolation of a large panel of monoclonal antibodies which bind holotoxin. In contrast, monoclonal antibodies isolated after immunization with holotoxin or toxoid bind to other toxin domains (H_N or light chain) or to nontoxin proteins present in crude toxin preparations and toxoid (*see* results from library 1, above, and Emanuel *et al.* (1996) *j. Immunol. Meth.,* 193: 189-197).

[0237] To produce and characterize the greatest number of monoclonal antibodies possible, we used phage display. This approach makes it possible to create and screen millions of different antibodies for binding. The resulting antibody fragments are already cloned and can easily be sequenced to identify the number of unique antibodies. Expression levels in *E. coli* are typically adequate to produce milligram quantities of scFv, which can easily be purified by IMAC after subcloning into a vector which attaches a hexahistidine tag to the C terminus. Ultimately, the V_H and V_L genes can be subcloned to construct complete IcG molecules, grafted to construct humanized antibodies, or mutated to create ultrahigh-affinity antibodies. By this approach, 28 unique monoclonal anti-BoNT/A H_c antibodies were produced and characterized.

[0238] The antibody sequences were diverse, consisting of 3 different V_H-gene families, at least 13 unique V-D-J rearrangements, and 3 V_K-gene families. Generation of this large panel of BoNT/A H_c antibodies was a result of the choice of antigen used for immunization and selection (BoNT/A H_c). For example, a Fab phage antibody library constructed from the V genes of mice immunized with pentavalent toxoid yielded only two Fab which bound pure toxin (in this case, BoNT/B). The majority of the Fab bound nontoxin proteins present in the toxoid (Emanuel, *et al., J. Immunol. Methods* 193:189-197 (1996)).

[0239] Despite the sequence diversity of the antibodies, epitope mapping revealed only four nonoverlapping epitopes. Epitopes 1 and 2 were immunodominant, being recognized by 21 of 28 (75%) of the antibodies. Interestingly, approximately the same, number (three to five) of immunodominant BoNT/A H_c peptide (nonconformational) epitopes are recognized by mouse and human polyclonal antibodies after immunization with pentavalent toxoid and by horse polyclonal antibodies after immunization with formaldehyde-inactivated BoNT/A (Atassi (1996) *J. Protein Chem.,* 15: 691-699).

[0240] scFv binding epitopes 1 and 2 resulted in partial antagonism of toxin-induced neuroparalysis at the mouse neuromuscular junction. When administered together, the two scFv had an additive effect, with the time to neuroparalysis increasing significantly. These results are consistent with the presence of two unique receptor binding sites on BoNT/A H_c. While the BoNT/A receptor(s) has not been formally identified, the results are consistent with those of ligand binding studies, which also indicate two classes of receptor binding sites on toxin, high and low affinity, and have led to a "dual receptor" model for toxin binding (Montecucco (1986) *Trends Biochem. Sci.* 11:314-317). Whether both of these sites are on H_c, however, is controversial. In two studies, BoNT/A H_c partially inhibited binding and neuromuscular paralysis (Black, *et al.* (1986) *J. Cell Biol.,* 103:521-534; Black, *et al.* (1980) *Am. J. Med.,* 69:567-570), whereas Daniels-Holgate *et al.* (1996) *J. Neurosci. Res.* 44:263-271, showed that BoNT/A H_c inhibited binding at motor nerve terminals but had no antagonistic effect on toxin-induced neuroparalysis at the mouse neuromuscular junction. Our results are consistent with the presence of two "productive" receptor binding sites on H_c which result in toxin internalization and toxicity. Differences in scFv potency may reflect differences in affinity of H_c for receptor binding sites or may reflect the greater than 10-fold difference in affinity of scFv for H_c. Finally, we have not formally shown that any of the scFv actually block binding of toxin to the cell surface. It is conceivable that the observed effect on time to neuroparalysis results from interference with a postbinding event.

[0241] ScFv antagonism of toxin-induced neuroparalysis in the mouse hemidiaphragm assay was less than that (7.5-fold prolongation of time to neuroparalysis) observed for 2.0 x 10^{-9} M polyclonal equine antitoxin (PerImmune Inc.). This difference could be due to the necessity of blocking additional binding sites, differences in antibody affinity or avidity, or a cross-linking effect leading to aggregated toxin which cannot bind. Affinity of antibody binding is also likely to be an important factor, since the toxin binds with high affinity to its receptor (Williams *et al.* (1983) *Eur. J. Biochem.,* 131: 437-445) and can be concentrated inside the cell by internalization. Of note, the most potent scFv has the highest affinity for H_c. Availability of other scFv described here, which recognize the same neutralizing epitope but with different K_ds, should help define the importance of affinity. These scFv, however, differ by many amino acids and may also differ in fine specificity, making interpretation of results difficult. Alternatively, mutagenesis combined with phage display can lead to the production of scFv which differ by only a few amino acids in sequence but vary by several orders of magnitude in affinity (Schier *et al.*(1996) *J. Mol. Biol.,* 263: 551-567). The same approach can be used to increase antibody affinity into the picomolar range (*Id.*).

[0242] The "gold standard" for neutralization is protection of mice against the lethal effects of toxin coinjected with antibody. While the relationship between *in vitro* and *in vivo* protection has not been formally established, equine antitoxin potentially neutralizes toxin in both types of assays (see above and Hatheway *et al.* (1984) *J. Infect. Dis.,* 150: 407-412). It is believed that this relationship holds for the scFv reported here, and this can be verified experimentally.

[0243] Such studies are not possible with small (25-kDa) scFv antibody fragments. The small size of scFv leads to rapid redistribution (the half-life at a phase is 2.4 to 12 min) and clearance (the half-life at β phase is 1.5 to 4 h) and antibody levels which rapidly become undetectable (Huston, *et al.*,(1996) *J. Nucl. Med.* 40: 320; Schier *et al.* (1995) *Immunotechnology,* 1: 73-81), while toxin levels presumably remain high (Hildebrand, *et al.* (1961) *Proc. Soc. Exp. Biol. Med.* 107-284-289). Performance of *in vivo* studies will be facilitated by the construction of complete IgG molecules from the V_H and V_L genes of scFv. Use of human constant regions will yield chimeric antibodies less immunogenic than murine monoclonals and much less immunogenic than currently used equine antitoxin. Immunogenicity can be further reduced by CDR grafting to yield humanized antibodies.

Example 2

Potent Neutralization Of Botulinum Neurotoxin By Recombinant Oligoclonal Antibody

[0244] The spore-forming bacteria *Clostridium botulinum* secrete botulinum neurotoxin (BoNT), the most poisonous substance known (Gill (1982) *Microbiol. Rev.* 46: 86–94). The protein toxin consists of a heavy and light chain that contain three functional domains (Simpson (1980) *J. Pharmacol. Exp. Ther.* 212: 16–21; Montecucco and Schiavo (1995) *Q. Rev. Biophys.* 28: 423–472; Lacy *et al.* (1998) *Nat. Struct. Biol.* 5: 898–902). The Cterminal portion of the heavy chain (HC) comprises the binding domain, which binds to a sialoganglioside receptor and a putative protein receptor on presynaptic neurons, resulting in toxin endocytosis (Dolly *et al.* (1984) *Nature (London)* 307: 457–460; Montecucco (1986) *Trends Biochem. Sci.* 11: 315–317). The N-terminal portion of the heavy chain (H_N) comprises the translocation domain, which allows the toxin to escape the endosome. The light chain is a zinc endopeptidase that cleaves different members of the SNARE complex, depending on serotype, resulting in blockade of neuromuscular transmission (Schiavo *et al.* (1992) *Nature (London)* 359: 832–835; Schiavo *et al.* (1993) *J. Biol. Chem.* 268: 23784–23787).

[0245] There are seven BoNT serotypes (A–G; Lacy and Stevens (1999) *J. Mol. Biol.* 291: 1091–1104), four of which (A, B, E, and F) cause the human disease botulism (Arnon *et al.* (2001) *J. Am. Med. Assoc.* 285: 1059–1070). Botulism is characterized by flaccid paralysis, which if not immediately fatal requires prolonged hospitalization in an intensive care unit and mechanical ventilation. The potent paralytic ability of the toxin has resulted in its use in low doses as a medicine to treat a range of overactive muscle conditions including cervical dystonias, cerebral palsy, posttraumatic brain injury, and poststroke spasticity (Mahant *et al.* (2000) *J. Clin. Neurosci.* 7: 389–394). BoNTs are also classified by the Centers for Disease Control (CDC) as one of the six highest-risk threat agents for bioterrorism (the ''Class A agents''), because of their extreme potency and lethality, ease of production and transport, and need for prolonged intensive care (Arnon *et al.* (2001) *J. Am. Med. Assoc.* 285: 1059–1070). Both Iraq and the former Soviet Union produced BoNT for use as weapons (United Nations Security Council (1995) *Tenth Report of the Executive Committee of the Special Commission Established by the Secretary-General Pursuant to Paragraph 9(b)(I) of Security Council Resolution 687 (1991), and Paragraph 3 of Resolution 699 (1991) on the Activities of the Special Commission* (United Nations Security Council, New York); Bozheyeva *et al.* (1999) *Former Soviet Biological Weapons Facilities in Kazakhstan: Past, Present, and Future* (Center for Nonproliferation Studies, Monterey Institute of International Studies, Monterey, CA)), and the Japanese cult Aum Shinrikyo attempted to use BoNT for bioterrorism (Arnon *et al.* (2001) *J. Am. Med. Assoc.* 285: 1059–1070). As a result of these threats, specific pharmaceutical agents are needed for prevention and treatment of intoxication.

[0246] No specific small-molecule drugs exist for prevention or treatment of botulism, but an investigational pentavalent toxoid is available from the CDC (Siegel (1988) *J. Clin. Microbiol.* 26: 2351–2356) and a recombinant vaccine is under development (Byrne and Smith (2000) *Biochimie* 82: 955–966). Regardless, mass civilian or military vaccination is unlikely because of the rarity of disease or exposure and the fact that vaccination would prevent subsequent medicinal use of BoNT. Postexposure vaccination is useless because of the rapid onset of disease. Toxin neutralizing antibody (Ab) can be used for pre- or postexposure prophylaxis or for treatment (Franz *et al.* (1993) Pp. 473-476 in *Botulinum and Tetanus Neurotoxins: Neurotransmission and Biomedical Aspects*, ed. DasGupta, B. R. Plenum, New York). Small quantities of both equine antitoxin and human botulinum immune globulin exist and are currently used to treat adult (Black and Gunn (1980) *Am. J. Med.* 69: 567–570; Hibbs *et al.* (1996) *Clin. Infect. Dis.* 23: 337–340) and infant botulism (Arnon (1993) Pp. 477-482 in *Botulinum and Tetanus Neurotoxins: Neurotransmission and Biomedical Aspects*, ed. DasGupta, B. R. Plenum, New York), respectively. Recombinant monoclonal antibody (mAb) could provide an unlimited supply of antitoxin free of infectious disease risk and not requiring human donors for plasmapheresis. Such mAbs must be of high potency to provide an adequate number of doses at reasonable cost. In some instances, the potency of polyclonal Ab can be recapitulated in a single mAb (Lang *et al.* (1993) *J. Immunol.* 151: 466–472). In the case of BoNT, potent neutralizing mAbs have yet to be produced: single mAb neutralizing at most 10 to 100 times the 50% lethal dose (LD50) of toxin in mice (Pless *et al.* (2001) *Infect. Immun.* 69: 570–574; Hallis *et al.* (1993) Pp. 433-436 In: *Botulinum and Tetanus Neurotoxins: Neurotransmission and Biomedical Aspects*, ed. DasGupta, B. R., Plenum, New York). In this example, we show that BoNT serotype A (BoNT/A) can be very potently neutralized *in vitro* and *in vivo* by combining two or three mAbs, providing a route to drugs for preventing and treating botulism and diseases caused by other pathogens and biologic threat agents.

Methods

IgG Construction.

[0247] V_H genes of C25, S25, and 3D12 single-chain fragment variable (scFv) were amplified using PCR from the respective phagemid DNA with the primer pairs GTC TCC TGA GCT AGC TGA GGA GAC GGT GAC CGT GGT (SEQ ID NO:183) and either GTA CCA ACG CGT GTC TTG TCC CAG GTC CAG CTG CAG GAG TCT (C25, SEQ ID NO:184), GTA CCA ACG CGT GTC TTG TCC CAG GTG AAG CTG CAG CAG TCA (S25, SEQ ID NO:185), or GTA CCA ACG CGT GTC TTG TCC CAG GTG CAG CTG GTG CAG TCT (3D12, SEQ ID NO:186). DNA was digested with Mlu1 and *NheI*, ligated into N5KG1Val- Lark (gift of Mitch Reff, IDEC Pharmaceuticals, San Diego) and clones containing the correct V_H identified by DNA sequencing. V_ genes of C25, S25, and 3D12 scFv were amplified from the respective phagemid DNA with the primer pairs TCA GTC GTT GCA TGT ACT CCA GGT GCA CGA TGT GAC ATC GAG CTC ACT CAG TCT (SEQ ID NO:187) and CTG GAA ATC AAA CGT ACG TTT TAT TTC CAG CTT GGT (C25, SEQ ID NO:188), TCA GTC GTT GCA TGT ACT CCA GGT GCA CGA TGT GAC ATC GAG CTC ACT CAG TCT (SEQ ID NO:189) and CTG GAA ATC AAA CGT ACG TTT GAT TTC CAG CTT GGT (S25, SEQ ID NO:190), or TCA GTC GTT GCA TGT ACT CCA GGT GCA CGA TGT GAC ATC GTG ATG ACC CAG TCT (SEQ ID NO:191) and CTG GAA ATC AAA CGT ACG TTT TAT CTC CAG CTT GGT (3D12, SEQ ID NO:192), cloned into pCR-TOPO (Invitrogen) and clones containing the correct V_ identified by DNA sequencing. V_ genes were excised from pCR-TOPO with *Dra*III and *Bsi*WI and ligated into *Dra*III- and BsiWI-digested N5KG1Val-Lark DNA containing the appropriate V_H gene. Clones containing the correct VH and Vκ gene were identified by DNA sequencing, and vector DNA was used to transfect CHO DG44 cells by electroporation. Stable cell lines were established by selection in G418 and expanded into 1L spinner flasks. Supernatant containing IgG was collected, concentrated by ultrafiltration, and purified on Protein G (Pharmacia).

Measurement of IgG Affinity and Binding Kinetics.

[0248] IgG binding kinetics were measured using surface plasmon resonance in a BIAcore (Pharmacia Biosensor) and used to calculate the K_d. Approximately 200–400 response units of purified IgG (10–20 μg/ml in 10 mM acetate, pH 3.5–4.5) was coupled to a CM5 sensor chip by using *N*-hydroxysuccinimide–*N*-ethyl-*N'*-(dimethylaminopropyl)-carbodiimide chemistry. The association rate constant for purified BoNT/AH_C was measured under continuous flow of 15 μl/min, using a concentration range of 50–800 nM. The association rate constant (k_{on}) was determined from a plot of (ln(dR/dt))/t vs. concentration. The dissociation rate constant (k_{off}) was determined from the dissociation part of the sensorgram at the highest concentration of scFv analyzed using a flow rate of 30 μl/min to prevent rebinding. K_d was calculated as k_{off}/k_{on}.

Measurement of in Vitro Toxin Neutralization.

[0249] Phrenic nervehemidiaphragm preparations were excised from male CD-1 mice (25–33g) and suspended in 135 mM NaCl, 5 mM KCl, 1 mM Na_2HPO_4, 15 mM $NaHCO_3$, 1 mM $MgCl_2$, 2 mM $CaCl_2$, and 11 mM glucose. The incubation bath was bubbled with 95% O_2/5% CO_2 and maintained at 36°C. Phrenic nerves were stimulated at 0.05 Hz with square waves of 0.2 ms duration. Isometric twitch tension was measured using a force-displacement transducer (Model FT03, Grass Instruments, Quincy, MA). Purified IgG were incubated with BoNT A for 30 min at room temperature and then added to the tissue bath resulting in a final IgG concentration of 6.0×10^{-8} M (S25 and 3D12 alone) or 2.0×10^{-8}M (C25 alone) and a final BoNT A concentration of 2.0×10^{-11} M. For pairs of IgG, the final concentration of each IgG was decreased 50%, and for studies of a mixture of all 3 IgG, the concentration of each IgG was decreased by 67%.

Measurement of in Vivo Toxin Neutralization.

[0250] Fifty micrograms of the appropriate IgG were added to the indicated number of mouse LD_{50} of BoNT/A neurotoxin (Hall strain) in a total volume of 0.5 ml of gelatin phosphate buffer and incubated at RT for 30 min. For pairs of Ab, 25 μg of each Ab was added, and for the combination of 3 Ab, 16.7 μg of each Ab was added. The mixture was then injected i.p. into female CD-1 mice (16–22 g). Mice were studied in groups of ten and were observed at least daily. The final death tally was determined 5 days after injection.

Measurement of Solution Affinity of mAbs.

[0251] Equilibrium binding studies were conducted using a KinExA flow fluorimeter to quantify the antibodies with unoccupied binding sites in reaction mixtures of the antibody with the antigen. Studies with reaction mixtures comprised of one, two, or three different antibodies were conducted in Hepes-buffered saline, pH 7.4, with total antibody concentrations of 342, 17.2, and 17.2 pM, respectively. In all cases, the concentration of soluble toxin was varied from less than 0.1 to greater than 10-fold the value of the apparent K_d (twelve concentrations, minimum). Reaction mixtures comprised of one, two, or three different antibodies were incubated at 25°C for 0.5, 3, and 17 h, respectively, to ensure that equilibrium was achieved.

Results

[0252] To generate mAbs capable of neutralizing BoNT/A, we previously generated scFv phage antibody libraries from mice immunized with recombinant BoNT/A binding domain (H_C) and from humans immunized with pentavalent botulinum toxoid (Amersdorfer *et al.* (1997) *Infect. Immun.* 65: 3743–3752; Amersdorfer *et al.* (2002) *Vaccine* 20: 1640–1648). After screening more than 100 unique mAbs from these libraries, three groups of scFv were identified that bound nonoverlapping epitopes on BoNT/AH_C and that neutralized toxin *in vitro* (prolonged the time to neuroparalysis in a murine hemidiaphragm model; Amersdorfer *et al.* (1997) *Infect. Immun.* 65: 3743–3752; Amersdorfer *et al.* (2002) *Vaccine* 20: 1640–1648). *In vitro* toxin neutralization increased significantly when two scFv binding nonoverlapping epitopes were combined. *In vivo* toxin neutralization could not be determined because of the rapid clearance of the 25-kDa scFv from serum (Colcher *et al.* (1990) *J. Natl. Cancer Inst.* 82: 1191–1197).

[0253] To evaluate *in vivo* BoNT neurotoxin neutralization, IgG were constructed from the VH and V_ genes of three BoNT/A scFv that neutralized toxin *in vitro*. V_H and Vκ genes were sequentially cloned into a mammalian expression vector, resulting in the fusion of the human Cκ gene to the Vκ and the human γ1 gene to the V_H. Stable expressing cell lines were established and IgG purified from supernatant yielding chimeric IgG with murine V-domains and human C-domains, for the murine scFv C25 and S25, and a fully human IgG for the human scFv 3D12. IgG equilibrium binding constants (K_d) were measured and found to be at least comparable to the binding constants of the scFv from which they were derived (Table 8). The antigen binding affinity of two of the IgG (S25 and 3D12) was significantly higher (lower K_d) than for the corresponding scFv, largely because of an increase in the association rate constant (k_{on}). We presume this reflects an increase in the stability of the molecule and hence an increase in the functional antibody concentration.

[0254] Table 8. Association (k_{on}) and dissociation (k_{off}) rate constants and equilibrium dissociation constants (K_d) for BoNT/A IgG and scFv from which the IgG were derived.

	IgG				scFv		
Ab	K_d	k_{on}	k_{off}		K_d	k_{on}	k_{off}
C25	1.69 x 10^{-9}	1.32 x 10^{6}	2.24 x 10^{-3}		1.10 x 10-9	3.00 x 10^{5}	3.30 x 10^{-4}
S25	3.90 x 10^{-9}	1.46 x 10^{6}	5.70 x 10^{-3}		7.30 x 10-8	1.10 x 10^{4}	8.10 x 10^{-4}
3D12	5.62 x 10^{-11}	2.26 x 10^{6}	1.27 x 10^{-4}		3.69 x 10-8	1.30 x 10^{4}	5.00 x 10^{-4}

[0255] *In vitro* toxin neutralization by IgG was determined in the mouse hemidiaphragm assay (Desphande *et al.* (1995) *Toxicon* 33: 551–557). Compared with toxin alone, each of the three IgG significantly increased the time to neuroparalysis, with C25 being the most potent (Figure 4). Significant synergy in toxin neutralization was observed when pairs of IgG were studied. For these studies, it was necessary to decrease the concentration of C25 IgG studied 3-fold to 20 nM because of its high potency and the fact that the hemidiaphragm preparations have an 8-h lifespan. Each pair of IgG significantly increased the time to neuroparalysis compared with the time for either single IgG (Figure 4). A mixture of all three IgG further increased the time to neuroparalysis, although this difference did not reach statistical significance compared with antibody pairs because of the small number of diaphragms studied.

[0256] *In vivo* toxin neutralization was studied using a mouse assay in which toxin and Ab are premixed and injected i.p., and time to death and number of surviving mice determined (Sheridan *et al.* (2001) *Toxicon* 39: 651–657). Fifty micrograms of each single mAb prolonged the time to death but failed to protect mice challenged with 20 LD_{50}s (Figure 5A). In contrast, any pair of mAbs completely protected mice challenged with 100 LD_{50}s of toxin (Figure 5B). At 500 LD_{50}s, the majority of mice receiving two of the pairs of mAbs (S25 + 3D12 or C25 + S25) died, whereas 80% of mice receiving the pair of C25 + 3D12 survived (Figure 3). All mice receiving a mixture of all three mAbs (oligoclonal Ab) survived challenge with 500 LD_{50}s of toxin (Figure 6). In these studies, the total amount of Ab administered was kept constant at 50 μg per mouse. To determine potency, mAb pairs and oligoclonal Ab were studied at increasing doses of toxin (Figure 6). The most potent mAb pair (C25 + 3D12) protected 90% of mice challenged with 1,000 LD_{50}s, with no mice surviving challenge with 2,500 LD_{50}s. In contrast, oligoclonal Ab completely protected all mice challenged with 5,000 LD_{50}s of toxin, with five of ten mice surviving challenge with 20,000 LD_{50}s of toxin. The potency of the oligoclonal Ab was titrated using a modification of the standard mouse neutralization bioassay (Hatheway and Dang (1994) Pp. 93-107 In: *Therapy with Botulinum Toxin*, ed. Jankovic, J., Dekker, New York) and was determined to be 45 international units (IU)/mg of Ab, 90 times more potent than the human botulinum immune globulin used to treat infant botulism (Arnon (1993) Pp. 477-482 in *Botulinum and Tetanus Neurotoxins: Neurotransmission and Biomedical Aspects*, ed. DasGupta, B. R. Plenum, New York). By definition, one IU neutralizes 10,000 LD50s of BoNT/A toxin (Bowmer (1963) *Bull. W. H. O.* 29: 701–709).

[0257] Two potential mechanisms could account for the increase in potency observed when mAbs were combined: an increase in the functional binding affinity of the Ab mixture for toxin and/or an increase in the blockade of the toxin surface that binds to cellular receptor(s). To determine the effect of combining antibodies on the functional binding affinities, apparent K_d were determined for each single mAb, pairs of mAbs, and the mixture of all three mAbs by using a flow fluorimeter to quantify the free antibody that remained in solution reaction mixtures. For single mAbs, the antigen binding affinities measured in homogeneous solution (both antigen and antibody in solution; Fig. 7) were lower (higher K_d) than those measured by surface plasmon resonance in a BIAcore (Table 8), where the antibody is immobilized and only the antigen is in solution. When antibody C25, which showed the greatest *in vitro* potency, was mixed in equimolar amounts with antibody 3D12, the resulting Ab combination bound to the toxin with an apparent K_d of 65 pM, an affinity 200- and 10-fold higher (lower K_d) than those observed with the individual antibodies alone. Addition of equimolar amounts of a third mAb (S25) to the mixture increased the apparent affinity further to 18 pM. An equimolar mixture of C25 with S25 yielded only a minor 2-fold increase in affinity, which may explain why this pair is less potent *in vivo* than the combination of C25 and 3D12. The increase in functional affinity observed with multiple mAbs may be due to either a conformational change in toxin that occurs on binding of the first mAb, resulting in higher affinity binding of the second and third mAbs, or from mAb binding changing the toxin from a monovalent to a multivalent antigen (Moyle *et al.* (1983) *J. Immunol.* 131: 1900–1905). This results in an ''avidity effect'' and an increase in affinity. Avidity effects have been well recognized and characterized for IgG binding to multivalent antigens (Crothers and Metzger (1972) *Immunochemistry* 9: 341–357), such as cell surfaces, but are not well appreciated as occurring in solution.

[0258] The increments in measured *Kd* are consistent with the increase in *in vivo* potency observed for mAb pairs and oligoclonal Ab. Rearranging the equilibrium binding equation:

$$\text{free toxin/bound toxin} = K_d/[\text{serum antibody}].$$

Assuming a 2-ml mouse blood volume, the serum antibody concentration is 160 nM when mice receive 50 μg of Ab. Because the administered amount of toxin is a large multiple of the LD_{50}, bound toxin ~ administered toxin. Thus, the above equation simplifies to:

$$\text{free toxin/administered toxin} = K_d/160\ \text{nM}.$$

To determine the amount of administered toxin that results in death of 50% of mice, one substitutes 1 LD_{50} for the amount of free toxin and solves for administered toxin, yielding the equation:

$$\text{administered toxin (in } LD_{50}\text{s)} = 1\ LD_{50} \times 160\ \text{nM}/K_d.$$

Using the solution *Kd* for C25, the predicted toxin dose at which 50% of the mice survive is 16 LD_{50}s (administered toxin = 1 LD_{50} x 160 nM/10 nM). When this calculation is applied to the C25 and 3D12 Ab pair, and to oligoclonal Ab, the magnitude of the increase in potency on combining antibodies parallels the increase in functional affinity (Table 9).

[0259] Table 9. Observed and predicted toxin neutralization by rewcombinant antibody.

Antibody	Predicted Toxin Neutralization	Observed Toxin Neutralization
C25	16 LD_{50}s	<20 LD_{50}s
C25 + 3D12	2,500 LD_{50}s	1,500 LD_{50}s
C25 + 3D12 + S25	8,900 LD_{50}s	20,000 LD_{50}s

[0260] The second potential mechanism for potent toxin neutralization by oligoclonal Ab is the need to block multiple epitopes on the toxin binding domain surface that bind to cellular receptors. It has been hypothesized that the toxin binds to cellular receptors via at least two sites on the toxin binding domain (. Dolly *et al.* (1984) *Nature (London)* 307: 457–460; Montecucco (1986) *Trends Biochem. Sci.* 11: 315–317). These include a ganglioside binding site and a putative protein receptor binding site. In fact, two spatially separated ganglioside binding sites have been observed in the co-crystal structure of the homologous tetanus toxin (Fotinou *et al.* (2001) *J. Biol. Chem.* 276: 32274–32281), and mAbs binding nonoverlapping tetanus toxin epitopes can block binding of toxin to GT1b ganglioside (Fitzsimmons *et al.* (2000) *Vaccine* 19: 114–121). Our prior epitope mapping studies are consistent with multiple mAbs blocking a large portion of the BoNT binding domain (HC) (Mullaney *et al.* (2001) *Infect. Immun.* 69: 6511–6514). T wo of the mAbs (S25 and 3D12) bind the C-terminal subdomain of BoNT HC. The C25 mAb binds a conformational epitope that consists of sequence from the N- and C-terminal subdomains of BoNT H_C. One model consistent with the epitope mapping places the three mAb epitopes on the same H_C face and overlapping the known docking sites for the putative cellular ganglioside receptor GT1b (Mullaney *et al.* (2001) *Infect. Immun.* 69: 6511–6514).

Discussion

[0261] In conclusion, we have shown that one of the six class A biowarfare agents, BoNT/A, can be potently neutralized by an oligoclonal Ab consisting of only three mAbs. Oligoclonal Ab is 90 times more potent than hyperimmune human globulin and approaches the potency of hyperimmune mono-serotype horse type A antitoxin (Sheridan *et al.* (2001) *Toxicon* 39: 651–657). Thus, the potency of polyclonal serum can be deconvoluted, or reduced, to mAbs binding only three nonoverlapping epitopes. This synergistic effect results in a more than 20,000-fold increase in potency for the three mAbs compared with the potency of any of the single mAbs. Others have previously shown synergy between monoclonal antibodies in neutralizing tetanus toxin or HIV infection. In the case of tetanus toxin, combining three to four monoclonal antibodies increased the potency of *in vivo* toxin neutralization up to 200-fold (Volk *et al.* (1984) *Infect. Immun.* 45: 604–609). In the case of HIV, combining three or four mAbs increased the potency of viral neutralization 10-fold compared with individual mAbs (Zwick *et al.* (2001) *J. Virol.* 75: 12198–12208). Thus, our observation is likely to prove general in many systems. We show, however, that the increased potency in the case of toxin neutralization likely results from a large increase in the functional affinity of the mixture antibodies. Whether such a mechanism holds true for viral neutralization is unclear.

[0262] One can hypothesize that the polyclonal humoral immune response to toxin is functionally dominated by Ab binding only a few nonoverlapping epitopes. The increase in potency appears to result primarily from a large decrease in the K_d of oligoclonal Ab compared with the individual mAb, and also to greater blockade of the toxin surface that interacts with cellular receptors Such mechanisms may be generally applicable to many antigens in solution, suggesting that oligoclonal Ab may offer a general route to more potent antigen neutralization than mAb. Although it might be possible to achieve a similar potency by engineering the K_d of the C25 mAb to near pM, oligoclonal Ab offers a simpler, more rapid route to a potent antitoxin.

[0263] Oligoclonal Ab also offers a safe and unlimited supply of drug for prevention and treatment of BoNT/A intoxication. Because the Ab consists of either chimeric or human IgG, production could be immediately scaled to produce a stockpile of safe antitoxin. Alternatively, we have already replaced the chimeric S25 IgG with a fully human IgG and increased potency of the oligoclonal Ab more than 2-fold. Work is ongoing to replace chimeric C25 with a fully human homologue. Chimeric, humanized, and human mAb represent an increasingly important class of therapeutic agents whose means of production are known. Ten mAbs have been approved by the FDA for human therapy and more then 70 other mAb therapeutics are in clinical trials (Reichert (2001) *Nat. Biotechnol.* 19: 819–822). With an elimination half-life of up to 4 weeks, Ab could provide months of protection against toxin or be used for treatment. Oligoclonal Ab would be applicable to the other BoNT toxin serotypes, as well as to other class A agents.

Anthrax is a toxin-mediated disease, and Ab has been shown to be protective for this agent (Little *et al.* (1997) *Infect. Immun.* 65: 5171–5175; Beedham *et al.* (2001) *Vaccine* 19: 4409–4416). Vaccinia immune globulin can be used to prevent or treat smallpox or complications arising from vaccination of immunocompromised hosts (Feery (1976) *Vox Sang.* 31: 68–76). Ab may also be useful for plague and disease caused by the hemorrhagic fever viruses (Hill *et al.* (1997) *Infect. immun.* 65: 4476–4482; Wilson *et al.* (2000) *Science* 287: 1664–1666). Our data support the rapid development and evaluation of oligoclonal Ab for countering BoNT and other agents of biowarfare and bioterrorism.

Example 3

Genetic And Immunological Comparison Of Anti-Botulinum Type A Antibodies From Immune And Non-Immune Human Phage Libraries

[0264] Understanding the antibody response in botulinum intoxication is important for vaccine design and passive prophylaxis. To investigate this activity, we have studied the immune response to BoNT/A (botulinum neurotoxin serotype A) binding domain (H_C) at the molecular level using phage display. The scFv antibodies were isolated from V-gene repertoires prepared from (a) human volunteer immunized with pentavalent botulinum toxoid and (b) non-immune human peripheral blood lymphocytes and spleenocytes. A large panel of serotype specific phage expressing botulinum binding scFv could be selected from both libraries. Epitope mapping of immune scFv binders towards BoNT/A HC revealed surprisingly a limited number of scFv recognizing conformational epitopes that corresponded to two distinct groups, clusters I and II. Only scFv from cluster I exhibited neutralizing activity in the mouse hemidiaphragm assay. Anti- BoNT/A HC clones derived from a non-immune library could be conveniently grouped into clusters III–XI and appeared to share no overlapping epitopes with cluster I or II. In addition they showed no neutralization of toxin at biologically significant concentrations. We therefore suggest that a vaccine based on the pentavalent botulinum toxoid directs the humoral immune response to a limited number of immunodominant epitopes exposed on the binding domain HC.

Introduction

[0265] Botulinum toxin is a paralytic neurotoxin existing as seven different serotypes (A–G) elaborated by a number of bacterial species belonging to the genus *Clostridium* (Hatheway (1989) Pp. 3-24 In: Simpson LL, editor. Botulinum neurotoxin and tetanus toxin. San Diego: Academic Press). They are produced as a single chain protein (Mr : 150,000) and fully activated by limited proteolysis, which results in formation of two chains, the heavy (M_r : 100,000) and light (Mr : 50,000) chains held together by a disulfide bond and non-covalent bonds (Niemann (1991) Pp. 303-348 In: Alouf JE, Freer JH, editors. Sourcebook of bacterial protein toxins. New York: Academic Press; Simpson (1990) *J Physiol.*, 84:143–151). Poisoning can occur by ingestion of clostridia-contaminated food (foodborne botulism), by infant bowel infection (infant botulism), and by deep subcutaneous infection of wounds (wound botulism). Human botulism is most frequently caused by types A, B, and E and rarely by F (Dowell (1984) *Rev Infect Dis.*, 6(Suppl 1):202–207; Botulism in the United States. Handbook for epidemiologists, clinicians and laboratory workers. Atlanta, Center for Disease Control, 1980). BoNTs (botulinum neurotoxin serotypes) act preferentially on cholinergic nerve endings to block acetylcholine release (Habermann *et al.* (1986) *Curr Top Microbiol Immunol.*, 129:93–179; Montecuccoe*t al.* (1994) *Mol Microbiol.*, 13:1–8). The action of BoNTs involves three steps (Simpson (1986) *Ann Rev Pharmacol Toxicol.*, 26:427–453): (1) binding to receptors on the presynaptic membranes via the C-terminus of the heavy chain HC; (2) translocation of the light chain into the cytosol via the N-terminus of the heavy chain HN; and (3) cleavage of one or more key components in the synaptic vesicle docking and fusion protein complex by the zinc protease activity of the light chain (Montecuccoet *al.* (1994) *Mol Microbiol.*, 13:1–8; Schiavo (1992) *J Biol Chem.*, 267:23479–23483; Schiavoet *al.* (1995) *Curr Top Microbiol Immun.*, 195:257–275). Passive immunotherapy has been established as a valuable prophylactic and therapeutic approach against human pathogens and their toxins (for review, see Gronskiet *al.* (1990) *Mol Immunol.*, 28:1321–1332 and Cross (1997) P. 97 In: Cryz SJ, editor. Immunotherapy and vaccines.Weinheim, Germany: VCH Verlagsgesellschaft). In the case of botulism it is believed that antibody preparations recognizing the C-terminal domain of the BoNT heavy chain (HC) are able to prevent binding of the toxin to its cellular receptor(s). Immunization of mice with recombinant HC conferred good protection in vivo to a challenge dose up to 1,000,000 mouse i.p. LD_{50} (Clayton *et al.* (1995) *Infect Immun.*, 63:2738–2742; Byrneet *al.* (1998) *Infect Immun.*, 66:10). Equine plasma-derived polyclonal anti-botulinum antibody preparations (equine HIG) have been administered to more than 80% of adult botulism patients in the past (Middlebrook and Brown (1995) *Curr Top Microbiol Immun.*, 195:89–122; Tacket *et al.* (1984) *Am J Med.*, 76:794–798; Morris (1981) P. 15 In: Lewis GE jr, editor. Biomedical aspects of botulism. New York: Academic Press). The large number of different epitopes recognized by polyclonal antibody preparations normally ensures the presence of protective antibodies, which are usually a small subpopulation of the total antibody. For prophylaxis, equine antibody is most effective when administered prior to exposure, but can prevent the disease up to 24 h post exposure (Middlebrook and Brown (1995) *Curr Top Microbiol Immun.*, 195:89–122). However, administration of equine antitoxin can cause adverse reactions, such as serum sickness and anaphylaxis in 9% of cases (Black and Gunn (1980) *Am J Med.*, 69:567–570). Recent efforts have been focused on the production of human immunoglobulin (human BIG) prepared from serum of immunized volunteer donors (Arnon (1993) Pp. 477-482 In: DasGupta BR, editor. Botulinum and tetanus neurotoxins,neurotransmission and biomedical aspects. New York: Plenum Press). Neutralizing monoclonal antibodies, especially if of human origin, would provide an unlimited source of antibody and replace the preparation of antibody from humans or horses.

[0266] We have been using antibody phage display to generate monoclonal antibodies capable of neutralizing BoNTs (Hoogenboom *et al.* (1991) *Nucl Acids Res.*, 19:4133–4137; McCaffertyet *al.* (1990) *Nature*, 348:552–554; Skerra and Pluckthun (1988) *Science*, 240:1038–1041). Using phage antibody libraries constructed from immunized mice, we identified two sets of monoclonal which bound two non-overlapping neutralizing epitopes on BoNT/A HC (Amersdorfer *et al.* (1997) *Infect. Immun.*, 65:3743–3752). In the present example, we describe the characterization of monoclonal antibodies selected from a phage antibody library constructed from a human volunteer immunized with pentavalent botulinum toxoid (A–E). The affinities and epitopes recognized by these monoclonal antibodies were compared to affinities and epitopes recognized by monoclonal antibodies selected from a non-immune human phage library. The results identify an additional neutralizing epitope and provide a path to generating a fully human antibody for botulism prevention and treatment.

Materials and methods:

Immune and non-immune V-gene antibody libraries

[0267] For construction of an immune phage antibody library, a human volunteer received immunization with pentavalent botulinum toxoid types A–E (Michigan Department of Public Health). The volunteer was immunized at 0, 2 and 12 weeks with 0.5 ml of pentavalent toxoid and boosted with 0.5 ml of toxoid 1 year later. The neutralization titer against BoNT/A was measured using the mouse serum neutralization bioassay (Hathewayet *al.* (1984) *J Infect Dis.*, 150: 407–412). PBLs were isolated by centrifugation in Histopaque 1077 and RNA prepared using a modified method of Cathala et al. (Cathala *et al.* (1983) *DNA*, 2:329–335). First strand cDNA was made from RNA prepared from 1.0 x 10^8 B cells, using an IgG constant region primer for heavy chain or κ and λ constant region primers for light chains [26]. *VH* , *Vκ* and *Vλ* genes were amplified from first strand cDNA as described (Marks*et al.* (1991) *J Mol Biol.*, 222:581–597). PCR products were gel purified, ethanol precipitated after extraction from the gel and used to construct *scFv* gene repertoires as previously described (*Id.*). The *scFv* gene repertoires were gel purified and then used as template for re-amplification with flanking oligonucleotides containing appended restriction sites (*Id.*). *scFv* gene repertoires (*VH -Vκ* , *VH -Vλ*) were gel purified, digested with *Sfi*I and *Not*I, extracted with phenol/ chloroform, and ligated into the vector pCANTAB-5E (Pharmacia Biotech, Milwaukee, WI) digested with *Sfi*I and *Not*I (Sambrook*et al.* (1991) New York: Cold Spring Harbor Laboratory). The ligation mix was extracted with phenol/ chloroform, ethanol precipitated, and electroporated into 50 μl E. *coli* TG1 cells (Gibson(1984) University of Cambridge: studies on the Epstein-Barr virus genome). Cells were plated on TYE plates containing 100 _g/ml ampicillin and 1% (w/v) glucose. Colonies were scraped off the plates into 2ml 2 x TY containing 100μg/ml ampicillin, 1% (w/v) glucose and 15% (v/v) glycerol for storage at -70°C. The products from four transformations resulted in a library of 7.7 x 10^5 individual recombinants. For the non-immune library, a previously reported phage-displayed human single chain antibody library containing 6.7 x 10^9 members was utilized (Sheets *et al.* (1997) *Proc Natl. Acad Sci USA*, 95:6157–6162).

Phage preparation and selections

[0268] Phagemid particles from both libraries were prepared by rescue withVCS-M13 helper phage (Stratagene) as previously described (Marks*et al.* (1991) *J Mol Biol.*, 222:581–597). Phage particles were purified and concentrated by two PEG precipitations (Sambrook*et al.* (1991) New York: Cold Spring Harbor Laboratory), resuspended in 2ml phosphate-buffered saline (PBS: 25mM NaH2PO4, 125mM NaCl, pH 7.4) and filtered through a 0.45 μm filter (Nalgene) to achieve a titer of approximately 10^{13} transducing units (TU)/ml.

[0269] Libraries were selected using 75mm x 12mm immunotubes (Nunc, Maxisorb) coated overnight at 4°C with 2ml of BoNT serotypes A, B, C, and E (50μg/ml each), or BoNT/A HC (50μg/ml) in PBS, pH 7.4 (Emanuel *et al.* (1996) *J Immunol Meth.*, 193:189–97). Tubes were blocked with 2% skimmed milk powder in PBS for 1 h at RT, and then the selection, washing and elution procedures were performed as previously described (Marks*et al.* (1991) *J Mol Biol.*, 222:581–597) using phage at a concentration of 5.0 x 10^{12} TU/ml. The 500 μl of the eluted phage were used to infect 10 ml log phase growing *E. coli* TG1, which were plated on 2 x TY-AMP-Glu plates. Phage were rescued, concentrated as described above, and used for the next selection round. The rescue-selection-plating cycle was typically repeated for four rounds.

ELISA screening and fingerprinting

[0270] After each round of selection, single ampicillin-resistant colonies were used to inoculate microtitre plate wells containing 150 μl of 2 x TY-AMP-0.1% glucose. The bacteria were grown to give an *A*600 of approximately 0.9, and scFv expression induced by addition of isopropyl-β-d-thiogalacto- pyranoside (IPTG) to a final concentration of 1mM (De Bellis and Schwartz (1990) *Nucl Acids Res.*, 18:1311). Bacteria were grown overnight with shaking at 25°C, the cells were pelleted by centrifugation, and the supernatant containing soluble scFv was collected. Screening of scFv for binding to BoNTs and BoNT/A HC was performed in 96-well microtitre plates (Falcon 3912) coated with 10 μg/ml of antigen in PBS, pH 7.4. The scFv derived from the non-immune library were detected using mouse monoclonal antibody 9E10 (1 μg/ml) (Santa Cruz Biotechnology, CA), which recognizes the C-terminal myc tag (Munro and Pelham (1986) *Cell*, 46:291–300) followed by peroxidase-conjugated anti-mouse Fc antibody (Sigma) as described (Griffiths and Malmqvist (1993) *EMBO J.*, 12:725–734). The scFvs derived from the immune library were detected using peroxidase-conjugated monoclonal antibody anti-E (2.5 μg/ml) (Pharmacia Biotech). The reaction was stopped after 30 min with NaF (3.2 mg/ml) and A405 nm was measured. The number of unique clones was determined by PCR-fingerprinting (Marks*et al.* (1991) *J Mol Biol.*, 222:581–597) followed by DNA sequencing of the V_H and V_L genes of at least two clones from each fingerprint pattern. The specificity of antibodies was determined by ELISA performed as above using wells coated with 10 μg/ml of BoNT/A, BoNT/B, BoNT/C, BoNT/E, BoNT/A H_C and recombinant translocation domain of serotype A (BoNT/A HN). Clones were identified as being specific for the selected antigen if they gave at least a five-fold higher signal than background.

Subcloning, expression and purification of scFv

[0271] scFv antibodies binding BoNT/A and BoNT/A HC as determined by ELISA were subcloned into the expression vector pUC119 Sfi-NotmycHis, resulting in the fusion of a hexa-histidine tag at the C-terminus of the scFv (Schier*et al.* (1995) *Immunotech.*, 1:73–81). The scFv was expressed and purified by immobilized metal affinity chromatography as previously described (Schier*et al.* (1996) *J Mol Biol.*, 255:28–43) and the concentration of purified monomeric scFv determined spectrophotometrically, assuming an A280 nm of 1.0 correlates to an scFv concentration of 0.7 mg/ml.

Epitope mapping and affinity determination

[0272] Epitope mapping and kinetic studies were performed using surface plasmon resonance in a BIAcore (Pharmacia Biosensor). In a BIAcore flow cell, approximately 600 resonance units (RU) of BoNT/A HC (15μg/ml in 10mM sodium acetate, pH 4.5) were coupled to a CM5 sensor chip using NHS-EDC chemistry (Johnson *et al.* (1991) *Anal Biochem.*, 198:268–277). This amount of coupled BoNT/A HC resulted in scFv RUmax of 100–175RU. The surface was regenerated after binding of scFv using 4M $MgCl_2$. For epitope mapping studies, the amount (RU) of scFv bound for each member of a pair was determined, and then the two scFv were mixed together to give a final concentration equal to the concentration used for measurements of the individual scFv (Amersdorfer *et al.* (1997) *Infect. Immun.*, 65:3743–3752). The *K*d of scFv was calculated from the association rate constants (k_{on}) and dissociation rate constants (k_{off}) determined in the BIAcore ($K_d = k_{off}/k_{on}$). Association was measured under continuous flow of 5 μl/min using a concentration range of scFv from 50 to 1000 nM. The k_{on} was determined from a plot of ln $(dR/dt)/t$ versus concentration (Karlsson *et al.* (1991) *J Immunol Meth.*, 145:229–240). The k_{off} was determined from the dissociation part of the sensorgram at the highest concentration of scFv analyzed using a flow rate of 30 μl/min to prevent rebinding.

***In vitro* bioassay**

[0273] In vitro neutralization studies were performed using a mouse hemidiaphragm preparation, as previously described (Desphande(1995) *Toxicon*, 33:551–557). Phrenic nerve-hemidiaphragm preparations were excised from male CD/1 mice (25–33 g) and suspended in 135mM NaCl, 5mM KCl, 1mM Na_2PO_4 15mM $NaHCO_3$ 1mM $MgCl_2$ 2mM $CaCl_2$, and 11mM glucose. The incubation bath was bubbled with 95% O2, 5% CO and maintained at 36°C. Phrenic nerves were stimulated at 0.05 Hz with square waves of 0.2 ms duration. Isometric twitch tension was measured using a force-displacement transducer (Model FT03, Grass) connected to a chart recorder. Purified scFv antibodies were incubated with BoNT/A for 30 min at RT and then added to the tissue bath resulting in a final scFv concentration of 2.0 x 10^{-8} M and a final BoNT/A concentration of 2.0 x 10^{-11} M. Toxin induced paralysis was defined as a 50% reduction of the initial muscle twitch. The ratio of prolongation was calculated from the value of 50% reduction by the antibody divided by 50% reduction of BoNT/A. The combination of 3D12 and C25 was studied at a final concentration of 2.0 x 10^{-8} M each. Differences between times to 50% twitch reduction were determined using two-tailed *t*-test, with $P < 0.05$ being significant.

Preparation of botulinum toxin and botulinum toxin domains

[0274] Purified botulinum toxin serotype A, B, C and E (150 kDa) were obtained from USAMRIID. The binding domain of botulinum toxin type A (BoNT/A HC) was expressed in *E. coli* and purified by immobilized metal affinity chromatography (IMAC) utilizing a C-terminal (His_6) tag (Ophidian Pharmaceuticals, Inc.). The translocation domain of botulinum toxin type A (BoNT/A HN) was a gift from Dr. R. Stevens (UC-Berkeley, CA).

[0275] Table 10. Specificity of BoNT binding scFv selected from immune and non-immune phage display libraries

scFv specificity	Number of unique scFv	
	Immune Library (pentavalent toxoid)	Non-Immune Library
BoNT/A	23	14
HC (binding domain)	6	10
HN (translocation domain)	4	1
Light chain (cat. domain)	13	3
BoNT/B	16	5
BoNT/C	6	5
BoNT/E	3	3

Results

Strategy for the synthesis of immune phage display library

[0276] PBLs from a human volunteer immunized with pentavalent botulinum toxoid were used to generate a scFv phage antibody library. The donors polyclonal serum was protective against BoNT/A with a titer of 2.56 IU (international units) in the mouse neutralization bioassay (Hathewayet *al.* (1984) *J Infect Dis.*, 150: 407–412). The V_H and V_L genes were amplified from RNA, spliced together to create *scFv* gene repertoires and cloned into pCANTAB-5E to create a phage antibody library of 7.7 x10^5 transformants. PCR screening of 15 randomly selected clones indicated that all carried full length inserts, 66% having $V\kappa$ light chains and 34% having V_λ light chains as determined by germline gene specific light chain primers (data not shown).

Selection of phage antibody libraries and ELISA screening

[0277] Both the immune library and a large non-immune human phage antibody library (Sheets *et al.* (1997) *Proc Natl. Acad Sci USA*, 95:6157–6162) were selected on BoNT serotypes A, B, C, E and BoNT/A HC. After three rounds of selection on BoNT/A or BoNT/A HC, the frequency of ELISA positive clones was 79 and 100%, respectively from the immune library. A similar frequency of ELISA positivity was observed for the other serotypes. After three rounds of selection on BoNT/A or BoNT/A HC, the frequency of ELISA positive clones was 28 and 94%, respectively from the non-immune library. A similar frequency of ELISA positivity was observed for the other serotypes. The number of unique scFv was determined by DNA fingerprinting followed by DNA sequencing, and specificity of each scFv was determined by ELISA. In screening, 100 colonies from each selection, 48 unique antibodies were identified from the immune library (23 BoNT/A, 16 BoNT/B, 6 BoNT/C and 3 BoNT/E) and 27 unique antibodies from the non-immune library (14 BoNT/A, 5 BoNT/B, 5 BoNT/C and 3 BoNT/E) (Table 10).

[0278] The fine specificity of each BoNT/A scFv was determined by ELISA on recombinant BoNT/A HC and BoNT/A HN domains (Figure 8). Of the 23 immune BoNT/A antibodies isolated after selection on toxin, 6 bound to BoNT/A HC (3A6, 3D12, 2A1, 3B8, 3F10, 2B11), 4 bound to BoNT/A HN (3D4, 3A11, 4A4, 3G4) (Figure 8A) and the remaining 13 antibodies presumably bound the light chain (Chen *et al.* (1997) *Infect Immun.*, 65:1626–1630). These findings suggest that immunization with botulinum toxoid directs the immune response towards the light chain, with fewer antibodies directed against the HC or HN domains.

[0279] Selection of the immune library on BoNT/A HC yielded only a single unique antibody (2A1), which was clonally related to toxin selected clones 3D12 and 3D6 (Table 11). When the *VL* gene usage of the six anti-HC clones was analyzed, all were found to use the *Vκ1* gene family (Table 11), although the library contained 2/3 *Vκ* and 1/3 *Vλ* light chain genes. Selection of the non-immune library on BoNT/A holotoxin yielded four antibodies, but none of these bound BoNT/A HC. Selection of the library on BoNT/A HC yielded 10 unique scFv, which used both *Vκ* or *Vλ* light chain genes (Table 11). Overall, only 50% of these scFv bound holotoxin, consistent with the observation that a significant portion of the HC surface is buried in the holotoxin (Lacy *et al.* (1998) *Nat Struct Biol.*, 5:898–902). All scFv antibodies were serospecific and domain specific, with no cross reactivity observed except for clone 2B11 from the non-immune library, which bound to BoNT/A HC and BoNT/A HN domain as determined by ELISA (Figure 8B).

[0280] Table 11. CDR 3-sequences and affinities for human scFv antibodies isolated from immune and non-immune libraries, selected on BoNT/A and BoNT/A H_C.[a]

Non-immune library Heavy Chain				
Clone	Family	Segment	Diff from Genome	V_H CDR3
2A9[b]	V_H3	DP54	5	GRGVN (SEQ ID NO:193)
2B1[b]	V_H3	DP46	0	NGDPEAFDY (SEQ ID NO:194)
2H6[b]	V_H3	DP47	6	ALQSDSPYFD (SEQ ID NO:195)
3C2[b]	V_H3	DP46	2	DLAIFAGNDY (SEQ ID NO:196)
2B6[b]	V_H3	DP47	3	VGVDRWYPADY (SEQ ID NO:197)
3F6[c]	V_H3	DP47	2	DLLDGSGAYFDY (SEQ ID NO:198)
2A2[b]	V_H3	DP46	0	DLDYGGNAGYFDL (SEQ ID NO:199)
2B10[b]	V_H3	DP46	0	DLDYGGNAGYFDL (SEQ ID NO:200)
2E6[b]	V_H3	DP46	0	DYTANYYYYGMDV (SEQ ID NO:201)
3D1b	V_H3	DP47	7	DLGYGSGTSSYYLDY (SEQ ID NO:202)
Non-immune library Light Chain				V_L CDR3
2A9[b]	Vκ1	L12A	6	QQANSFPRT (SEQ ID NO:203)
2B1[b]	Vκ1	L1	11	LQDYNGWT

				(SEQ ID NO:204)
2H6 [b]	Vλ3	DPL16	7	NSRDSSGNHVV (SEQ ID NO:205)
3C2 [b]	Vλ3	DPL16	9	KSRDSRGNHLAL (SEQ ID NO:206)
2B6 [b]	Vκ1	L12A	5	QQYHTISRT (SEQ ID NO:207)
3F6 [c]	Vλ3	DPL16	3	NSRDSSGNHVV (SEQ ID NO:208)
2A2 [b]	Vλ3	DPL16	10	HSRDSSVTNLD (SEQ ID NO:209)
2B10 [b]	Vλ3	DPL16	4	NSRDSSGNHQV (SEQ ID NO:210)
2E6 [b]	Vλ2	DPL12	14	NSRDSSGVV (SEQ ID NO:211)
3D1 [b]	Vλ3	DPL16	5	NSRDSSGNHVV (SEQ ID NO:212)
Immune Library Heavy Chain				
Clone	Family	Segment	Diff from Genome	V_H CDR3
3B8 [c]	V_H1	V1-2	10	LATYYYFGLDV (SEQ ID NO:213)
3F10 [c]	V_H1	V1-2	10	LATYYYFGLDV (SEQ ID NO:214)
2B11 [c]	V_H1	DP10	11	GPWELVGYFDS (SEQ ID NO:215)
3A6c	V_H3	DP50	18	EPDWLLWGDRGALDV (SEQ ID NO:216)
3D12 [c]	V_H3	DP50	13	EPDWLLWGDRGALDV (SEQ ID NO:217)
2A1 [b]	V_H3	DP50	14	EPDWLLWGDRGALDV (SEQ ID NO:218)
Immune Library Light Chain				
Clone	Family	Segment	Diff from Genome	V_L CDR3
3B8 [c]	Vκ1	DPK7	12	QQYNSYVYT (SEQ ID NO:219)
3F10 [c]	Vκ1	DPK8	10	QQLNSYPLT (SEQ ID NO:220)
2B11 [c]	Vκ1	L12	11	QQLISYPLT (SEQ ID NO:221)
3A6 [c]	Vκ1	L12	8	QHYNTYPYT (SEQ ID NO:222)
3D12 [c]	Vκ1	L12	10	QHYNTYPYT (SEQ ID NO:223)
2A1 [b]	Vκ1	L12	4	QHYNTYPYT (SEQ ID NO:224)

[a] Human germline VH , Vκ and Vλ segments have been assigned as detailed in the V-BASE database (MRC Centre for Protein Engineering, Cambridge, UK). Listed clones, with identical VH or VL CDR 3 regions, showed different CDR 1, CDR 2 and framework regions, as indicated by their differences from the germline genes; accession can be made through GenBank with nos. AF090405–AF090420.

[b] Library selected on BoNT/A.

[c] Library selected on BoNT/A HC.

Epitope mapping of BoNT/A HC specific antibody fragments

[0281] BoNT/A HC binding scFv were epitope mapped to determine the number of non-overlapping epitopes recognized. Epitope mapping was performed using surface plasmon resonance in a BIAcoreTM studying pairs of scFv at concentrations resulting in near saturation of the chip surface and at least 100RU of scFv bound. The amount of scFv bound was determined for each member of a pair, and then the two scFv were mixed together to give a final concentration equal to the concentration used for measurements of the individual scFv. Antibodies recognizing identical epitopes showed minimal increase in RU bound when injected together (Figure 9A), while scFv recognizing different epitopes showed an additive increase in RU (Figure 9B). As depicted in Tables 2 and 3, scFv 3A6, 3D12 and 2A1, referred to as cluster I, share high homology of the *VH* and *VL* gene segments (DP 50 and L12, respectively) and recognize overlapping epitopes. They differ in sequence only by mutations in the heavy and light chain genes introduced by somatic mutations. The scFv 3B8 and 3F10, referred to as cluster II, form a second set of antibodies binding to a different epitope compared to cluster I. Clone 2B11, representing a possible unique epitope, could not be analyzed due to poor expression levels. When scFv antibodies derived from the non-immune library were analyzed, we found that all bound to unique epitopes, referred to as clusters III–XI as depicted in Table 3. Members of the non-immune library (clusters III–XI) showed no overlapping binding with members of the immune library (clusters I and II). The epitopes recognized by both the immune and non-immune scFv do not overlap with the epitopes bound by two previously reported murine scFv, C25 and S25 (Amersdorfer *et al.* (1997) *Infect. Immun.*, 65:3743–3752).

Kinetic measurements and neutralization assay

[0282] The *k*on and *k*off were measured using surface plasmon resonance in a BIAcore and used to calculate the equilibrium dissociation constant. The scFv selected from the immune library had K_d's of 3.69 x 10^{-8} and 7.8 x10^{-9} M, values comparable to those reported for monoclonal IgG produced from hybridomas (Foote and Milstein (1991) *Nature*, 352:530–532) (Table 12). Non-immune scFv had lower Kd's ranging from 4.6 x 10^{-7} to 2.61×10^{-8} M. To determine the ability of scFv to neutralize toxin induced neuroparalysis, in vitro studies were performed on one representative member from each epitope cluster using phrenic nerve-hemidiaphragm preparations. Values were reported in time to 50% twitch reduction for BoNT/A alone and in the presence of 2.0 x 10^{-8} M scFv. As shown in Table 12 and Figure 10A and 10B, a significant difference in neutralization of the different anti-BoNT/A H_C scFvs were found, depending on which library was used. From the immune library, 3D12 (cluster I) significantly prolonged the time to neuroparalysis 1.5-fold, whereas 3F10 (cluster II) exhibited no effect on toxin neutralization. Representatives of the non-immune library (clusters III–XI) showed no protective effect in the hemidiaphragm assay, even after combination of all members of clusters III–XI at a final concentration of 1.8 x 10^{-7} M. When using a combination of 3D12 (cluster I) with a previous isolated murine scFv, C25 (Amersdorfer *et al.* (1997) *Infect. Immun.*, 65:3743–3752), time to paralysis increased significantly to 3.2-fold, demonstrating a synergistic effect on toxin neutralization. We observed similar synergy with murine scFv S25 and 3D12 (data not shown).

[0283] Table 12. Affinities, binding kinetics, and in vitro toxin neutralization results of scFv selected from phage antibody libraries.

Clone	Cluster	K_d (M)[a]	k_{on} (x 10^5 $(Ms)^{-1}$)	k_{off} (x $10^{-3}s^{-1}$)	Paralysis Time[b]
Immune Library					
3D12[c]	I	3.69 x 10^{-8}	0.13	0.50	85 ± 5.0[d]
3F10[c]	II	7.80 x 10^{-9}	0.80	0.62	55 ± 5.0[e]
Non-Immune Library					
2B10[f]	III	1.29 x 10^{-7}	5.57	71.6	62.3 ± 6.7[e]
2E6[f]	IV	1.93 x 10^{-7}	1.19	23.0	60.9 ± 8.2[e]
2H6[f]	V	3.86 x 10^{-8}	2.20	8.50	63.0 ± 5.0[e]
2B1[f]	VI	1.07 x 10^{-7}	0.83	8.88	58.4 ± 4.0[e]
2A9[f]	VII	2.61 x 10^{-8}	0.25	0.66	71.0 ± 3.0[e]
2B6[f]	VIII	7.15 x 10^{-8}	1.09	7.80	61.9 ± 5.0[e]
3D1[f]	IX	4.60 x 10^{-7}	1.31	60.3	58.3 ± 3.8[e]
3F6[c]	X	6.60 x 10^{-8}	4.69	30.9	60.4 ± 3.6[e]
3C2[f]	XI	3.90 x 10^{-8}	2.10	82.0	61.9 ± 4.8[e]
Murine Library					
S25	XII	7.30 x 10^{-8}	0.11	0.82	85 ± 10[d]
C25	XIII	1.10 x 10^{-9}	3.0	0.33	151 ± 12[d]
Combination C25 + S25					218 ± 22[g]
C25 + 3D12					179 ± 2.3[d]
Non-immune scFv (Clusters III-XI)					65 ± 2.3[g]
BoNT/A pure toxin (control)					56 ± 3.8

[a] The variables kon and koff were measured by surface plasmon resonance and Kd calculated as koff /kon.
[b] Time (min) to 50% twitch reduction in mouse hemidiaphragm assay using 20nM scFv + 20pM BoNT/A, compared to time for BoNT/A alone. Each value is the mean ± S.E.M. of at least three observations.
[c] Library selected on BoNT/A.
[d] P <0.01 compared to BoNT/A.
[e] Not significant.
[f] Library selected on BoNT/A HC.
[g] P <0.01 compared to BoNT/A HC.

Discussion

[0284] We previously demonstrated that immunization of mice with the recombinant binding domain of BoNT/A HC directs the immune response towards generation of antibodies which bind epitope(s) involved in HC binding to presynaptic toxin receptors (Amersdorfer *et al.* (1997) *Infect. Immun.*, 65:3743–3752). These experiments indicated that neutralization of toxin by scFv could be correlated to both scFv affinity and ability to compete with the holotoxin for receptor binding sites. Here we have carried out a more systematic approach by using immune and non-immune phage display libraries to map human humoral immune and non-immune responses to BoNT/A. The source of antibody genes for the two antibody libraries were (a) PBL of a human volunteer immunized with pentavalent toxoid (A–E) and (b) non-immune peripheral blood lymphocytes and spleenocytes. One limitation of this approach is the extent of which one immune human donor used for these studies represents broad genetic diversity generated upon exposure to botulism. The fact that the humoral immune response in mice and human resulted in a rather limited number of protective epitopes, suggests significant conservation of antigenic epitopes conferring protection. The selection procedure involved panning both combinatorial libraries against four immobilized botulinum neurotoxins, serotypes A, B, C, and E. After three to four panning cycles, antibodies against each serotype were obtained from both libraries, with decreasing frequency in this order, BoNT/A, BoNT/B, BoNT/C and BoNT/E. Similar frequency of binders was also observed for the non-immune library, with the exception of BoNT/B. These results correlate with the findings of Siegel (Siegel (1989) *J Clin Microbiol.*, 26:2351–2356), where they studied serum specimens from 25 human recipients of botulinum pentavalent toxoid. Immunogenicity of the various serotypes was determined by a mouse serum neutralization bioassay--serotype A ranged between 5.7 and 51.6 IU/ml, followed by serotype B from 0.78 to 18 IU/ml and serotype E, from 0.61 to 10 IU/ml.

[0285] Human immunization with toxoid resulted in production of antibodies directed largely against the toxin light chain, with fewer antibodies binding HC. Similar results were observed after immunization of mice with BoNT/A HC followed by holotoxin boosts. Since antibody neutralization activity results largely from blockade of cellular receptor binding by HC, these analyses indicate that an HC vaccine will be more protective than a toxin based vaccine, as more HC antibodies are generated. Human immune HC scFv recognized at least two non-overlapping epitopes. The scFv binding one of these epitopes (cluster I) could neutralize toxin in vitro. Potency of toxin neutralization increased when scFv binding cluster I were combined with immune mouse scFv binding either one of two non-overlapping HC epitopes. This result suggests that HC docks with either multiple cellular receptors, or docking occurs over a broad surface area (Mullaney *et al.* (2001) *Infect Immun.*, 69:6511–6514).

[0286] The repertoire of human scFv recognizing HC was extended to a range of other epitopes (clusters III–XI) by selecting a large non-immune library on BoNT/A. Interestingly, this result is consistent with the concept that the primary immune repertoire contains antibodies capable of recognizing much of the solvent accessible area of an antigen, but that immunization directs this recognition to a limited number of immunodominant epitopes. All of the antibodies obtained from the non-immune library, however, were directed against non-neutralizing epitopes (or at least did not neutralize toxin in vitro). One explanation for the failure of neutralization could be due to low affinity of the antibodies for the HC domain (e.g. 2B10, 2E6, 2B1, 3D1), ranging from 107 to 460nM compared to the high affinity interaction of the toxin to its receptor(s), which is 0.3–2.3nM (Schengrund (1999) *J Toxicol Toxin Rev.*, 18:35–44).

[0287] In conclusion, we report here the successful isolation of specific human antibodies toward botulinum neurotoxins and their subdomains using combinatorial libraries prepared from immune and non-immune human donors. The use of phage display to screen the antibody repertoire of any person with infectious diseases or pathogens allows us to access a very large pool of human monoclonal antibodies with therapeutic and research potential.

Example 4

Neutralizing antibodies evolved for higher affinity

[0288] To improve detection and treatment of botulism, molecular evolution and yeast display was used to increase the affinity of two neutralizing single chain Fv (scFv) antibodies binding BoNT serotype A (BoNT/A), HuC25 and 3D12.

Affinity maturation of the mAb HuC25

[0289] The affinity of HuC25 for BoNT/A was sequentially increased using a series of mutant yeast display libraries (Figure 20). First, the HuC25 gene was subcloned into the yeast display vector pYD2 as a NcoI-NotI fragment. The scFv gene successfully displayed on the yeast surface and the KD of the displayed scFv for pure BoNT/A was determined by flow cytometry to be 8.44×10^{-10} M (Figure 21). This is comparable to the K_D measured for purified HuC25 scFv binding to recombinant BoNT/A HC as previously measured using SPR in a BIAcore (1.4 x 10^{-9} M). The HuC25 scFv gene was then randomly mutated by PCR using error prone conditions and the resulting gene repertoire cloned into pYD2 using gap repair to create a library of 2.0 x 10^5 transformants (Figure 20). The library was grown, induced, and then analyzed by flow cytometry for frequency of scFv display (27%) and antigen binding (3.65%).

[0290] The library was then subjected to four rounds of selection using decreasing concentrations of pure BoNT/A. The scFv gene was PCR amplified from 6 individual colonies obtained after the final round of sorting, revealing the presence of 1 unique sequence, AR1 (Figure 18). The AR1 clone was grown, scFv display induced, and the KD of the displayed scFv for BoNT/A was measured to be 1.69 x 10^{-10} M, a 5 fold improvement from HuC25 (Figure 21).

[0291] To increase affinity further, two mutant yeast display libraries were constructed based on the sequence of AR1. For one library, the AR1 scFv gene was randomly mutated by using error prone PCR; for the second library, site directed mutagenesis was used to diversify four amino acids (SNED) in the L3. This loop was selected for mutagenesis since this it was shown from the selection of AR1 that mutations here could increase affinity and it was likely that the error prone method had not fully sampled mutations in this loop. Four rounds of selection were performed for each library, with a final round of off rate selection performed by labeling with purified BoNT/A followed by a 12 hour dissociation in the presence of BoNT/A binding domain (HC) to prevent rebinding. BoNT/A labeled yeast were then sorted using a mAb (7C1) which bound the catalytic domain of the toxin. Screening of individual colonies from the final round of sorting revealed only wild type AR1 sequence for the site directed library, suggesting that L3 was already optimized. From the error prone library, a single unique clone was isolated (AR2, Figure 18), whose KD as a yeast displayed scFv was determined to be 6.14 x 10^{-11} M, a 2.8 fold increase from the parental AR1 (Figure 21).

[0292] Additional yeast display libraries were created to further increase the affinity of AR2. These included a library where random mutations were introduced into the AR2 gene and two site directed libraries based on the sequence of AR2 which diversified either five amino acids in the H1 or 4 amino acids in L2. Libraries were selected on pure BoNT/A using the strategy described for the selection of AR1, individual colonies sequenced, and the affinities of the unique yeast displayed scFv measured. No clones of higher affinity were identified from the error prone library or the library of L2 mutants. Two clones of higher affinity were identified from the H1 library (Figure 18), AR3 and AR4 (KDs of 1.9 and 2.3 x 10^{-11} M, an approximate three fold increase in affinity from AR2, Figure 21).

Affinity maturation of the mAb 3D12

[0293] For affinity maturation, the 3D12 scFv gene was cloned as a NcoI-NotI fragment from the phagemid vector pCANTAB5E into the yeast display vector pYD2. Random mutations were then introduced into the 3D12 scFv gene using PCR under error prone conditions and the resulting gene repertoire cloned into pYD2 using gap repair to create a library of 2.1 x 10^6 transformants. The library was grown, induced, and then analyzed by flow cytometry for frequency of scFv display (27%) and antigen binding (3.65%). The library was then subjected to five rounds of selection using decreasing concentrations of BoNT/A. A final round of off rate selection was then performed by labeling with purified BoNT/A followed by a 15 hour dissociation in the presence of BoNT/A binding domain (HC) to prevent rebinding. BoNT/A labeled yeast were then sorted using a mAb (7C1) which bound the catalytic domain of the toxin. The scFv gene was PCR amplified from 6 individual colonies obtained after the final round of sorting, revealing the presence of 3 unique sequences (Table 13, clones 3-1 (also known as RAZ1, Figure 19A), 3-8, and 3-10). Each unique clone was grown, scFv display induced, and the KD of the displayed scFv for BoNT/A measured using flow cytometry, along with the wild type 3D12 scFv. All three mutant scFv had higher affinity than the wild type 3D12 scFv. For the highest affinity scFv (RAZ1, KD in Figure 21), mutations were located entirely within the VL, in CDRs 1, 2, and 3 (Figure 19A).

[0294] Table 13. Amino acid sequences for affinity matured and/or modified antibodies.

Heavy Chains				
Clone	Framework 1	CDR1	Framework 2	CDR2
HuC25	QVQLQESGGGLVQPGGSLRLSCAASGFTFS (SEQ ID NO:225)	DYYMY(SEQ ID NO:226)	WVRQAPGKGLEWVA(SEQ ID NO:227)	TISDGGSYTYYPDSVKG(SEQ ID NO:228)
AR1	QVQLQESGGGLVQPGGSLRLSCAASGFTFS (SEQ ID NO:229)	DYYMY(SEQ ID NO:230)	WVRQAPGKGLEWVA(SEQ ID NO:231)	TISDGGSYTYYPDSVKG(SEQ ID NO:232)
AR2	QVQLQESGGGLVQPGGSLRLSCAASGFTFS(SEQ ID NO:233)	DHYMY(SEQ ID NO:234)	WVRQAPGKGLEWVA(SEQ ID NO:235)	TISDGGSYTYYPDSVKG(SEQ ID NO:236)
WR1(V)	QVQLQESGGGLVQPGGSLRLSCAASGFTSS (SEQ ID NO:237)	DHYMY(SEQ ID NO:238)	WVRQAPGKGLEWVA(SEQ ID NO:239)	TISDGGSYTYYPDSVKG(SEQ ID NO:240)
WR1(T)	QVQLQESGGGLVQPGGSLRLSCAASGFTSS (SEQ ID NO:241)	DHYMY(SEQ ID NO:242)	WVRQAPGKGLEWVA(SEQ ID NO:243)	TISDGGSYTYYPDSVKG(SEQ ID NO:244)
3D12	QVQLVQSGGGVVHPGRSLKLSCAGSGFTFS(SEQ ID NO:245)	DYDMH(SEQ ID NO:246)	WVRQAPGKGLEWVA(SEQ ID NO:247)	VMWFDGTEKYSAESVKG(SEQ ID NO:248)
RAZ1	QVQLVQSGGGVVHPGRSLKLSCAGSGFTFS(SEQ ID NO:249)	DYDMH(SEQ ID NO:250)	WVRQAPGKGLEWVA(SEQ ID NO:251)	VMWFDGTEKYSAESVKG(SEQ ID NO:252)
3-8	QVQLVQSGGGVVHPGRSLKLSCAGSGFTFS(SEQ ID NO:253)	DYDMH(SEQ ID NO:254)	WVRQAPGKGLEWVA(SEQ ID NO:255)	VIWFDGTEKYSAESVKG(SEQ ID NO:256)
3-10	QVQLVQSGGGVVHPGRSLKLSCAGSGFTFS(SEQ ID NO:257)	DYDMH(SEQ ID NO:258)	WVRQAPGKGFEWVA(SEQ ID NO:259)	VMWFDGTEKYSAESVKG(SEQ ID NO:260)
ING1	QVQLQQSGGGLVQPGGSLRLSCAASGFTFS(SEQ ID NO:40)	NYAMT(SEQ ID NO:41)	WVRQAPGKGLEWVS(SEQ ID NO:42)	SISVGGSDTYYADSVKG(SEQ ID NO:43)
Heavy Chains cont'd				
	Framework 3	CDR3	Framework 4	
HuC25	RFTISRDNSKNTLYLQMNSLRAEDTAMYYCSR(SEQ ID NO:261)	YRYDDAMDY(SEQ ID NO:262)	WGQGTLVTVSS(SEQ ID NO:263)	
AR1	RFTISRDNSKNTLYLQMNSLRAEDTAIYYCSR(SEQ ID NO:264)	YRYDDAMDY(SEQ ID NO:265)	WGQGTLVTVSS(SEQ ID NO:266)	
AR2	RFTTSRDNSKNTLYLQMNSLRAEDTAIYYCSR(SEQ ID NO:267)	YRYDDAMDY(SEQ ID NO:268)	WGQGTLVTVSS(SEQ ID NO:269)	

WR1(V)	RFTVSRDNSKNTLYLQMNSLRAEDTAIYYCSR(SEQ ID NO:270)	YRYDDAMDY(SEQ ID NO:271)	WGQGTLVTVSS(SEQ ID NO:272)	
WR1(T)	RFTTSRDNSKNTLYLQMNSLRAEDTAIYYCSR(SEQ ID NO:273)	YRYDDAMDY(SEQ ID NO:274)	WGQGTLVTVSS(SEQ ID NO:275)	
3D12	RFTISRDNSKNTLFLQMNSLRADDTAVYYCAR(SEQ ID NO:276)	EPDWLLWGDRGALDV(SEQ ID NO:277)	WGQGTTVTVSS(SEQ ID NO:278)	
RAZ1	RFTISRDNSKNTLFLQMNSLRADDTAVYYCAR(SEQ ID NO:279)	EPDWLLWGDRGALDV(SEQ ID NO:280)	WGQGTTVTVSS(SEQ ID NO:281)	
3-8	RFTISRDNSKNTLFLQMNSLRADDTAVYYCAR(SEQ ID NO:282)	EPDWLLWGDRGALDV(SEQ ID NO:283)	WGQGTTVTVSS(SEQ ID NO:284)	
3-10	RFTISRDNSKNTLFLQMNSLRADDTAVYYCAR(SEQ ID NO:285)	EPDRLLWGDRGALDV(SEQ ID NO:286)	WGQGTTVTVSS(SEQ ID NO:287)	
ING1	RFTVSRDNSKNTLLLQMNSLRAEDTAVYYCAK (SEQ ID NO:68)	VRTKYCSSLSCFAGFDS (SEQ ID NO:69)	WGQGTRVTVSS (SEQ ID NO:70)	
Light Chains				
Clone	Framework 1	CDR1	Framework 2	CDR2
HuC25	EIVLTQSPATLSLSPGERATISC(SEQ ID NO:288)	RASESVDSYGHSFMQ(SEQ ID NO:289)	WYQQKPGQAPRLLIY(SEQ ID NO:290)	RASNLEP(SEQ ID NO:291)
AR1	EIVLTQSPATLSLSPGERATISC(SEQ ID NO:292)	RASESVDSYGHSFMQ(SEQ ID NO:293)	WYQQKPGQAPRLLIY(SEQ ID NO:294)	RASNLEP(SEQ ID NO:295)
AR2	EIVLTQSPATLSLSPGERATISC(SEQ ID NO:296)	RASESVDSYGHSFMQ(SEQ ID NO:297)	WYQQKPGQAPRLLIY(SEQ ID NO:298)	RASNLEP(SEQ ID NO:299)
WR1(V)	EIVLTQSPATLSLSPGERATISC(SEQ ID NO:300)	RASESVDSYGHSFMQ(SEQ ID NO:301)	WYQQKPGQAPRLLIY(SEQ ID NO:302)	RASNLEP(SEQ ID NO:303)
WR1(T)	EIVLTQSPATLSLSPGERATISC(SEQ ID NO:304)	RASESVDSYGHSFMQ(SEQ ID NO:305)	WYQQKPGQAPRLLIY(SEQ ID NO:306)	RASNLEP(SEQ ID NO:307)
3D12	DIVMTQSPSTLSASVGDRVTITC(SEQ ID NO:308)	RASQSISSWLA (SEQ ID NO:309)	WYQQKPGKAPKLLMY(SEQ ID NO:310)	EASSLES(SEQ ID NO:311)
RAZ1	DIVMTQSPSTLSASVGDRVTITC(SEQ ID NO:312)	WASQSISSRLA (SEQ ID NO:313)	WYQQKPGKAPKLLMY(SEQ ID NO:314)	EATSLGS(SEQ ID NO:315)
3-8	DIVMTQSPSTLSASVGDRVTITC(SEQ ID NO:316)	RASQSISSWLA (SEQ ID NO:317)	WYQQKPGKAPKLLMY(SEQ ID NO:318)	GASSLGS(SEQ ID NO:319)
3-10	DIVMTQSPSTLSASVGDRVTITC(SEQ ID NO:320)	RASQSISSWLA (SEQ ID NO:321)	WYQQKPGKAPKLLMY(SEQ ID NO:322)	EASSLGR(SEQ ID NO:323)
ING1	DIVMTQSPSSLSASVGDRVTIT	RASQSISSYLN	WYQQKPGKAPKL	AASSLQS(SEQ

	C (SEQ ID NO:96)	(SEQ ID NO:97)	LIY(SEQ ID NO:98)	ID NO:99)
Light Chains cont'd.				
Clone	Framework 3	CDR3	Framework 4	
HuC25	GIPARFSGSGSGTDFTLTISSLEPEDFAVYYC(SEQ ID NO:324)	QQSNEDPFT(SEQ ID NO:325)	FGQGTKVEIKR(SEQ ID NO:326)	
AR1	GIPARFSGSGSGTDFTLTISSLEPEDFAVYYC(SEQ ID NO:327)	QQGNEVPFT(SEQ ID NO:328)	FGQGTKVEIKR(SEQ ID NO:329)	
AR2	GIPARFSGSGSGTDFTLTISSLEPEDFAVYYC(SEQ ID NO:330)	QQGNEVPFT(SEQ ID NO:331)	FGQGTKVEIKR(SEQ ID NO:332)	
WR1(V)	GIPARFSGSGSGTDFTLTISSLEPEDFAVYYC(SEQ ID NO:333)	QQGNEVPFT(SEQ ID NO:334)	FGQGTKVEIKR(SEQ ID NO:335)	
WR1(T)	GIPARFSGSGSGTDFTLTISSLEPEDFAVYYC(SEQ ID NO:336)	QQGNEVPFT(SEQ ID NO:337)	FGQGTKVEIKR(SEQ ID NO:338)	
3D12	GVPSRFSGSGSGTEFTLTISSLQPDDFAAYYC(SEQ ID NO:339)	QHYNTYPYT(SEQ ID NO:340)	FGQGTKLEIKR(SEQ ID NO:341)	
RAZ1	GVPSRFSGSGSGTEFTLTISSLQPDDFAAYYC(SEQ ID NO:342)	QHYDTYPYT(SEQ ID NO:343)	FGQGTKLEIKR(SEQ ID NO:344)	
3-8	GVPSRFSGSGSGTEFTLTISSLHPDDFAAYYC(SEQ ID NO:345)	QHYNTYPYT(SEQ ID NO:346)	FGQGTKLEIKR(SEQ ID NO:347)	
3-10	GVPSRFSGSGSGTEFTLTISSLQPDDFAAYYC(SEQ ID NO:348)	QHYSTYPYT(SEQ ID NO:349)	FGQGTKLEIKR(SEQ ID NO:350)	
ING1	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC(SEQ ID NO:124)	QQSYSTPRTT(SEQ ID NO:125)	FGGGTKVDIKR(SEQ ID NO:126)	

*Sequence for complete heavy chain is heavy chain framework 1+ CDR1 + framework 2 + CDR2 + framework 3 + CDR3 + framework 4.

Sequence for complete light chain is light chain framework 1+ CDR1 + framework 2 + CDR2 + framework 3 + CDR3 + framework 4.

Impact of conversion of yeast displayed scFv to IgG on affinity

[0295] For many immunologic assays, as well as *in vivo* neutralization studies, it is necessary to utilize IgG. We therefore converted HuC25, AR1, AR2, AR3, AR4, 3D12, and RAZ1 to full length IgG consisting of the human gamma 1 constant region and the human kappa constant region by sequential cloning of the VH and Vk genes into a mammalian expression vector driven by dual CMV promoters. Stable CHO DG44 cell lines were established for each of the 7 antibodies and IgG was purified from cell culture supernatant in yields of 5-20 mg/L for six of the seven antibodies. We were unable to express any significant quantities of the AR3 IgG.

[0296] The affinities of each IgG was measured kinetic exclusion analysis (Kinexa). The affinities of the HuC25 family of mutants and of RAZ1 were significantly higher as IgG than yeast displayed scFv, but the relative increase in affinity of the IgG, were consistent with the relative affinities determined on yeast displayed scFv (Table 14). For example the AR4 scFv had a 37 fold higher affinity than HuC25 scFv by yeast display and the AR4 IgG had a

34 fold higher affinity than the HuC25 IgG as measured by Kinexa. The RAZ1 scFv had a 45 fold higher affinity than 3D12 scFv by yeast display and the RAZ1 IgG had a 35 fold higher affinity than the 3D12 IgG as measured by Kinexa.

[0297] Table 14. Affinity of antibodies on A1 and A2 toxins.

Antibody	K_D on Hall (A1) toxin	K_D on Honey (A2) toxin
HuC25	1.24 nM	250 nM
AR1	200 pM	100 nM
AR2	47 pM	ND
WR1 (V)	450 pM	9.0 nM
WR1 (T)	310 pM	3.7 nM
3D12	940 pM	2.2 nM
3D12.3-1 (RAZ1)	17 pM	70 pM
3D12.3-8	21 pM	67 pM
3D12.3-10	28 pM	81 pM

Impact of affinity on detection of BoNT/A by flow cytometry

[0298] Higher affinity scFv displayed on yeast were able to detect significantly lower concentrations of BoNT/A compared to lower affinity yeast displayed scFv (Figure 22). The highest affinity scFv (AR4) was able to detect as little as 0.1 pM of BoNT/A, a value lower than that reported for other non-amplified BoNT detection systems. Thus the results validate the utility of increasing antibody affinity to increase detection sensitivity.

Impact of affinity on neutralization of BoNT/A

[0299] The wild type and higher affinity antibodies were studied in the in vivo mouse neutralization assay. For a single antibody, higher affinity led to small (approximately 2 fold) increase in protection of mice challenged with intraperitoneal BoNT/A (Figure 23), with the highest affinity AR4 antibody providing complete protection against 100 mouse LD50s of toxin but not against 200 LD50s. When two antibodies were combined, protection increased significantly, with the combination of AR4+3D12 providing approximately a 2 fold increase in protection, from 2500 LD50s to 5000 LD50s. When RAZ1 was substituted for 3D12 in the antibody pairs, protection was seen out to 10,000 mouse LD50s for the combination of AR4 and RAZ1. Thus the data indicate that using higher affinity antibodies in antibody combinations leads to more potent toxin neutralization. This is even more clear for combinations of three antibodies (Table 15).

[0300] Table 15. Potency of neutralization of antibody combinations.

	1000 LD_{50}	2500 LD_{50}	5000 LD_{50}	10,000 LD_{50}	20,000 LD_{50}	40,000 LD_{50}
HuC25:B4:3D12, 50 μg					10/10	20/20
HuC25:B4:3D12, 10 μg	10/10	10/10	1/10	0/10		
HuC25:B4:RAZ1, 10 μg					8/10	
CR1:RAZ1:ING1, 5 μg				10/10		
CR1:RAZ1:ING1, 2 μg				18/20		

CR1:RAZ1:ING1, 1 μg				8/10		
CR1:RAZ1:ING1, 0.5 μg				3/10		

[0301] Here the replacement of 3D12 with the higher affinity RAZ1 in a combination of HuC25/B4/3D12 or RAZ1, provides complete protection at a 10,000 LD50 challenge dose of toxin. With the wildtype 3D12 in the combination, no mice survive challenge at 10,000 LD50s. Replacing B4 with the higher affinity ING1 and HuC25 with the higher affinity CR1 allows a decrease in the antibody dose from 50ug to 1 ug with still 80% survival at a 10,000 LD50 challenge dose of toxin. Thus increasing the affinity of single antibodies used in antibody combinations increases potency and allows for a decrease in antibody dose.

Example 5

Sequence Variation Within Botulinum Neurotoxin Serotypes Impacts Antibody Binding And Neutralization

Materials and methods

Toxin gene sequences:

[0302] The NCBI databases and Medline were searched to identify published or archived sequences of botulinum neurotoxin genes or proteins. The neurotoxin gene of Clostridial strain FRI-A2H was sequenced for this work (manuscript in preparation). The neurotoxin gene sequence of Clostridial strain was a gift of Michael Peck. Gene sequences were entered into Vector NTI (Invitrogen, San Diego, CA), translated, classified by serotype and aligned. Phylogenetic trees were constructed using ClustalW.

Toxins and antibodies:

[0303] Purified pure and complexed botulinum neurotoxins A1 (Hall hyper) and A2 (FRI-A2H) were purchased from Metabiologics Inc (Madison, WI). Antibodies S25 and C25 were derived from a single chain Fv phage display library constructed from the V-genes of an immunized mouse (Amersdorfer *et al.* (1997) *Infect. Immun.* 65: 3743-3752; Nowakowski *et al.* (2002) *Proc. Natl. Acad. Sci. U S A*, 99: 11346-50). Antibody 3D12 was derived from a single chain Fv phage display library constructed from the V-genes of an immunized human volunteer donor (Amersdorfer *et al.* (2002) *Vaccine* 20: 1640-1648; Amersdorfer *et al.* (1997) *Infect. Immun.* 65: 3743-3752). Antibody B4 was derived from a single chain Fv phage display library constructed from the V-genes of an immunized mouse transgenic for the human immunoglobulin locus (Xenomouse), (I.Geren and J.D. Marks, submitted). The V-genes of each of these four antibodies were cloned into a mammalian expression vector containing human IgG1 and kappa constant regions as previously described (Nowakowski *et al.* (2002) *Proc. Natl. Acad. Sci. U S A*, 99: 11346-50). Stable CHO DG44 cell lines were established and IgG purified using protein G as previously described (Nowakowski *et al.* (2002) *Proc. Natl. Acad. Sci. U S A*, 99: 11346-50). Antibody purity and concentration was determined by SDS-PAGE and absorbance at 280 nm. Antibodies 9D8 (murine IgG1/kappa) and 7C1 (murine IgG1/kappa) were derived from hybridomas generated from mice immunized with rBoNT/A H_C and boosted with BoNT/A toxin. IgG were purified from hybridoma supernatants using protein G and purity and concentration determined by SDS-PAGE and BCA assay (Pierce Chemical Co.). For subsequent studies, IgG antibodies were stored in PBS, pH 7.4 at approximately 1-3 mg/ml.

Toxin capture ELISA:

[0304] For toxin capture ELISA, 96 well microtiter plates (Immunolon 2, Dynatech) were coated with antibody at 2 μg/ml overnight at 4°C. After blocking for 30 minutes in 5% skim milk-PBS, toxins were applied in half-log dilutions from 100 nM to 1 pM in duplicate and A incubated for 90 minutes at 37°C. Plates were washed and incubated with equine anti-BoNT antibody (PerImmune), diluted to 0.2 IU/ml, for 60 minutes, followed by washing and incubation with a 1:1000 dilution of goat anti-horse antibody conjugated to horseradish peroxidase (KPL) for 60 minutes. Plates were developed with ABTS (KPL). Average absorbance at 405 nm after subtraction of background control was plotted against toxin concentration.

Measurement of antibody affinity for toxin:

[0305] IgG association and dissociation rate constants for purified BoNT/A1 or A2 toxins were measured using surface plasmon resonance in a BIAcore 1000 (Pharmacia Biosensor) and used to calculate the KD as previously described (Nowakowski *et al.* (2002) *Proc. Natl. Acad. Sci. U S A,* 99: 11346-11350). Briefly, approximately 100-400 RU of purified IgG (10-20 ug/ml in 10 mM acetate, pH 3.5-4.5) was coupled to a CM5 sensor chip using NHS-EDC chemistry. The association rate constant for purified BoNT/A1 or A2 neurotoxins was measured under continuous flow of 15 ul/min using a concentration range of 50 nM to 800 nM toxin. Association rate constant (kon) was determined from a plot of (ln(dR/dt))/t vs. concentration. The dissociation rate constant (koff) was determined from the dissociation part of the sensorgram at the highest concentration of toxin analyzed using a flow rate of 30 μl/min to prevent rebinding. KD was calculated as koff/kon.

Measurement of in vivo toxin neutralization:

[0306] Fifty μg of the appropriate IgG were added to the indicated number of mouse LD_{50}s of BoNT/A1 neurotoxin complex (Hall strain) or BoNT/A2 neurotoxin complex (FRI-A2H strain) in a total volume of 0.5 ml of gelatin phosphate buffer and incubated at RT for 30 min. For pairs of mAbs, 25 μg of each mAb was added, and for the combination of 3 mAbs, 16.7 μg of each mAb was added. The mixture was then injected intraperitoneally into female CD-1 mice (16-22 grams on receipt). Mice were studied in groups of 10 and were observed at least daily. The final death tally was determined 5 days after injection. Studies using mice were conducted in compliance with the Animal Welfare Act and other Federal statutes and regulations relating to animals and experiments involving animals and adhere to principles stated in the Guide for the Care and Use of Laboratory Animals, National Research Council, 1996. The facility where this research was conducted is fully accredited by the Association for Assessment and Accreditation of Laboratory Animal Care International.

Results

Sequence variation within botulinum neurotoxin serotypes

[0307] To determine the extent of sequence variability within toxin serotypes, the literature was searched revealing 60 published neurotoxin sequences. This data included 49 complete toxin gene sequences and 11 partial toxin gene sequences (Table 16). The 49 complete sequences were classified by serotype, aligned, and the extent of sequence identity determined (Table 17 and Figure 11). Of the 49 sequences analyzed, there were 7 BoNT/A, 9 BoNT/B, 6 BoNT/C, 5 BoNT/D, 17 BoNT/E, 4 BoNT/F, and 1 BoNT/G. Within serotypes, two types of toxin gene sequences were observed; those that were virtually identical to each other (vide infra) and those that differed by at least

2.6% at the amino acid level. Such sequence variability was observed within all six serotypes where more than 1 toxin gene had been sequenced (BoNTs A, B, C, D, E, and F). Within serotypes, variability ranged from a high of 32% for BoNT/F to a low of 2.6% for BoNT/E (Table 17). Three BoNT C/D and two BoNT D/C mosaic strains were sequenced. These strains typically contained light chains and N terminal heavy chains that matched their parental serotype, with the terminal third of the neurotoxin sequence having strong, but not absolute, identity with the alternative serotype of the mosaics (Table 16).

[0308] Table 16. Clostridial strains used in sequence analyses. Accession numbers are from the NCI nucleotide database.

serotype	subtype	strain(s)	accession #	reference(s)
A	A1	NCTC 2916	X52066	Thompson, 1990 [1]
		62A	M30196	Binz, 1990b [2]
		ATCC 3502		(Dr. Michael Peck, unpublished)
		Hall hyper	AF461540	Dineen, 2003 [3]
		Hall Allergan	AF488749	Zhang, 2003 [4]
	A2	Kyoto-F	X73423	Willems, 1993 [5]
		FRI-A2H		(Bradshaw et al, unpublished)
B	B1	Danish	M81186	Whelan, 1992 [6]
		BGB		Kirma, 2004 [7]
		okra		Ihara, 2003 [8]
	B2	strain 111	AB084152	Ihara, 2003 [8]
	nonproteolytic B	Eklund 17B	X71343	Hutson, 1994 [9]
	bivalent B	CDC 588	AF300465	Kirma, 2004 [7]
		CDC 593	AF300466	Kirma, 2004 [7]
		CDC 1436	AF295926	Kirma, 2004 [7]
		CDC 3281	Y13630	Santos-Buelga, 1998
C	C1	Stockholm	X66433	Hauser, 1990;
			X62389	Kimura, 1990 [10, 11]
		C 468	X72793	Hauser, 1994 [12]
		Yoichi	AB061780	Sagane, 2001 [13]
	C/D	6813	D49440	Moriishi, 1996 [14]
		6814	AB037166	
		TW/2003	AY251553	
D	D	BVD/-3	X54254	Binz, 1990 [15]
		CB-16	S49407	Sunagawa, 1992 [16]
		1873	AB012112	Nakajima, 1998 [17]
	D/C	South Africa	D38442	Moriishi, 1996 [14]
		D 4947	AB037920	Kouguchi, 2002 [18]
E	E botulinum	NCTC 11219	X62683	Whelan, 1992 [19]
		Beluga	X62089	Poulet, 1992 [20]
		35396	AB082519	Tsukamota, 2002 [21]
	E butyricum	BL5262, BL6340	X62088	Poulet, 1992 [20]
			X62088	
		BL5520	Q9FAR6	Wang, 2000 [22]
		KZ 1886	AB037708	Wang, 2000 [22]
		KZ 1887	AB037709	Wang, 2000 [22]
		KZ 1889	AB037710	Wang, 2000 [22]
		KZ 1890	AB037711	Wang, 2000 [22]
		KZ 1891	AB037712	Wang, 2000 [22]
		KZ 1897	AB037706	Wang, 2000 [22]
		KZ 1898	AB037707	Wang, 2000 [22]
		KZ 1899	AB037705	Wang, 2000 [22]
		LCL 063	AB037713	Wang, 2000 [22]
		LCL 095	AB037714	Wang, 2000 [22]
		LCL 155	AB037704	Wang, 2000 [22]

F	proteolytic F	Langeland	X81714 L35496	Hutson, 1994 [9]; Elmore, unpublished
	nonproteolytic F	Eklund 202F	M92906	East, 1992 [23]
	F baratii	ATCC 43756	X68262	Thompson, 1993 [24]
	bivalent F	CDC 3281 (Bf)	Y13631	Santos-Buelga, 1998 [25]
G	G	113/30	X74162	Campbell, 1993 [26]

[0309] 1. Thompson *et al.* (1990) *Eur. J. Biochem.*, 189(1): 73-81.

[0310] 2. Binz *et al.* (1990) *J. Biol. Chem.*, 265(16): 9153-9158.

[0311] 3. Dineen *et al.* (2003) *Cur.r Microbiol.*, 46(5): 345-352.

[0312] 4. Zhang *et al.* (2003) *Gene*, 315: 21-32.

[0313] 5. Willems *et al.*(1993) *Res. Microbiol.*, 144(7): 547-556.

[0314] 6. Whelan *et al.* (1992) *Appl. Environ. Microbiol.*, 58(8): 2345-2354.

[0315] 7. Kirma *et al.* (2004) *FEMS Microbiol. Lett.*, 231(2): 159-164.

[0316] 8. Ihara *et al.* (2003) *Biochim. Biophys. Acta*, 1625(1): 19-26.

[0317] 9. Hutson *et al.* (1994) *Curr. Microbiol.*, 28(2): 101-110.

[0318] 10. Hauser *et al.* (1990) *Nucleic Acids Res.*, 18(16): 4924.

[0319] 11. Kimura *et al.* (1990) *Biochem. Biophys. Res. Commun.*, 171(3): 1304-1311.

[0320] 12. Hauser *et al.* (1994) *Mol. Gen. Genet.*, 243(6): 631-640.

[0321] 13. Sagane *et al.* (2001) *Biochem. Biophys. Res. Commun.*, 288(3): 650-657.

[0322] 14. Moriishi *et al.* (1996) *Biochim. Biophys. Acta*, 1307: 123-126.

[0323] 15. Binz *et al.* (1990) *Nucleic Acids Res.*, 18(18): 5556.

[0324] 16. Sunagawa *et al.* (1992) *J. Vet. Med. Sci.*, 54(5): 905-913.

[0325] 17. Nakajima *et al.* (1998) *Microbiol. Immunol.*, 42(9): 599-605.

[0326] 18. Kouguchi *et al.* (2002) J. Biol. Chem., 277(4): 2650-2656.

[0327] 19. Whelan *et al.* (1992) *Eur. J. Biochem.*, 204(2): 657-667.

[0328] 20. Poulet *et al.* (1992) *Biochem. Biophys. Res. Commun.*, 183(1): 107-113.

[0329] 21. Tsukamoto *et al.* (2002) *Microb. Pathog.*, 33(4): 177-184.

[0330] 22. Wang *et al.* (2000) *Appl. Environ. Microbiol.*, 66(11): 4992-4997.

[0331] 23. East *et al.* (1992) *FEMS Microbiol. Lett.*, 75(2-3): 225-230.

[0332] 24. Thompson *et al.* (1993) *FEMS Microbiol. Lett.*, 108(2): 175-182.

[0333] 25. Santos-Buelga *et al.* (1998) *Curr Microbiol.*, 37(5): 312-318.

[0334] 26. Campbell *et al.* (1993) *Biochim Biophys Acta*, 1216(3): 487-491.

[0335] The two toxin serotypes causing more than 90% of human botulism (BoNT/A and B, (Control (1998) Botulism in the United States, 1899-1998. Handbook for epidemiologists, clinicians,and laboratory workers. Atlanta, Georgia U.S. Department of Health and Human Services, Public Health Service: downloadable at www.bt.cdc.gov/agent/botulism/index.asp) were analyzed in more detail. Of the seven published BoNT/A toxin sequences, five (62A, NCTC 2916, ATCC 3502, and Hall hyper (Hall Allergan)) were virtually identical (99.9-100% identity) and have been classified as subtype A1 (Figure 12A). The other two BoNT/A sequences (Kyoto-F and FRI-A2H) were 100% identical and have been classified as subtype A2 (Figure 12A). The A1 toxins differed from the A2 toxins by 10.1 %, with the greatest difference in sequence in the receptor binding domain (C-terminal heavy chain, HC). (Table 18). Besides being greater in number, the HC amino acid differences tended to be located in solvent accessible amino acids exposed on the toxin surface (Figure 12B). A number of these differences clustered around the putative ganglioside binding site (Figure 12B). The sequence of the catalytic domain (light chain) was more conserved (Table 18), 1 with the differences more likely to be buried (Figure 12B).

[0336] Table 17. Classification of Clostridial botulinum neurotoxin gene sequences. Subtypes were defined as differing by at least 2.6% at the amino acid level.

serotype	complete sequences	partial sequences	subtypes	Minimum and maximum amino acid differences within serotype
A	7		2	10.1 %
B	9	3	4	3.6-7.7%
C	6		2	24.0-24.2 %
D	5		2	23.7-23.9 %
E	17	6	3	2.6-5.1 %
F	4	2	4	10.7-31.6 %
G	1		1	
total:	49	11	18	

[0337] Table 18. Percent amino acid identity between BoNT A1 and A2 strains.

	holotoxin	light chain	heavy chain	H_N	H_C
BoNT A1 versus BoNT A2	89.9	95.1	87.1	87.1	87.2

[0338] The nine published BoNT/B sequences could be grouped into 4 subtypes based on DNA and protein homology (Figure 13). These groups included the bivalent BoNT/B (BoNT Ab 1436, BoNT Ab 588, BoNT Ab 593, and BoNT Bf 3281), BoNT/B1 (BoNT/B Danish), BoNT/B2 (BoNT/B strain 111), and the nonproteolytic BoNT/B (BoNT/B Eklund). These toxins differed from each other by 3.6% to 7.7% at the amino acid level, with greater differences in the heavy chain compared to the light chain (Table 19).

[0339] Table 19. Percent amino acid identity among BoNT B strains.

	holotoxin	light chain	heavy chain	H_N	H_C
BoNT B1 vs:					
BoNT B2	95.7	99.5	93.6	95.8	91.8

BoNT B np	92.8	97.7	90.2	92.5	88.2
BoNT B bivalent	96.0-96.4	98.9-99.1	94.6-94.9	94.3-95.0	94.7-94.9

Impact of BoNT/A toxin sequence variation and antibody binding

[0340] To determine the impact of BoNT/A toxin sequence variability on immune recognition we measured the ability of six monoclonal antibodies raised against BoNT/A1 to bind to BoNT/A1 and BoNT/A2 by capture ELISA. Binding to both pure neurotoxin and neurotoxin complex was determined. Four mAbs (3D12, C25, B4, and S25) bound to non-overlapping epitopes on the BoNT/A HC, as determined by ELISA on recombinant HC. 3D12 and S25 have been previously epitope mapped to the C-terminal subdomain of BoNT/A HC, while C25 recognizes a complex epitope formed by the two HC subdomains (Mullaney *et al.*(2001) *Inf. Immun.*, 69: 6511-6514). One mAb (9D8) bound the BoNT/A translocation domain (HN) as determined by ELISA on recombinant HN (data not shown). One mAb (7C1) bound the BoNT/A light chain, as determined by ELISA on recombinant light chain.

[0341] Three of the four antibodies which bound the BoNT/A HC showed a marked reduction in binding to BoNT/A1 toxin compared to BoNT/A2 toxin (Figure 14). In contrast, non HC binding mAbs showed comparable ELISA signals on both A1 and A2 toxins (Figure 15). To quantitate the difference in binding to A1 and A2 toxins, the equilibrium dissociation constant and binding rate kinetics were measured for the binding of each mAb to purified A1 and A2 toxins (Table 17). All mAbs bound A1 toxin with high affinity (KD ranging between 6 and 0.17 nM). The three mAbs which demonstrated decreased binding to A2 toxin by capture ELISA (C25, S25, and B4) showed a 553 to more than 1200 fold reduction in affinity for A2 toxin compared to A1 toxin. It was not possible to measure a KD for the B4 mAb binding to BoNT/A2 due to very low affinity binding. The majority of the reduction in affinity was due to a large decrease in the association rate constant (Table 20). In contrast, three mAbs (3D12, 9D8 and 7C1) showed comparable high affinity for both A1 and A2 toxins.

[0342] Table 20. Association (k_{on}) and dissociation (k_{off}) rate constants and equilibrium dissociation constants (K_d) for BoNT/A IgG binding to BoNT/A1 and BoNT/A2. Association and dissociation rate constants were determined by surface plasmon resonance in a BIAcore and K_D calculated as k_{off}/k_{on}. NM = not meas*urable

Antibody	BoNT/A1			BoNT/A2		
	K_d (M^{-1})	k_{on} (M^{-1} s^{-1})	k_{off} (s^{-1})	K_d (M^{-1})	k_{on} (M^{-1} s^{-1})	k_{off} (s^{-1})
C25	$2.98x10^{-10}$	$1.5x10^{6}$	$4.47x10^{-4}$	$1.65x10^{-7}$	$2.09 x10^{4}$	$3.63x10^{-3}$
S25	$1.69x10^{-9}$	$4.82x10^{5}$	$8.15x10^{-4}$	$2.14x10^{-6}$	$1.34 x10^{3}$	$2.87x10^{-3}$
3D12	$1.68x10^{-10}$	$1.45x10^{6}$	$2.44x10^{-4}$	$1.04x10^{-9}$	$3.48x10^{5}$	$3.62x10^{-4}$
B4	$1.8x10^{-9}$	$7.2x10^{5}$	$1.31x10^{-3}$	NM	NM	NM
7C1	$5.9x10^{-9}$	$2.89x10^{5}$	$1.71x10^{-3}$	$5.1x10^{-9}$	$3.38x10^{5}$	$1.73x10^{-3}$
9D8	$1.21x10^{-9}$	$1.73x10^{5}$	$2.11x10^{-4}$	$1.3x10^{-9}$	$2.08x10^{5}$	$2.73x10^{-4}$

Impact of antibody binding on neutralization of A1 and A2 neurotoxins

[0343] We previously studied the in vivo neutralization capacity of three mAbs described here, 3D12, S25, and C25, for BoNT/A1 toxin. Despite showing significant in vitro neutralization of BoNT/A1, none of these three mAbs showed significant in vivo protection of mice receiving 50 ug of antibody and challenged with 20 mouse LD50s of BoNT/A1 (only 10-20% survival, (Nowakowski *et al.* (2002) *Proc. Natl. Acad. Sci. U S A*, 99: 11346-11350)). Similarly, none of the remaining three mAbs reported here showed significant in vivo protection when mice were challenged with 20 mouse LD_{50}s of BoNT/A1 (only 10-20% survival, data not shown). Since we previously reported significant synergy in in vivo protection when mAbs were combined, we studied the ability of mAb pairs and triplets to neutralize toxin in vivo. As previously observed, antibody pairs showed significantly greater BoNT/A1 neutralization than single mAbs, with even greater potency observed for combinations of three mAbs (Figures 16 and 17A). Synergy was observed for mAb pairs that included only 1 binding domain antibody (C25+9D8) or no binding domain antibodies (9D8+7C1) (Figure 16) or combinations of three mAbs that included only one binding domain antibody (C25+9D8+7C1) (Figure 17A). With respect to neutralization of BoNT/A2 toxin, only mAb pairs or triplets containing mAbs which bound BoNT/A2 with high affinity showed significant synergy for neutralization (Figure 17B). The most potent mAb triplet (3D12+9D8+7C1) was able to completely protect mice from a challenge of 10,000 mouse LD_{50}s of A1 or A2 toxin. While this combination (3D12+9D8+7C1) was not as potent for neutralization of A1 toxin as a combination of three binding domain mAbs (C25+3D12+B4), only one binding domain mAb bound A2 toxin with any affinity, and as a result the C25+3D12+B4 triplet neutralized less than 200 mouse LD_{50}s of A2 toxin.

Discussion

[0344] Analysis of 49 complete published botulinum neurotoxin sequences revealed that within serotypes, toxin gene sequences were either virtually identical or differed from each other by at least 3.6% at the amino acid level. We have termed those toxins with this minimum difference (3.6%) to be subtypes of a given serotype. Such analysis revealed an average of 2.8 subtypes for the six serotypes where more than one toxin gene has been sequenced (range 2-4 subtypes/serotype). While this analysis probably reveals the most frequent toxin subtypes, it is likely that additional toxin subtypes remain to be identified, given the relatively small number of toxin genes sequenced (on average 8 toxin genes/serotype).

[0345] The importance of toxin subtypes is their impact on diagnostic tests and the development of toxin therapeutics. Clearly, this level of nucleotide polymorphism can affect DNA probe based assays such as PCR. Importantly, the extent of amino acid substitution can affect the binding of monoclonal antibodies used for ELISA and other immunologic based diagnostic tests. We have clearly shown that the 10% amino acid difference between BoNT/A1 and BoNT/A2 subtypes has a dramatic effect on the binding affinity and ELISA signals of three of six monoclonal antibodies analyzed. Interestingly, the kinetic basis for the reduced mAb affinity is largely due to a decrease in the association rate constant, rather than an increase in the dissociation rate constant. The impact of the difference in toxin amino acid sequence on the binding of polyclonal antibody is unknown. Clearly, toxin assays based on immunologic recognition will need to be validated using the different toxin subtypes.

[0346] The differences in binding affinity translate into significant differences in the potency of *in vivo* toxin neutralization. Since we have not observed potent *in vivo* toxin neutralization by single mAbs, we studied the impact of toxin sequence variation on the potency of mAb combinations. As with the binding studies, only mAb combinations binding tightly to both A1 and A2 subtypes potently neutralized toxin *in vivo*. Thus the impact of subtype variability on potency must be evaluated in the development of antibody based toxin therapy, whether such therapy is oligoclonal or polyclonal. Similarly, toxin vaccines based on a single subtype may need to be evaluated for their ability to protect against related subtypes.

[0347] An unexpected finding in these studies was that mAbs binding to the translocation domain and/or catalytic domains of BoNT had neutralizing activity, either when combined with each other or when combined with a mAb recognizing the BoNT receptor binding domain (HC). Neutralizing activity has also been reported for mAbs binding the catalytic domain of tetanus toxin (Kozaki *et al.* (1995) *Microbiol. Immunol.*, 39: 767-774) and ricin (Lang *et al.* (1993) *J. Immunol.* 151: 466-472). Since mAbs which do not bind to the BoNT receptor binding domain cannot strictly block the interaction of BoNT binding domain epitopes to cellular receptors and subsequent BoNT endocytosis, the mechanism by which they contribute to neutralization remains unknown. Possibilities include enhancement of BoNT clearance from the circulation upon binding of multiple mAbs (Montero-Julian *et al.* (1995) *Blood* 85: 917-924), interference of receptor binding by a steric effect, interference with required intracellular toxin processes (endosomal escape or catalytic activity) (Koriazova and Montal (2003) *Nat. Struct. Biol.*, 10: 13-18), and/or altering intracellular BoNT trafficking. Regardless of the mechanism, the ability of non-binding domain mAbs to neutralize toxin significantly increases the number of epitopes available for neutralizing mAb generation, increasing the likelihood of finding mAbs binding and neutralizing all BoNT subtypes.

[0348] While we only studied the impact of sequence variability on antibody binding and neutralization for a single serotype (BoNT/A), three serotypes (BoNT/C, D, and F) have subtypes which differ from each other by more than the 10% difference between BoNT/A1 and BoNT/A2 (10.7% to 31.6%). For these three serotypes, the impact of sequence variability on immune recognition is likely to be greater than for BoNT/A. For two serotypes (BoNT/B and E), sequence variability was less than observed for BoNT/A (2.6% to 7.6%). The impact of this level of sequence variability will need to be evaluated, but is clearly in a range that could affect mAb binding, as shown in previous evaluations of mAb binding to BoNT/B toxin (Gibson *et al.* (1988) *J. Appl. Bacteriol.*, 64: 285-291; Kozaki *et al.* (1998) *Infect. Immun.*, 66: 4811-4816) and BoNT E (Kozaki *et al.* (1986) *Infect. Immun.*, 52: 786-791).

[0349] In conclusion, we report the existence of considerable sequence variability within six of the seven botulinum neurotoxin serotypes and show that this level of variability can significantly affect antibody binding and neutralization. Determining the full extent of such toxin diversity is an important step in the development of immunological botulinum toxin assays, therapeutics and vaccines. Once the sequence variability has been defined, it is likely that some number of these toxin variants will need to be produced for validation of detection assays, therapeutics, and vaccines.

Example 6

Neutralizing antibodies selected and evolved for cross neutralization of BoNT/A subtypes A1, A2, and A3

[0350] The discovery of different subtypes of botulinum neurotoxins, including BoNT/A, poses a challenge for the development of diagnostic and therapeutic antibodies. Ideally, mAbs or mixtures of mAbs would bind to and detect/neutralize most or all of the different BoNT subtypes. This would result in a detection system that did not miss the detection of some subtypes. For therapeutic antibodies, cross reactivity ensures that the antibody does not fail to neutralize one or more of the subtypes.

Selection of antibodies binding BoNT/A1 and BoNT/A2

[0351] To generate monoclonal antibodies capable of binding BoNT/A1 and BoNT/A2, immune phage or yeast scFv antibody libraries were sequentially selected, first on BoNT/A1 and then on BoNT/A2. After multiple rounds of selection, phage or yeast antibodies were screened for binding to both BoNT subtypes. Two scFv antibodies were identified that bound both BoNT/A1 and BoNT/A2 with comparable affinities, (ING1, scFv KD BoNT/A1 = 1.17×10^{-9} M; scFv KD BoNT/A2 = 1.18×10^{-9} M: and ING2, scFv K_D BoNT/A1 = 4.17×10^{-10} M; scFv K_D BoNT/A2 = 4.5×10^{-10} M. See Table 13 for sequences of ING1 and ING2. For *in vivo* studies, these two scFv were converted to IgG. The IgG maintained high affinity binding for both A1 and A2 BoNT (Table 21).

[0352] Table 21. Affinities of cross reactive IgG binding both BoNT/A1 and A2 with high affinity. Affinities and binding kinetics were determined by flow fluorimetry.

Antibody	Antigen	Kd	On Rate	Off Rate
CR-1	A1	2.96 pM	$3.54e^{6}$	$1.06e^{-5}$
CR-1	A2	1.73 nM	$1.62e^{7}$	$2.81e^{-2}$
ING-1	A1	314 pM	$2.02e^{5}$	$6.35e^{-5}$
ING-1	A2	719 pM		
ING-2	A1	9.57 pM	$1.09e^{6}$	$1.05e^{-5}$
ING-2	A2	7.42 pM	$9.78e^{5}$	$7.26e^{-6}$

<u>Generation of a HuC25 variant capable of binding both BoNT/A1 and A2 with high affinity.</u>

[0353] Neither HuC25 nor its higher affinity derivatives bind BoNT/A2 with high affinity (see Table 22 for affinities of AR2 for boNt/A1 and BoNT/A2). To increase affinity for BoNT/A2, we started with the higher affinity variant AR2. This antibody as an IgG has a more than 10,000 lower affinity for BoNT/A2 than BoNT/A1 and a very low affinity for BoNT/A2 of 2.0 x 10-7 M (Table 22).

[0354] Table 22. Affinity and binding kinetics of AR2 IgG and yeast displayed scFv for BoNT/A1 and BoNT/A2.

Method		**BoNT/A1**				**BoNT/A2**	
	K_d (M^{-1})	k_{on} (M^{-1} s^{-1})	k_{off} (s^{-1})c		K_d (M^{-1})	k_{on} (M^{-1} s^{-1})	k_{off} (s^{-1})
<u>IgG/SPR in BIAcore</u>	$1.46x10^{-11}$	$1.09x10^{6}$	$1.6x10^{-5}$		$1.7x10^{-7}$	$2.0x10^{4}$	$3.4x10^{-3}$
<u>IgG/Kinexa</u>	$6.8x10^{-12}$	$3.69x10^{6}$	$2.66x10^{-5}$		$2.01x10^{-7}$		
ScFv yeast display	$6.1x10^{-11}$				$1.08x10^{-7}$		

[0355] Libraries of AR2 mutants were generated using spiked oligonucleotides or error prone PCR and the mutants displayed on the surface of yeast as scFv. Libraries were serially selected, first on BoNT/A1 and BoNT/A2, yielding the mutants WR1(T), K_D BoNT/A2 = 3.7 nM, WR1(V), K_D BoNT/A2 = 9.0 nM and CR1 K_D BoNT/A2 = 850 pM (Table 20 for sequences). The highest affinity scFv, CR1 was converted to an IgG, which had an approximately 80 fold higher affinity for BoNT/A2 toxin compard to the parental AR2 IgG, while also increasing its affinity for BoNT/A1 approximately 10 fold (Table 23). To further increase affinity for BoNT/A2, the CR1 scFv gene was randomly mutated, displayed on yeast and higher affinity scFv selected sequentially on BoNT/A1 and BoNT/A2, yielding the mutant CR2 (see sequence listing or Table 13 for sequence). After conversion to an IgG, CR2 had an approximately 6 fold higher affinity for BoNT/A2 than CR1 and maintained high affinity binding for BoNT/A1 (Table 23).

[0356] Table 23. Affinities and binding kinetics of AR2, CR1, and CR2 IgG for BoNT/A1 and BoNT/A2 as determined by flow flourimetry,

Method		**BoNT/A1**			**BoNT/A2**		
	K_d (M^{-1})	k_{on} (M^{-1} s^{-1})	k_{off} (s^{-1})		K_d (M^{-1})	k_{on} (M^{-1} s^{-1})	k_{off} (s^{-1})
AR2	$6.8x10^{-12}$	$3.69x10^{6}$	$2.66x10^{-5}$		$2.01x10^{-7}$		
CR1	$2.96x10^{-12}$	$3.54x10^{6}$	$1.06x10^{-5}$		$1.73x10^{-9}$	$1.62x10^{7}$	$2.81x10^{-2}$
CR2					$2.9x10^{-10}$		

<u>**Antibodies with higher affinity for BoNT/A2 neutralize BoNT/A2 with high potency.**</u>

[0357] In example 5, it was shown that 50 ug of the combination of antibodies HuC25, B4, and 3D12 could neutralize 40,000 mouse LD50s of BoNT/A1 but less than 200 LD50s of BoNT/A2. Neither B4 nor HuC25 bound BoNT/A2 with high affinity. We therefore studied the ability of the CR1 antibody, derived from HuC25 but with high affinity for BoNT/A1 and BoNT/A2, combined with RAZ1, and either ING1 or ING2 to neutralize BoNT/A1 and BoNT/A2. Using an antibody dose of 50 ug total antibody, the combination of CR1+RAZ1+either ING1 or ING2 completely protected mice challenged with 40,000 mouse LD50s of BoNT/A1. The same doses of antibody showed significant protection of mice challenged with BoNT/A2, with the combination CR1+RAZ1+ING1 being the most potent, completely protecting mice challenged with 40,000 mouse LD50s of BoNT/A2 (Figure 25). Thus we have shown that it is possible to generate as well as evolve antibodies that can bind multiple BoNT subtypes with high affinity, in this case BoNT/A1 and A2, and that this leads to potent neutralization when the antibodies are combined

[0358] It is understood that the examples and embodiments described herein are for illustrative purposes only and that various modifications or changes in light thereof will be suggested to persons skilled in the art and are to be included within the spirit and purview of this application and scope of the appended claims. All publications, patents, and patent applications cited herein are hereby incorporated by reference in their entirety for all purposes.

CLAIMS

What is claimed is:

1. A method of neutralizing botulinum neurotoxin in a mammal said method comprising administering to said mammal at least two different neutralizing anti-antibodies for a BoNT serotype, wherein at least one of said two antibodies binds at least two different subtypes of said BoNT serotype with an affinity greater than about 10 nM.

2. The method of claim 1, wherein said BoNT serotype is selected from the group consisting of BoNT/A, BoNT/B, BoNT/C, BoNT/D, BoNT/E, and BoNT/F.

3. The method of claim 1, wherein said BoNT serotype is BoNT/A or BoNT/B.

4. The method of claim 1, wherein said BoNT serotype is BoNT/A.

5. The method of claim 4, wherein at least one of said antibodies binds at least two different subtypes selected from the group consisting of BoNT/A1, BoNT/A2, and BoNT/A3 each with an affinity greater than about 10 nM.

6. The method of claim 4, wherein at least one of said antibodies binds BoNT/A1 and BoNT/A2 each with an affinity greater than about 10 nM.

7. The method of claim1, 2, 3, or 4 where the antibodies neutralize at least 10,000 mouse LD50s/mg of antibody.

8. The method of claims 1 or 4, wherein both antibodies simultaneously bind at least one of said subtypes.

9. The method of claim 8, wherein the antibodies neutralize at least 10,000 mouse LD50s/mg of antibody.

10. The method of claim 1, wherein said antibodies each comprise at least one CDR selected from the group consisting of RAZ1 VL CDR1, RAZ1 VL CDR2, RAZ1 VL CDR3, RAZ1 VH CDR1, RAZ1 VH CDR2, RAZ1 VH CDR3, 1D11 VL CDR1, 1D11 VL CDR2, 1D11 VL CDR3, 1D11 VH CDR1, 1D11 VH CDR2, 1D11 VH CDR3, 2G11 VL CDR1, 2G11 VL CDR2, 2G11 VL CDR3, 2G11 VH CDR1, 2G11 VH CDR2, 2G11 VH CDR3, 5G4 VL CDR1, 5G4 VL CDR2, 5G4 VL CDR3, 5G4 VH CDR1, 5G4 VH CDR2, 5G4 VH CDR3, 3D12 VL CDR1, 3D12 VL CDR2, 3D12 VL CDR3, 3D12 VH CDR1, 3D12 VH CDR2, 3D12 VH CDR3, CR1 VL CDR1, CR1 VL CDR2, CR1 VL CDR3, CR1 VH CDR1, CR1 VH CDR2, CR1 VH CDR3, CR2 VL CDR1, CR2 VL CDR2, CR2 VL CDR3, CR2 VH CDR1, CR2 VH CDR2, CR2 VH CDR3, ING1 VL CDR1, ING1 VL CDR2, ING1 VL CDR3, ING1 VH CDR1, ING1 VH CDR2, ING1 VH CDR3, ING2 VL CDR1, ING2 VL CDR2, ING2 VL CDR3, ING2 VH CDR1, ING2 VH CDR2, and ING2 VH CDR3.

11. The method of claim 1, wherein said antibodies each comprise at least three CDRs selected from the group consisting of RAZ1 VL CDR1, RAZ1 VL CDR2, RAZ1 VL CDR3, RAZ1 VH CDR1, RAZ1 VH CDR2, RAZ1 VH CDR3, 1D11 VL CDR1, 1D11 VL CDR2, 1D11 VL CDR3, 1D11 VH CDR1, 1D11 VH CDR2, 1D11 VH CDR3, 2G11 VL CDR1, 2G11 VL CDR2, 2G11 VL CDR3, 2G11 VH CDR1, 2G11 VH CDR2, 2G11 VH CDR3, 5G4 VL CDR1, 5G4 VL CDR2, 5G4 VL CDR3, 5G4 VH CDR1, 5G4 VH CDR2, 5G4 VH CDR3, 3D12 VL CDR1, 3D12 VL CDR2, 3D12 VL CDR3, 3D12 VH CDR1, 3D12 VH CDR2, 3D12 VH CDR3, CR1 VL CDR1, CR1 VL CDR2, CR1 VL CDR3, CR1 VH CDR1, CR1 VH CDR2, CR1 VH CDR3, CR2 VL CDR1, CR2 VL CDR2, CR2 VL CDR3, CR2 VH CDR1, CR2 VH CDR2, CR2 VH CDR3, ING1 VL CDR1, ING1 VL CDR2, ING1 VL CDR3, ING1 VH CDR1, ING1 VH CDR2, ING1 VH CDR3, ING2 VL CDR1, ING2 VL CDR2, ING2 VL CDR3, ING2 VH CDR1, ING2 VH CDR2, and ING2 VH CDR3.

12. The method of claim 1, wherein said antibodies each comprise a VH CDR1, CDR2, and CDR3 all selected from a VH domain selected from the group consisting of a RAZ1 VH domain, a CR1 VH domain, a CR2 VH domain, an ING1 VH domain, an ING2 VH domain, a 1D11 VH domain, a 2G11 VH domain, a 3D12 VH domain, and a 5G4 VH domain.

13. The method of claim 1, wherein said antibodies each comprise a VL CDR1, CDR2, and CDR3 all selected from a VL domain selected from the group consisting of a RAZ1 VL domain, a CR1 VL domain, a CR2 VL domain, an ING1 VL domain, an ING2 VL domain, a 1D11 VL domain, a 2G11 VL domain, a 3D12 VL domain, and a 5G4 VL domain.

14. The method of claim 1, wherein said antibodies each comprise:

a VH CDR1, CDR2, and CDR3 all selected from a VH domain selected from the group consisting of a RAZ1 VH domain, a CR1 VH domain, a CR2 VH domain, an ING1 VH domain, an ING2 VH domain, a 1D11 VH domain, a 2G11 VH domain, a 3D12 VH domain, and a 5G4 VH domain; and

a VL CDR1, CDR2, and CDR3 all selected from a VL domain selected from the group consisting of a RAZ1 VL domain, a CR1 VL domain, a CR2 VL domain, an ING1 VL domain, an ING2 VL domain, a 1D11 VL domain, a 2G11 VL domain, a 3D12 VL domain, and a 5G4 VL domain.

15. The method of claim 1, wherein at least one of said antibodies comprises a VH CDR1, VH CDR2, VH CDR3, VL CDR1, VL CDR2, and VL CDR3 selected from an antibody selected from the group consisting of RAZ1, CR1, CR2, ING1, ING2, 1D11, 2G11, 3D12, and 5G4.

16. The method of claim 15, wherein at least one of said antibodies is a single chain Fv (scFv).

17. The method of claim 15, wherein at least one of said antibodies is an IgG.

18. The method of claim 15, wherein at least one of said antibodies is a Fab.

19. The method of claim 15, wherein at least one of said antibodies is a $(Fab')_2$.

20. The method of claim 15, wherein at least one of said antibodies is a $(scFv')_2$.

21. The method of claim 1, wherein at least one of said antibodies is selected from the group consisting of RAZ1, CR1, CR2, ING1, ING2, 1D11, 2G11, 3D12, and 5G4.

22. The method of claim 1, wherein at least two of said antibodies are selected from the group consisting of RAZ1, CR1, CR2, ING1, ING2, 1D11, 2G11, 3D12, and 5G4.

23. A composition for neutralizing a Botulinum neurotoxin (BoNT), said composition comprising:

at least two different neutralizing antibodies for a BoNT serotype, wherein at least one of said two antibodies binds at least two different subtypes of said BoNT serotype with an affinity greater than about 10 nM.

24. The composition of claim 23, wherein said BoNT serotype is selected from the group consisting of BoNT/A, BoNT/B, BoNT/C, BoNT/D, BoNT/E, and BoNT/F.

25. The composition of claim 23, wherein said BoNT serotype is BoNT/A or BoNT/B.

26. The composition of claim 23, wherein said BoNT serotype is BoNT/A.

27. The composition of claim 23, wherein at least one of said antibodies binds at least two different subtypes selected from the group consisting of BoNT/A1, BoNT/A2, and BoNT/A3 each with an affinity greater than about 10 nM.

28. The composition of claim 23, wherein at least one of said antibodies binds BoNT/A1 and BoNT/A2 each with an affinity greater than about 10 nM.

29. The composition of claim 23 or 26 , wherein both antibodies simultaneously bind at least one of said subtypes.

30. The composition of claim 23, wherein said antibodies each comprise at least one CDR selected from the group consisting of RAZ1 VL CDR1, RAZ1 VL CDR2, RAZ1 VL CDR3, RAZ1 VH CDR1, RAZ1 VH CDR2, RAZ1 VH CDR3, 1D11 VL CDR1, 1D11 VL CDR2, 1D11 VL CDR3, 1D11 VH CDR1, 1D11 VH CDR2, 1D11 VH CDR3, 2G11 VL CDR1, 2G11 VL CDR2, 2G11 VL CDR3, 2G11 VH CDR1, 2G11 VH CDR2, 2G11 VH CDR3, 5G4 VL CDR1, 5G4 VL CDR2, 5G4 VL CDR3, 5G4 VH CDR1, 5G4 VH CDR2, 5G4 VH CDR3, 3D12 VL CDR1, 3D12 VL CDR2, 3D12 VL CDR3, 3D12 VH CDR1, 3D12 VH CDR2, 3D12 VH CDR3, CR1 VL CDR1, CR1 VL CDR2, CR1 VL CDR3, CR1 VH CDR1, CR1 VH CDR2, CR1 VH CDR3, CR2 VL CDR1, CR2 VL CDR2, CR2 VL CDR3, CR2 VH CDR1, CR2 VH CDR2, CR2 VH CDR3, ING1 VL CDR1, ING1 VL CDR2, ING1 VL CDR3, ING1 VH CDR1, ING1 VH CDR2, ING1 VH CDR3, ING2 VL CDR1, ING2 VL CDR2, ING2 VL CDR3, ING2 VH CDR1, ING2 VH CDR2, and ING2 VH CDR3.

31. The composition of claim 23, wherein said antibodies each comprise at least three CDRs selected from the group consisting of RAZ1 VL CDR1, RAZ1 VL CDR2, RAZ1 VL CDR3, RAZ1 VH CDR1, RAZ1 VH CDR2, RAZ1 VH CDR3, 1D11 VL CDR1, 1D11 VL CDR2, 1D11 VL CDR3, 1D11 VH CDR1, 1D11 VH CDR2, 1D11 VH CDR3, 2G11 VL CDR1, 2G11 VL CDR2, 2G11 VL CDR3, 2G11 VH CDR1, 2G11 VH CDR2, 2G11 VH CDR3, 5G4 VL CDR1, 5G4 VL CDR2, 5G4 VL CDR3, 5G4 VH CDR1, 5G4 VH CDR2, 5G4 VH CDR3, 3D12 VL CDR1, 3D12 VL CDR2, 3D12 VL CDR3, 3D12 VH CDR1, 3D12 VH CDR2, 3D12 VH CDR3, CR1 VL CDR1, CR1 VL CDR2, CR1 VL CDR3, CR1 VH CDR1, CR1 VH CDR2, CR1 VH CDR3, CR2 VL CDR1, CR2 VL CDR2, CR2

VL CDR3, CR2 VH CDR1, CR2 VH CDR2, CR2 VH CDR3, ING1 VL CDR1, ING1 VL CDR2, ING1 VL CDR3, ING1 VH CDR1, ING1 VH CDR2, ING1 VH CDR3, ING2 VL CDR1, ING2 VL CDR2, ING2 VL CDR3, ING2 VH CDR1, ING2 VH CDR2, and ING2 VH CDR3.

32. The composition of claim 23, wherein said antibodies each comprise a VH CDR1, CDR2, and CDR3 all selected from a VH domain selected from the group consisting of a RAZ1 VH domain, a CR1 VH domain, a CR2 VH domain, an ING1 VH domain, an ING2 VH domain, a 1D11 VH domain, a 2G11 VH domain, a 3D12 VH domain, and a 5G4 VH domain.

33. The composition of claim 23, wherein said antibodies each comprise a VL CDR1, CDR2, and CDR3 all selected from a VL domain selected from the group consisting of a RAZ1 VL domain, a CR1 VL domain, a CR2 VL domain, an ING1 VL domain, an ING2 VL domain, a 1D11 VL domain, a 2G11 VL domain, a 3D12 VL domain, and a 5G4 VL domain.

34. The composition of claim 23, wherein said antibodies each comprise:

a RAZ1 VH domain, a CR1 VH domain, a CR2 VH domain, an ING1 VH domain, an ING2 VH domain, a 1D11 VH domain, a 2G11 VH domain, a 3D12 VH domain, and a 5G4 VH domain; and

a VL CDR1, CDR2, and CDR3 all selected from a VL domain selected from the group consisting of a RAZ1 VL domain, a CR1 VL domain, a CR2 VL domain, an ING1 VL domain, an ING2 VL domain, a 1D11 VL domain, a 2G11 VL domain, a 3D12 VL domain, and a 5G4 VL domain.

35. The composition of claim 23, wherein at least one of said antibodies comprises a VH CDR1, VH CDR2, VH CDR3, VL CDR1, VL CDR2, and VL CDR3 selected from an antibody selected from the group consisting of RAZ1, CR1, CR2, ING1, ING2, 1D11, 2G11, 3D12, and 5G4.

36. The composition of claim 35, wherein at least one of said antibodies is a single chain Fv (scFv).

37. The composition of claim 35, wherein at least one of said antibodies is an IgG.

38. The composition of claim 35, wherein at least one of said antibodies is a Fab.

39. The composition of claim 35, wherein at least one of said antibodies is a $(Fab')_2$.

40. The composition of claim 35, wherein at least one of said antibodies is a $(scFv')_2$.

41. The composition of claim 23, wherein at least one of said antibodies is selected from the group consisting of RAZ1, CR1, CR2, ING1, ING2, 1D11, 2G11, 3D12, and 5G4.

42. The composition of claim 23, wherein at least two of said antibodies are selected from the group consisting of RAZ1, CR1, CR2, ING1, ING2, 1D11, 2G11, 3D12, and 5G4.

43. The composition of claim 23, wherein said antibodies are in a pharmaceutically acceptable excipient.

44. The composition of claim 43, wherein said composition is a unit dosage formulation.

45. An antibody that neutralizes botulinum neurotoxin (BontA), wherein said antibody binds at least two different BontA subtypes with an affinity of greater than about 10 nM for each subtype.

46. The antibody of claim 45, wherein said antibody binds both the Bont A1 and A2 subtypes each with an affinity greater than about 10 nM.

47. The antibody of claim 45, wherein said antibody comprises at least one CDR selected from the group consisting of RAZ1 VL CDR1, RAZ1 VL CDR2, RAZ1 VL CDR3, RAZ1 VH CDR1, RAZ1 VH CDR2, RAZ1 VH CDR3, 1D11 VL CDR1, 1D11 VL CDR2, 1D11 VL CDR3, 1D11 VH CDR1, 1D11 VH CDR2, 1D11 VH CDR3, 2G11 VL CDR1, 2G11 VL CDR2, 2G11 VL CDR3, 2G11 VH CDR1, 2G11 VH CDR2, 2G11 VH CDR3, 5G4 VL CDR1, 5G4 VL CDR2, 5G4 VL CDR3, 5G4 VH CDR1, 5G4 VH CDR2, 5G4 VH CDR3, 3D12 VL CDR1, 3D12 VL CDR2, 3D12 VL CDR3, 3D12 VH CDR1, 3D12 VH CDR2, 3D12 VH CDR3, CR1 VL CDR1, CR1 VL CDR2, CR1 VL CDR3, CR1 VH CDR1, CR1 VH CDR2, CR1 VH CDR3, CR2 VL CDR1, CR2 VL CDR2, CR2 VL CDR3, CR2 VH CDR1, CR2 VH CDR2, CR2 VH CDR3, ING1 VL CDR1, ING1 VL CDR2, ING1 VL CDR3, ING1 VH CDR1, ING1 VH CDR2, ING1 VH CDR3, ING2 VL CDR1, ING2 VL CDR2, ING2 VL CDR3, ING2 VH CDR1, ING2 VH CDR2, and ING2 VH CDR3.

48. The antibody of claim 45, wherein said antibody comprises at least three CDRs selected from the group consisting of RAZ1 VL CDR1, RAZ1 VL CDR2, RAZ1 VL CDR3, RAZ1 VH CDR1, RAZ1 VH CDR2, RAZ1 VH CDR3, 1D11 VL CDR1, 1D11 VL CDR2, 1D11 VL CDR3, 1D11 VH CDR1, 1D11 VH CDR2, 1D11 VH CDR3, 2G11 VL CDR1, 2G11 VL CDR2, 2G11 VL CDR3, 2G11 VH CDR1, 2G11 VH CDR2, 2G11 VH CDR3, 5G4 VL CDR1, 5G4 VL CDR2, 5G4 VL CDR3, 5G4 VH CDR1, 5G4 VH CDR2, 5G4 VH CDR3, 3D12 VL CDR1, 3D12 VL CDR2, 3D12 VL CDR3, 3D12 VH CDR1, 3D12 VH CDR2, 3D12 VH CDR3, CR1 VL CDR1, CR1 VL CDR2, CR1 VL CDR3, CR1 VH CDR1, CR1 VH CDR2, CR1 VH CDR3, CR2 VL CDR1, CR2 VL CDR2, CR2 VL CDR3, CR2 VH CDR1, CR2 VH CDR2, CR2 VH CDR3, ING1 VL CDR1, ING1 VL CDR2, ING1 VL CDR3, ING1 VH CDR1, ING1 VH CDR2, ING1 VH CDR3, ING2 VL CDR1, ING2 VL CDR2, ING2 VL CDR3, ING2 VH CDR1, ING2 VH CDR2, and ING2 VH CDR3.

49. The antibody of claim 45, wherein said antibody comprises a VH CDR1, CDR2, and CDR3 all selected from a VH domain selected from the group consisting of a RAZ1 VH domain, a CR1 VH domain, a CR2 VH domain, an ING1 VH domain, an ING2 VH domain, a 1D11 VH domain, a 2G11 VH domain, a 3D12 VH domain, and a 5G4 VH domain.

50. The antibody of claim 45, wherein said antibody comprises a VL CDR1, CDR2, and CDR3 all selected from a VL domain selected from the group consisting of a RAZ1 VL domain, a CR1 VL domain, an ING1 VL domain, an ING2 VL domain, a 1D11 VL domain, a 2G11 VL domain, a 3D12 VL domain, and a 5G4 VL domain.

51. The antibody of claim 45, wherein said antibody comprises:

a RAZ1 VH domain, a CR1 VH domain, a CR2 VH domain, an ING1 VH domain, an ING2 VH domain, a 1D11 VH domain, a 2G11 VH domain, a 3D12 VH domain, and a 5G4 VH domain; and

a VL CDR1, CDR2, and CDR3 all selected from a VL domain selected from the group consisting of a RAZ1 VL domain, a CR1 VL domain, a CR2 VL domain, an ING1 VL domain, an ING2 VL domain, a 1D11 VL domain, a 2G11 VL domain, a 3D12 VL domain, and a 5G4 VL domain.

52. The antibody of claim 45, wherein said antibody comprises a VH CDR1, VH CDR2, VH CDR3, VL CDR1, VL CDR2, and VL CDR3 selected from an antibody selected from the group consisting of RAZ1, CR1, CR2, ING1, ING2, 1D11, 2G11, 3D12, and 5G4.

53. The antibody of claim 45, wherein said antibody comprises a RAZ1 VH and a RAZ1 VL.

54. The antibody of claim 45, wherein said antibody comprises a CR1 VH and a CR1 VL.

55. The antibody of claim 45, wherein said antibody comprises a CR2 VH and a CR2 VL.

56. The antibody of claim 45, wherein said antibody comprises an ING1 VH and a ING1 VL.

57. The antibody of claim 45, wherein said antibody comprises an ING2 VH and an ING2 VL.

58. The antibody of claim 45, wherein said antibody comprises a 1D11 VH and a 1D11 VL.

59. The antibody of claim 45, wherein said antibody comprises a 2G11 VH and an 1G11 VL.

60. The antibody of claim 45, wherein said antibody comprises a 5G4 VH and a 5G4 VL.

61. The antibody of claim 45, wherein said antibody comprises a 3D12 VH and a 3D12 VL.

62. The antibody of claim 45, wherein said antibody is a single chain Fv (scFv).

63. The antibody of claim 45, wherein said antibody is an IgG.

64. The antibody of claim 52, wherein said antibody is a Fab.

65. The antibody of claim 45, wherein said antibody is a $(Fab')_2$.

66. The antibody of claim 45, wherein said antibody is a $(scFv')_2$.

67. The antibody of claim 45, wherein said antibody is selected from the group consisting of RAZ1, CR1, CR2, ING1, ING2, 3D12, 1D11, 2G11, and 5G4.

68. An antibody that binds a botulinum neurotoxin (BontA), wherein said antibody comprises at least one CDR selected from the group consisting of AR2 VL CDR1, AR2 VL CDR2, AR2 VL CDR3, AR2 VH CDR1, AR2 VH CDR2, AR2 VH CDR3, AR3 VL CDR1, AR3 VL CDR2, AR3 VL CDR3, AR3 VH CDR1, AR3 VH CDR2, AR3 VH CDR3, AR4 VL CDR1, AR4 VL CDR2, AR4 VL CDR3, AR4 VH CDR1, AR4 VH CDR2, and AR4 VH CDR3.

69. The antibody of claim 68, wherein said antibody comprises at least three CDRs selected from the group consisting of AR2 VL CDR1, AR2 VL CDR2, AR2 VL CDR3, AR2 VH CDR1, AR2 VH CDR2, AR2 VH CDR3, AR3 VL CDR1, AR3 VL CDR2, AR3 VL CDR3, AR3 VH CDR1, AR3 VH CDR2, AR3 VH CDR3, AR4 VL CDR1, AR4 VL CDR2, AR4 VL CDR3, AR4 VH CDR1, AR4 VH CDR2, and AR4 VH CDR3.

70. The antibody of claim 68, wherein said antibody comprises a VH CDR1, CDR2, and CDR3 all selected from a VH domain selected from the group consisting of an AR2 VH domain, an AR3 VH domain, and an AR4 VH domain.

71. The antibody of claim 68, wherein said antibody comprises a VL CDR1, CDR2, and CDR3 all selected from a VL domain selected from the group consisting of an AR2 VL domain, an AR3 VL domain, and an AR4 VL domain.

72. The antibody of claim 68, wherein said antibody comprises:

a VH CDR1, CDR2, and CDR3 all selected from a VH domain selected from the group consisting of an AR2 VH domain, an AR3 VH domain, and an AR4 VH domain; and

a VL CDR1, CDR2, and CDR3 all selected from a VL domain selected from the group consisting of an AR2 VL domain, an AR3 VL domain, and an AR4 VL.

73. The antibody of claim 68, wherein said antibody comprises a VH CDR1, VH CDR2, VH CDR3, VL CDR1, VL CDR2, and VL CDR3 selected from an antibody selected from the group consisting of AR2, AR3 and AR4.

74. The antibody of claim 68, wherein said antibody is a single chain Fv (scFv).

75. The antibody of claim 68, wherein said antibody is an IgG.

76. The antibody of claim 68, wherein said antibody is a Fab.

77. The antibody of claim 68, wherein said antibody is a $(Fab')_2$.

78. The antibody of claim 68, wherein said antibody is a $(scFv')_2$.

79. The antibody of claim 68, wherein said antibody is selected from the group consisting of AR2, AR3 and AR4.

80. A nucleic acid that encodes an antibody according to any of claim 45-79.

81. A cell containing a nucleic acid that encodes an antibody according to any of claim 45-79.

82. A kit for neutralizing a Botulinum neurotoxin, said kit comprising:

a composition according to any of claims 23-44; and

instructional materials teaching the use of said composition to neutralize a Botulinum neurotoxin.

83. The kit of claim 82, wherein said composition is stored in a disposable syringe.

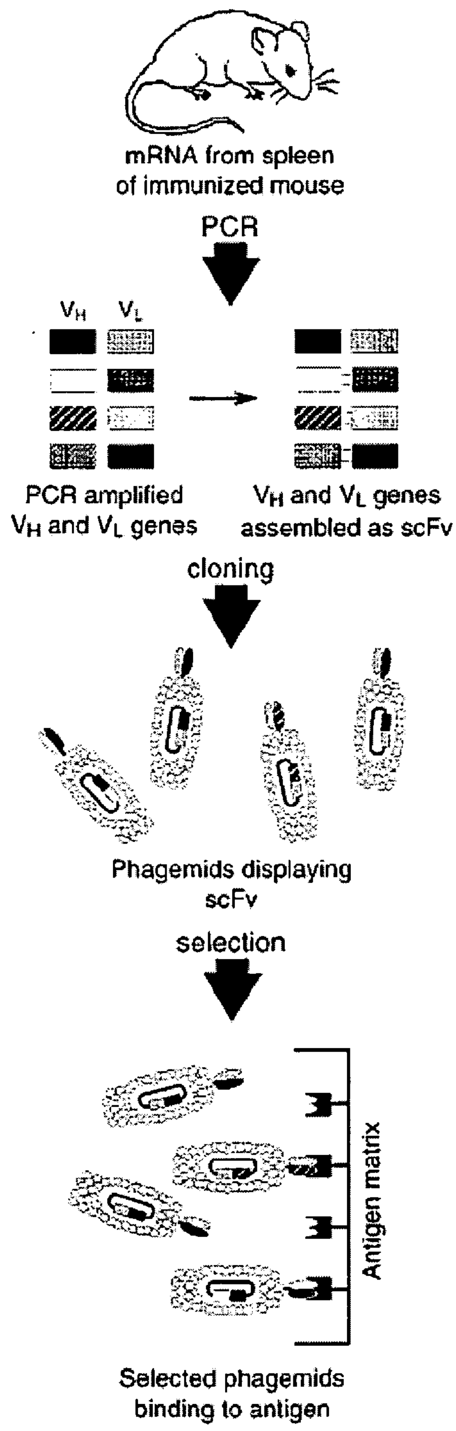

mRNA from spleen
of immunized mouse
PCR
V_H V_L
PCR amplified
V_H and V_L genes
V_H and V_L genes
assembled as scFv
cloning
Phagemids displaying
scFv
selection
Antigen matrix
Selected phagemids
binding to antigen

Fig. 1

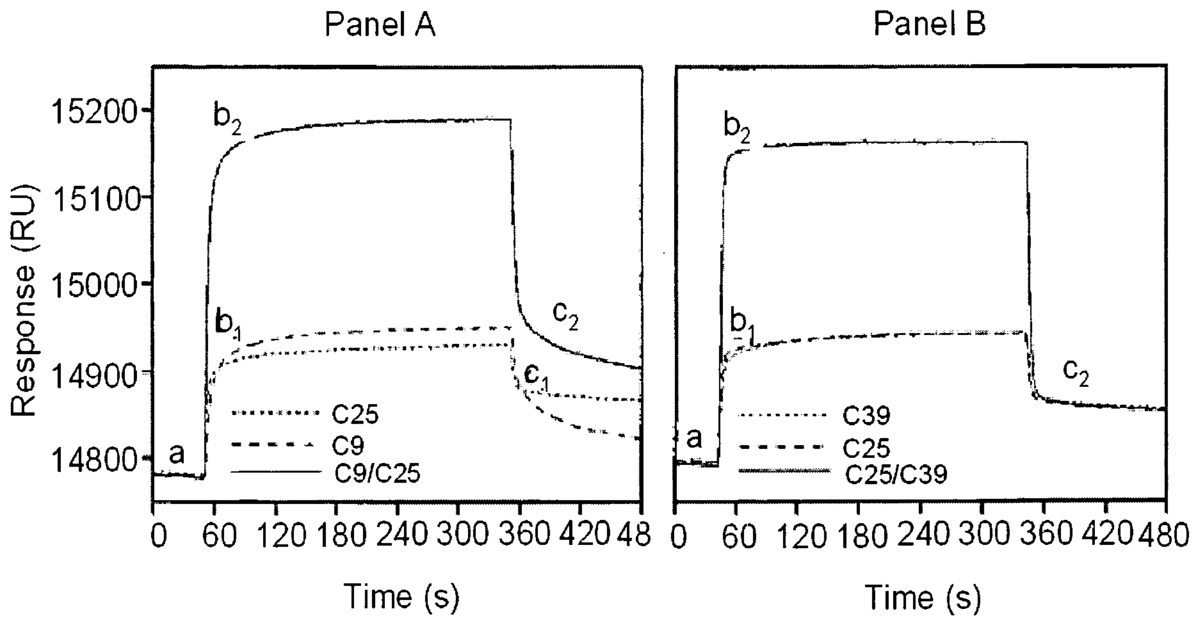
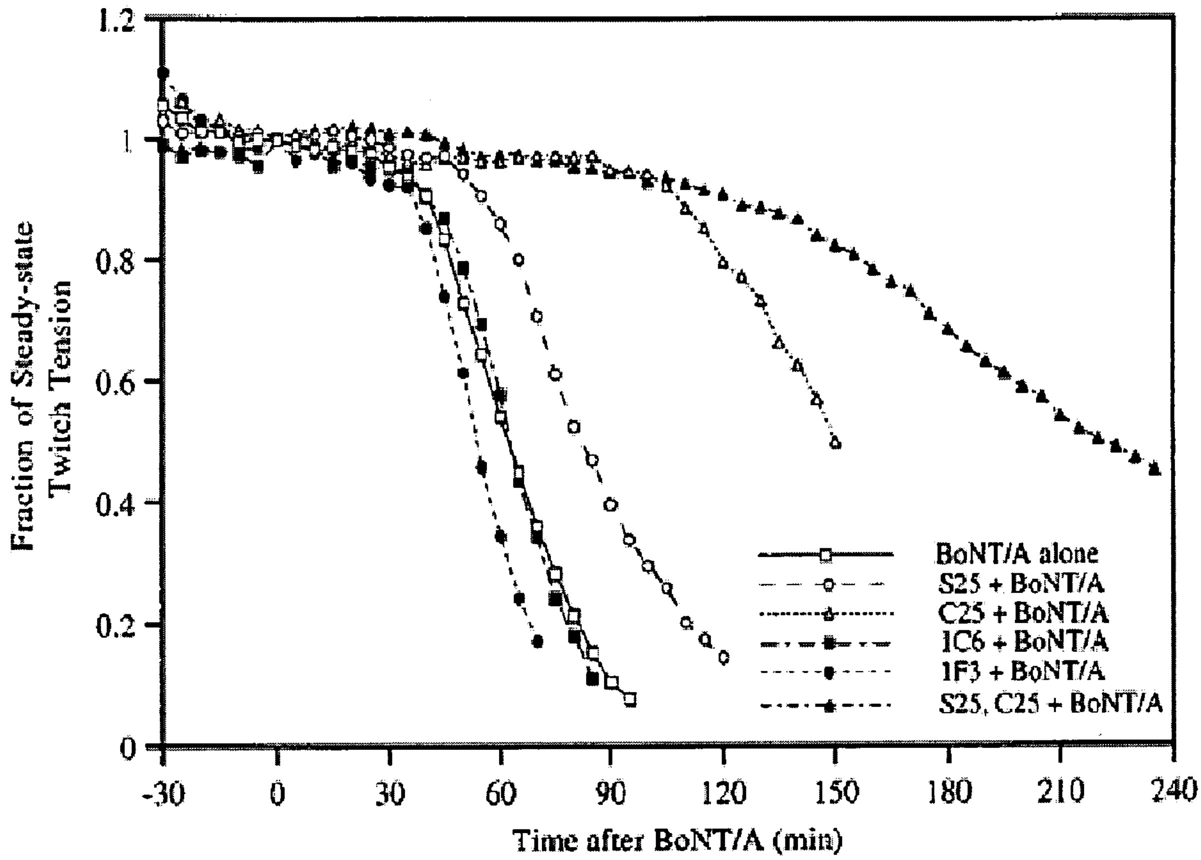
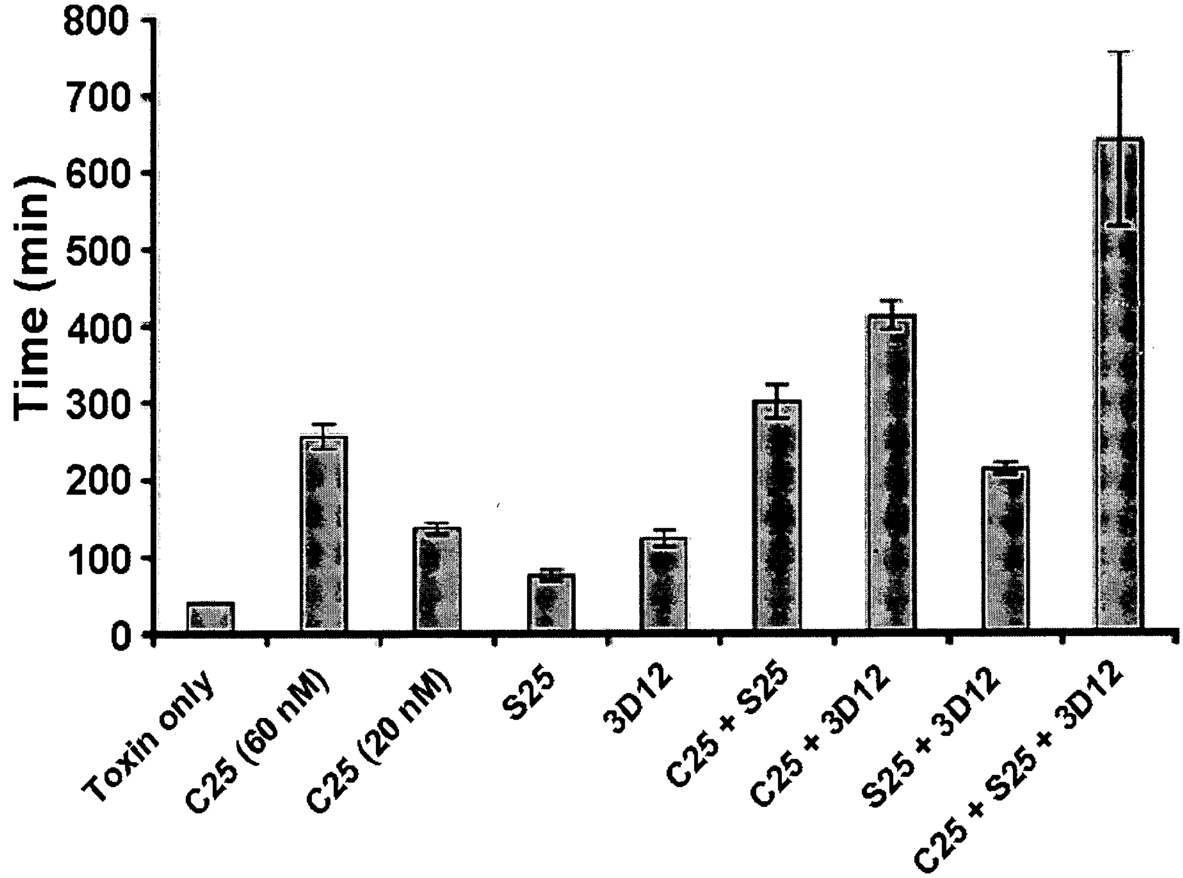

Panel A
Panel B
Response (RU)
15200
15100
15000
14900
14800
b2
b1
c2
c1
a
C25
C9
C9/C25
C39
C25
C25/C39
0 60 120 180 240 300 360 420 48
0 60 120 180 240 300 360 420 480
Time (s)
Time (s)

Fig. 2



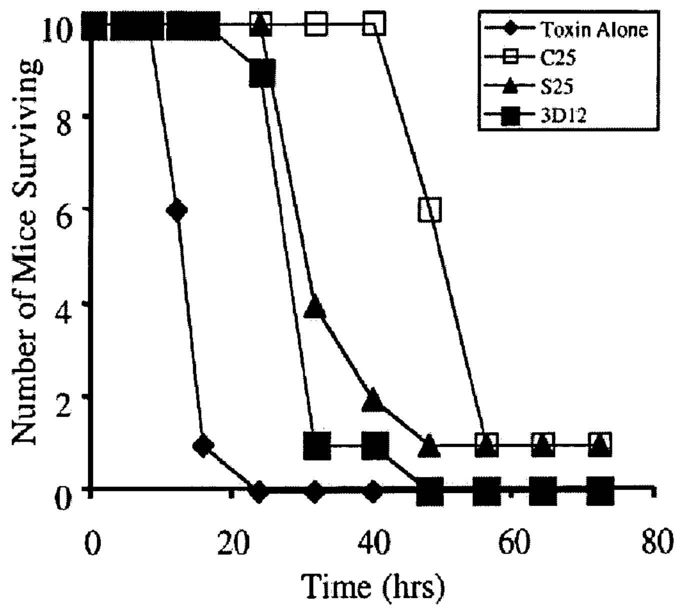
Fraction of Steady-state Twitch Tension
Time after BoNT/A (min)
BoNT/A alone
S25 + BoNT/A
C25 + BoNT/A
1C6 + BoNT/A
1F3 + BoNT/A
S25, C25 + BoNT/A

Fig. 3



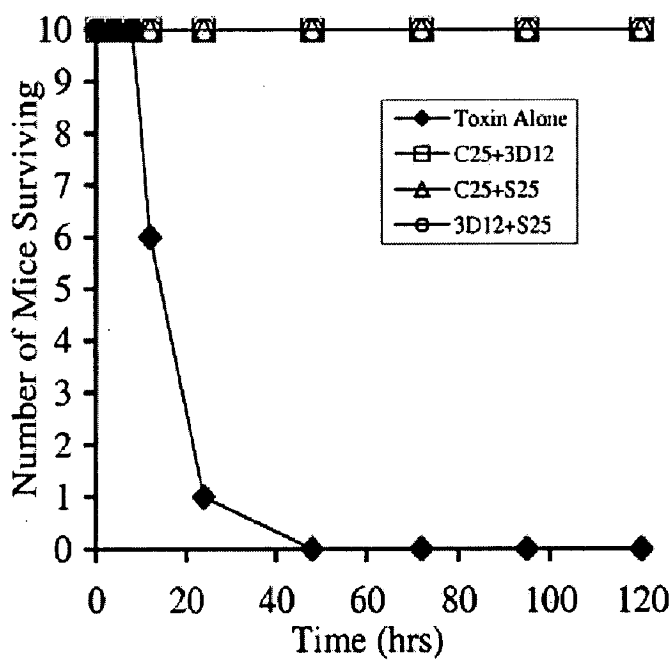
Time (min)
800
700
600
500
400
300
200
100
0
Toxin only
C25 (60 nM)
C25 (20 nM)
S25
3D12
C25 + S25
C25 + 3D12
S25 + 3D12
C25 + S25 + 3D12

Fig. 4



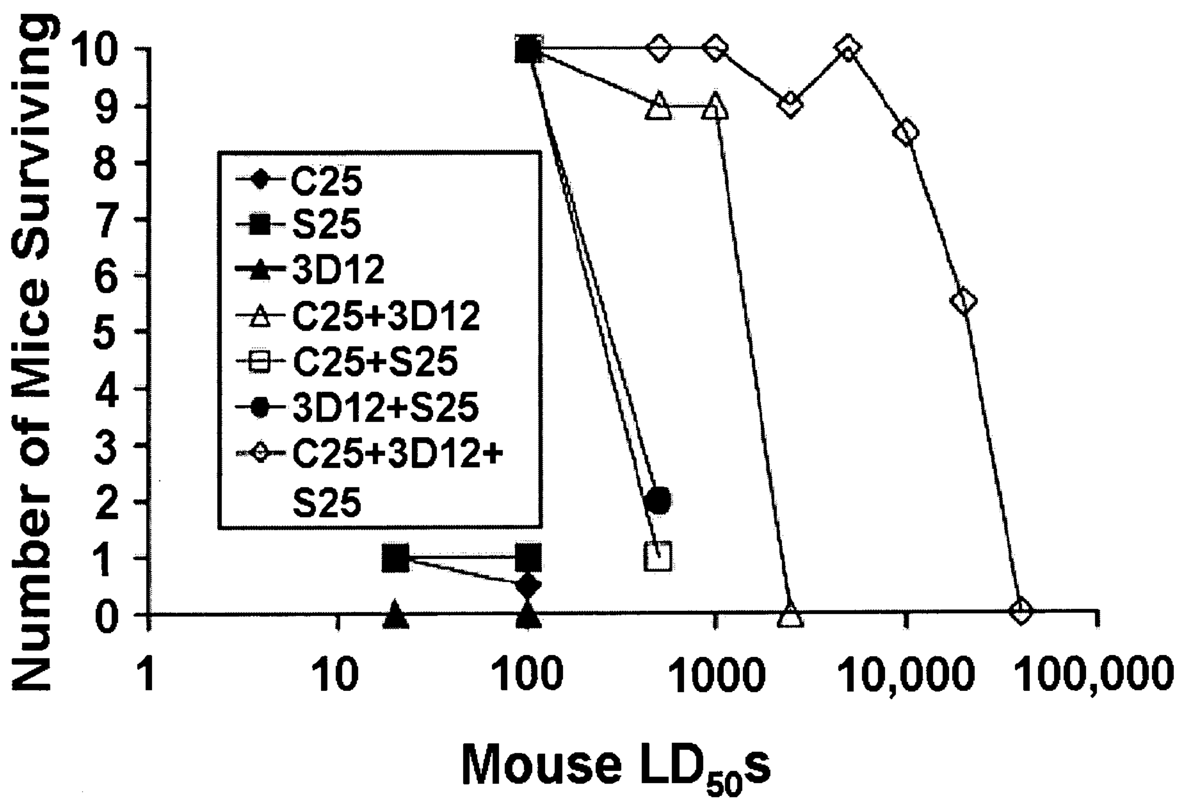
Toxin Alone
C25
S25
3D12
Number of Mice Surviving
10
8
6
4
2
0
0
20
40
60
80
Time (hrs)

Fig. 5A



Toxin Alone
C25+3D12
C25+S25
3D12+S25
Number of Mice Surviving
10
9
8
7
6
5
4
3
2
1
0
0
20
40
60
80
100
120
Time (hrs)

Fig. 5B



Number of Mice Surviving
10
9
8
7
6
5
4
3
2
1
0
C25
S25
3D12
C25+3D12
C25+S25
3D12+S25
C25+3D12+
S25
1
10
100
1000
10,000
100,000
Mouse LD_{50}s

Fig. 6

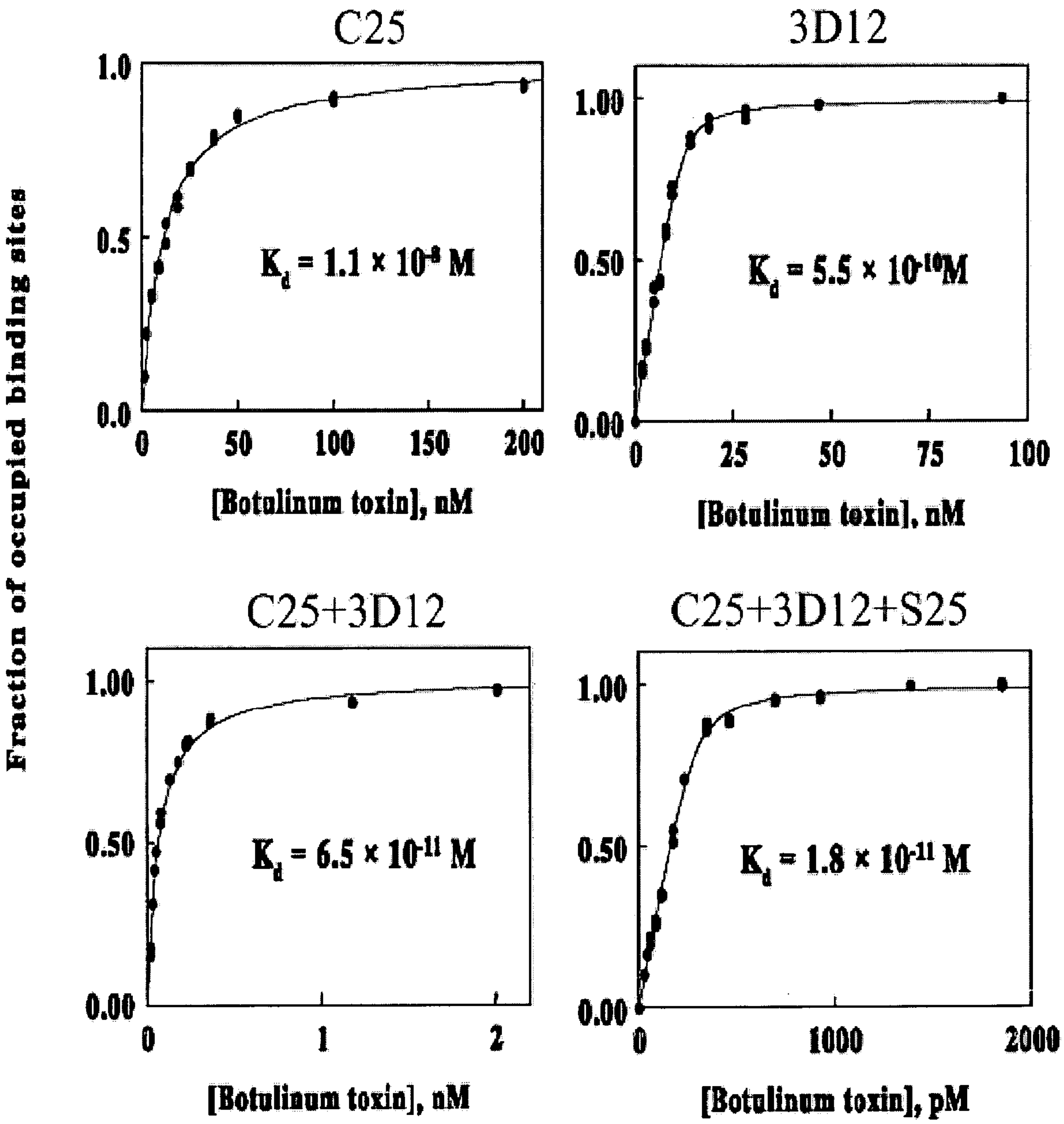
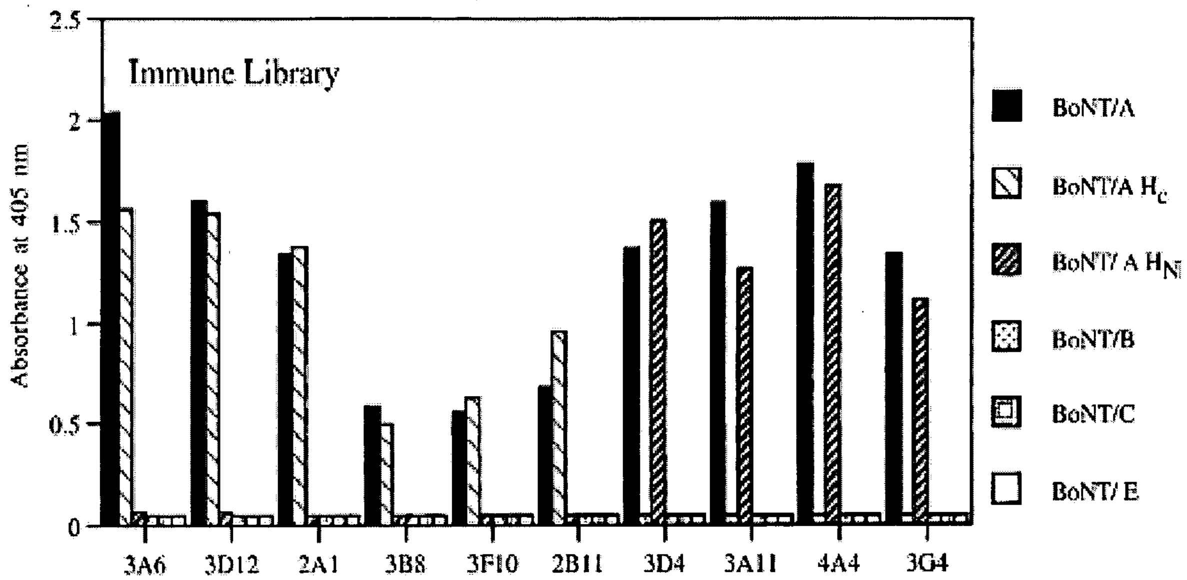
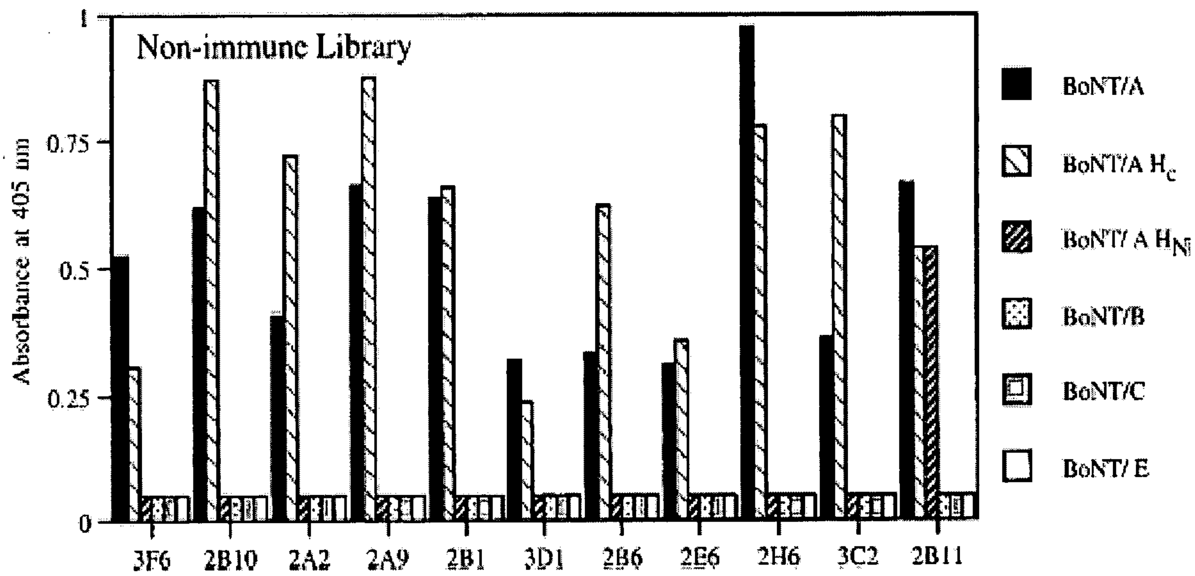

C25
3D12
C25+3D12
C25+3D12+S25
Fraction of occupied binding sites
$K_d = 1.1 \times 10^{-8}$ M
$K_d = 5.5 \times 10^{-10}$M
$K_d = 6.5 \times 10^{-11}$ M
$K_d = 1.8 \times 10^{-11}$ M
[Botulinum toxin], nM
[Botulinum toxin], nM
[Botulinum toxin], nM
[Botulinum toxin], pM

Fig. 7



Immune Library
Absorbance at 405 nm
2.5
2
1.5
1
0.5
0
3A6
3D12
2A1
3B8
3F10
2B11
3D4
3A11
4A4
3G4
BoNT/A
BoNT/A H_c
BoNT/ A H_N
BoNT/B
BoNT/C
BoNT/ E

Fig. 8A



Non-immune Library
Absorbance at 405 nm
1
0.75
0.5
0.25
0
3F6
2B10
2A2
2A9
2B1
3D1
2B6
2E6
2H6
3C2
2B11
BoNT/A
BoNT/A H_c
BoNT/ A H_N
BoNT/B
BoNT/C
BoNT/ E

Fig. 8B

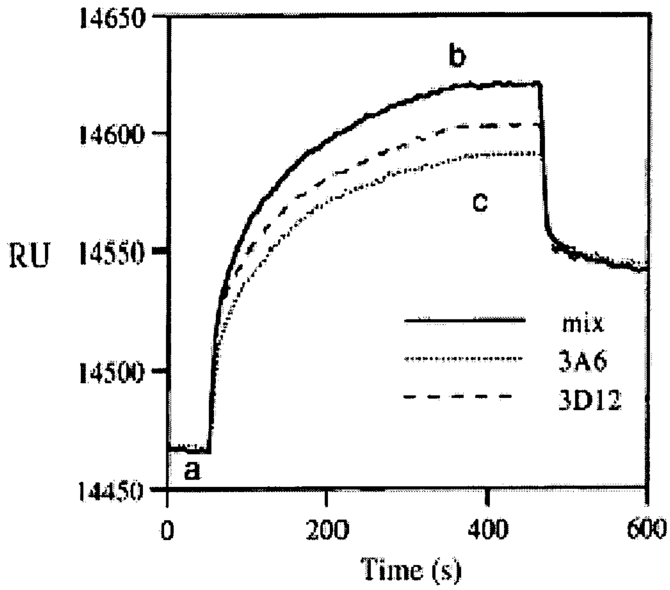

14650
14600
14550
14500
14450
RU
b
c
a
mix
3A6
3D12
0
200
400
600
Time (s)

Fig. 9A

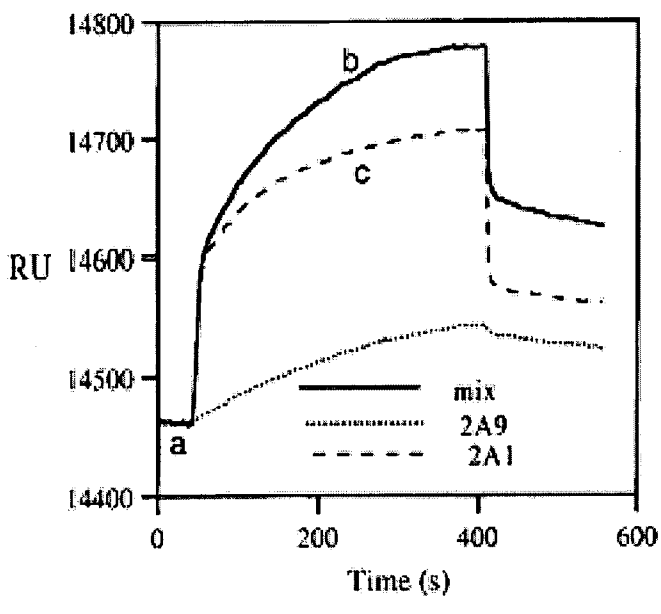

14800
14700
14600
14500
14400
RU
b
c
a
mix
2A9
2A1
0
200
400
600
Time (s)

Fig. 9B

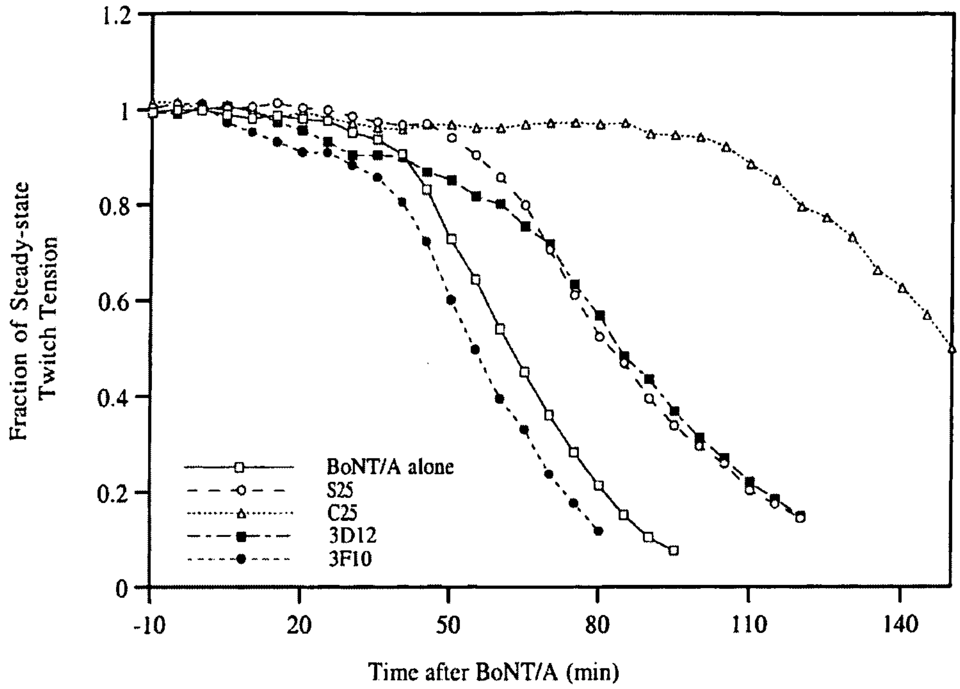


Fig. 10A

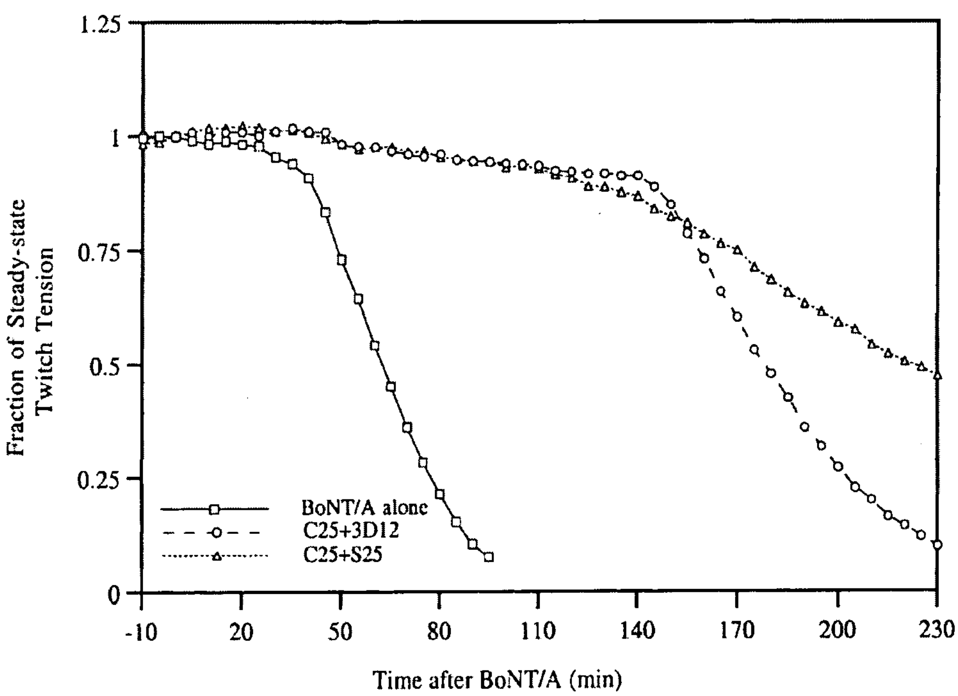


Fig. 10B

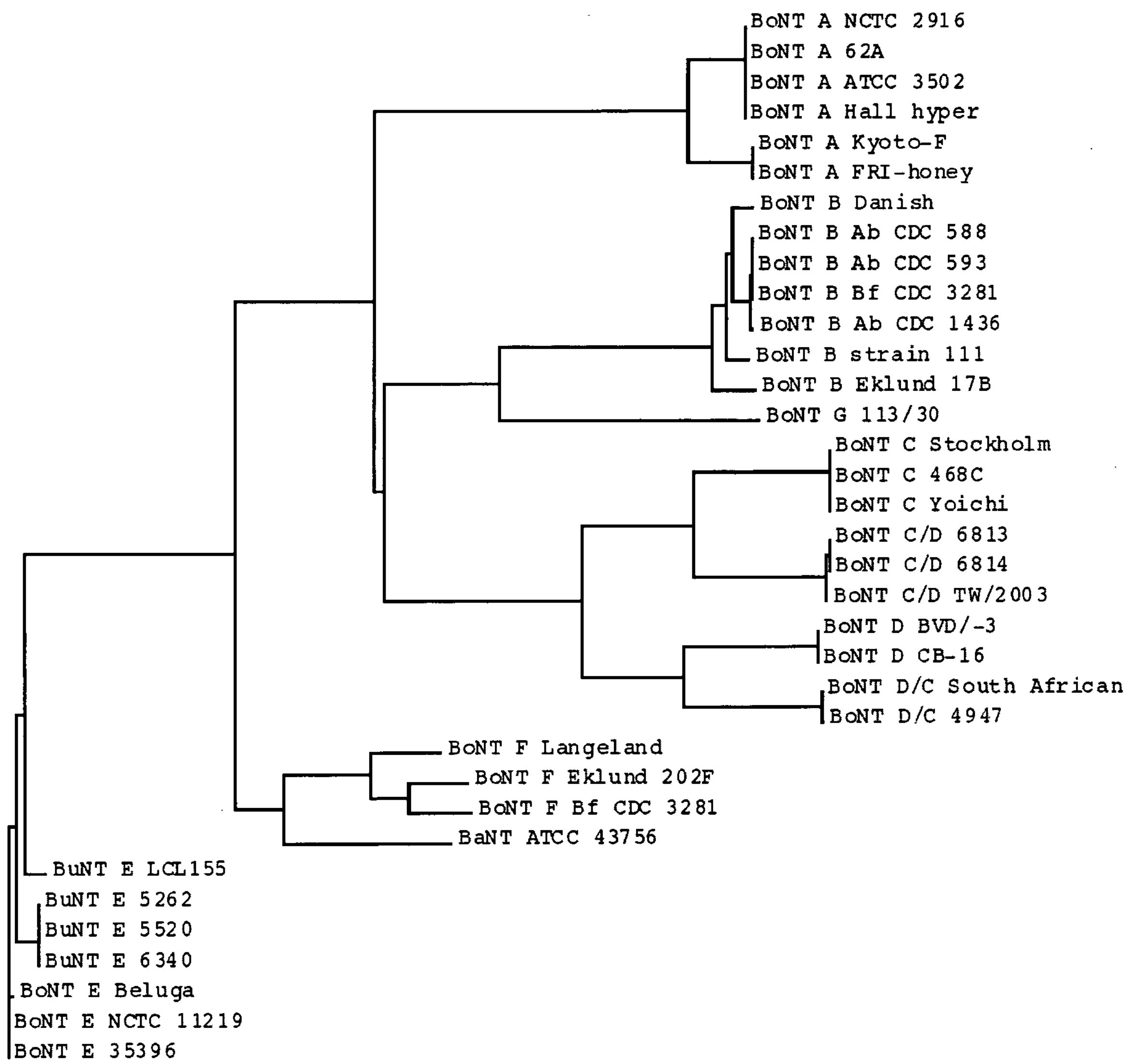

BoNT A NCTC 2916
BoNT A 62A
BoNT A ATCC 3502
BoNT A Hall hyper
BoNT A Kyoto-F
BoNT A FRI-honey
BoNT B Danish
BoNT B Ab CDC 588
BoNT B Ab CDC 593
BoNT B Bf CDC 3281
BoNT B Ab CDC 1436
BoNT B strain 111
BoNT B Eklund 17B
BoNT G 113/30
BoNT C Stockholm
BoNT C 468C
BoNT C Yoichi
BoNT C/D 6813
BoNT C/D 6814
BoNT C/D TW/2003
BoNT D BVD/-3
BoNT D CB-16
BoNT D/C South African
BoNT D/C 4947
BoNT F Langeland
BoNT F Eklund 202F
BoNT F Bf CDC 3281
BaNT ATCC 43756
BuNT E LCL155
BuNT E 5262
BuNT E 5520
BuNT E 6340
BoNT E Beluga
BoNT E NCTC 11219
BoNT E 35396

Fig. 11

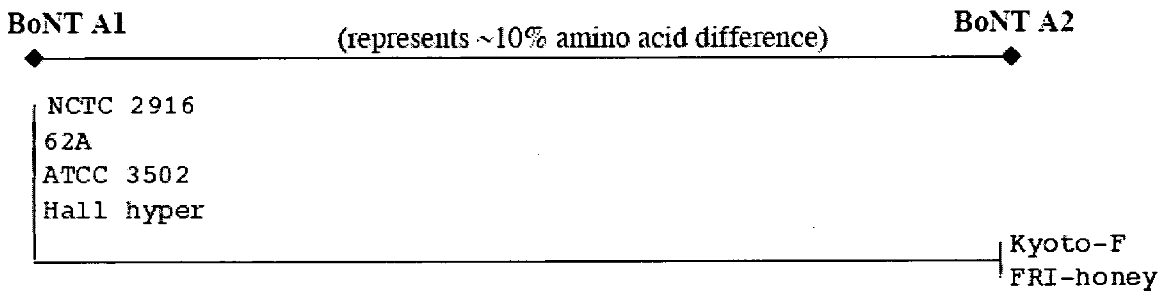


Fig. 12A

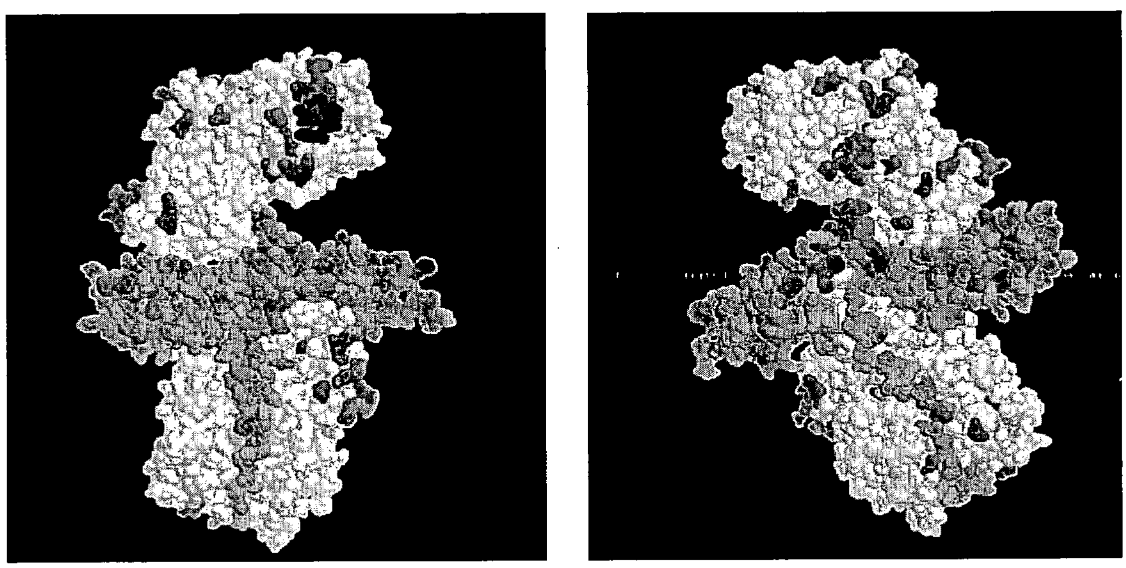


Fig. 12B

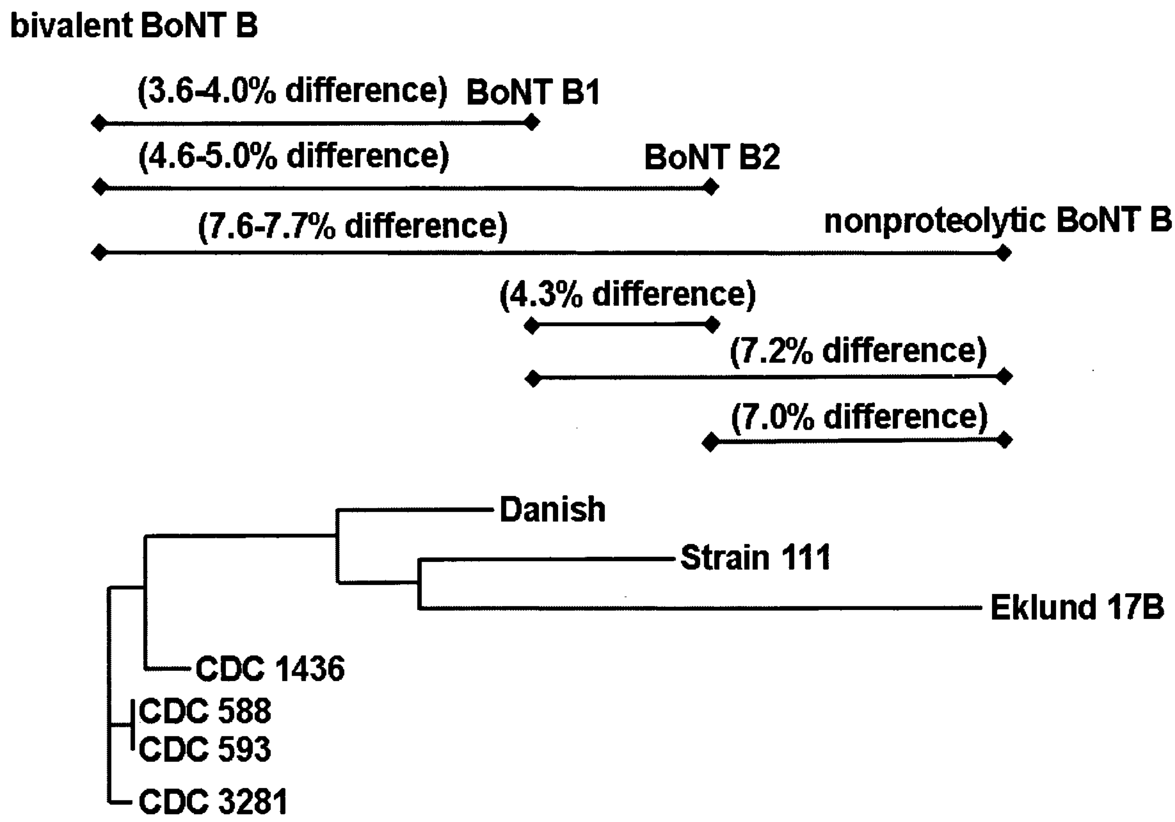

bivalent BoNT B
(3.6-4.0% difference)
BoNT B1
(4.6-5.0% difference)
BoNT B2
(7.6-7.7% difference)
nonproteolytic BoNT B
(4.3% difference)
(7.2% difference)
(7.0% difference)
Danish
Strain 111
Eklund 17B
CDC 1436
CDC 588
CDC 593
CDC 3281

Fig. 13

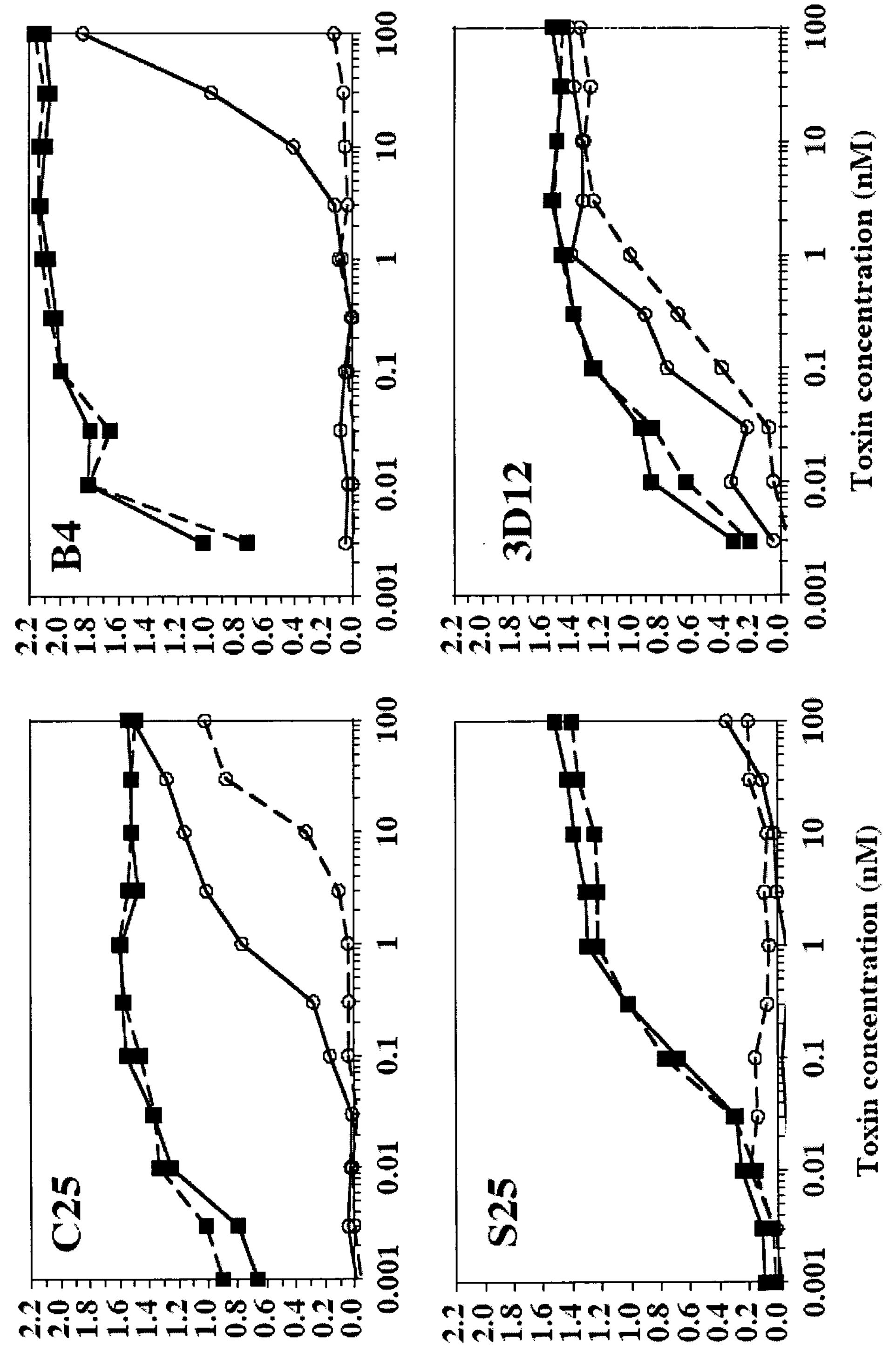
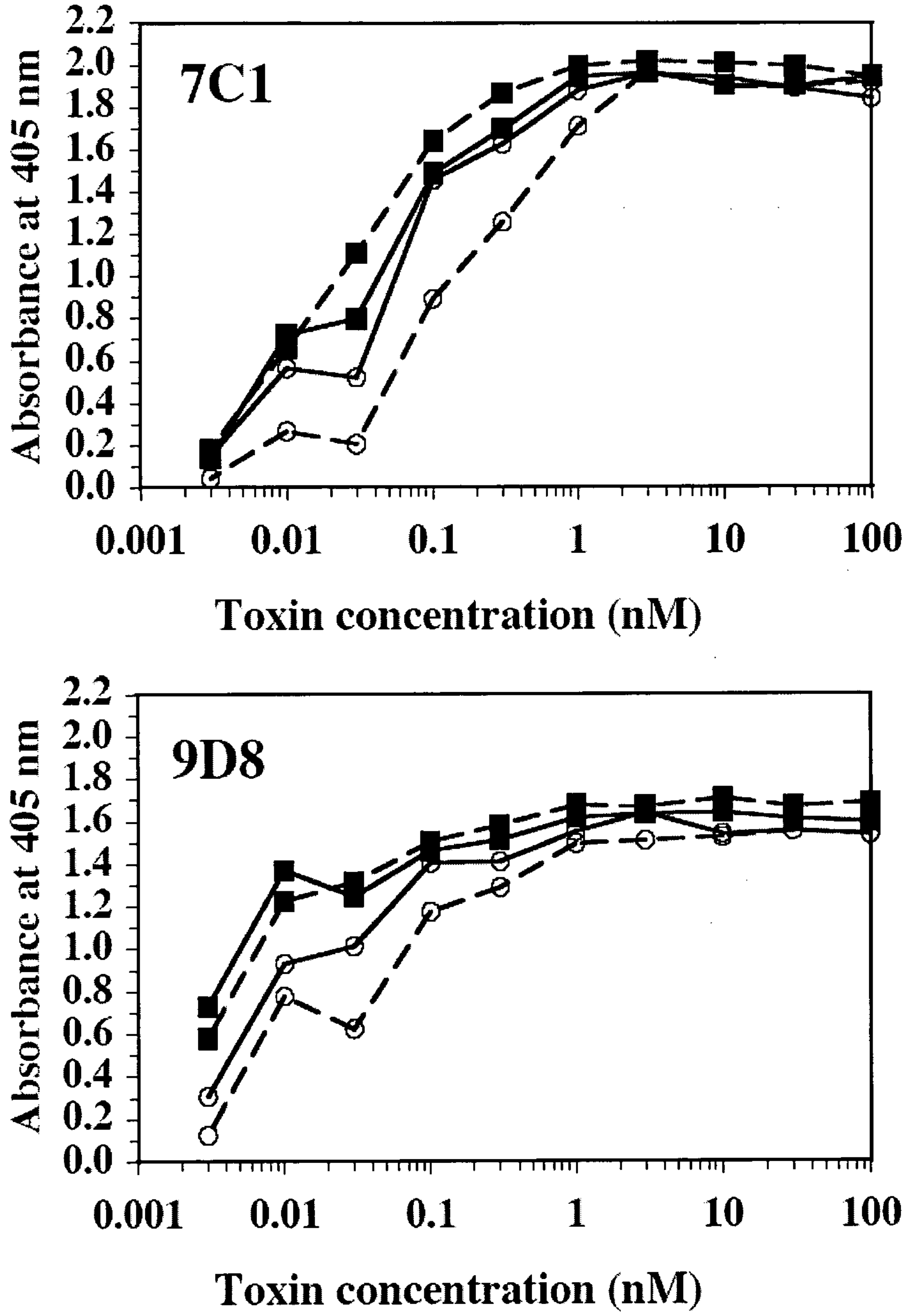

C25
B4
S25
3D12
Absorbance at 405 nm
Absorbance at 405 nm
Toxin concentration (nM)
Toxin concentration (nM)
0.001
0.01
0.1
1
10
100
0.0
0.2
0.4
0.6
0.8
1.0
1.2
1.4
1.6
1.8
2.0
2.2

Fig. 14



7C1
Absorbance at 405 nm
2.2
2.0
1.8
1.6
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
0.001
0.01
0.1
1
10
100
Toxin concentration (nM)
9D8
Absorbance at 405 nm
Toxin concentration (nM)

Fig. 15

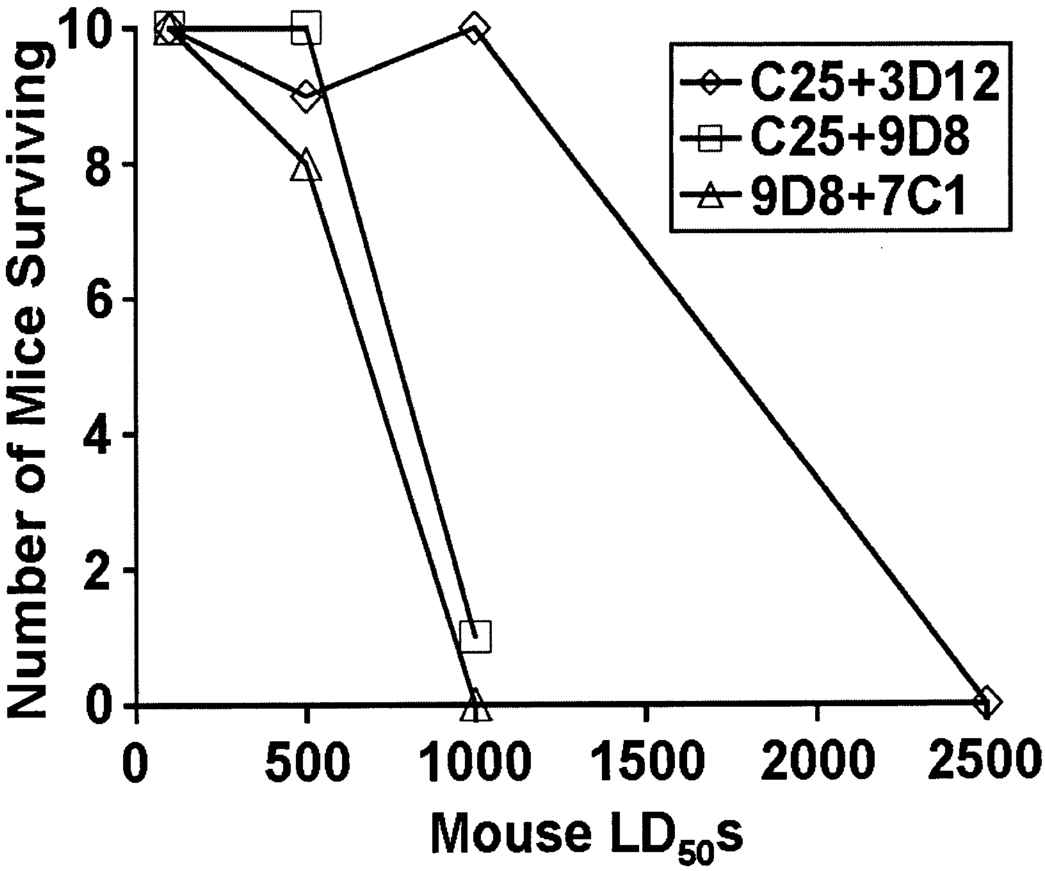

Number of Mice Surviving
10
8
6
4
2
0
0
500
1000
1500
2000
2500
Mouse LD50s
C25+3D12
C25+9D8
9D8+7C1

Fig. 16

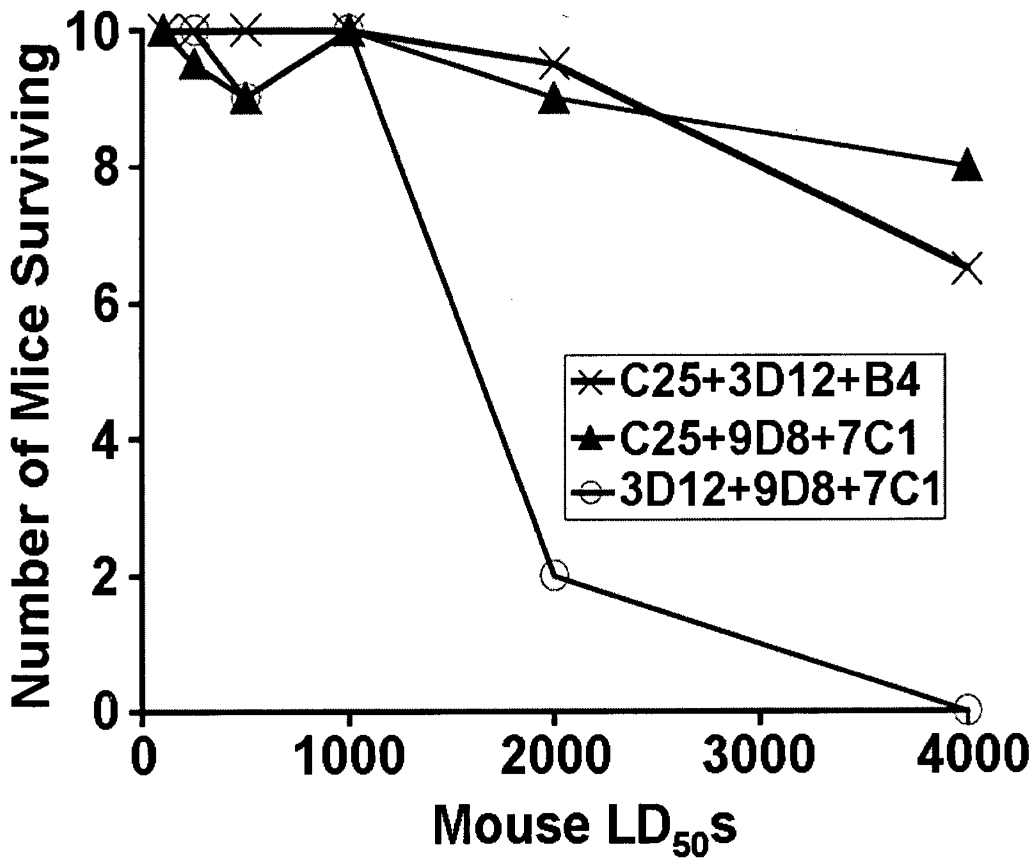
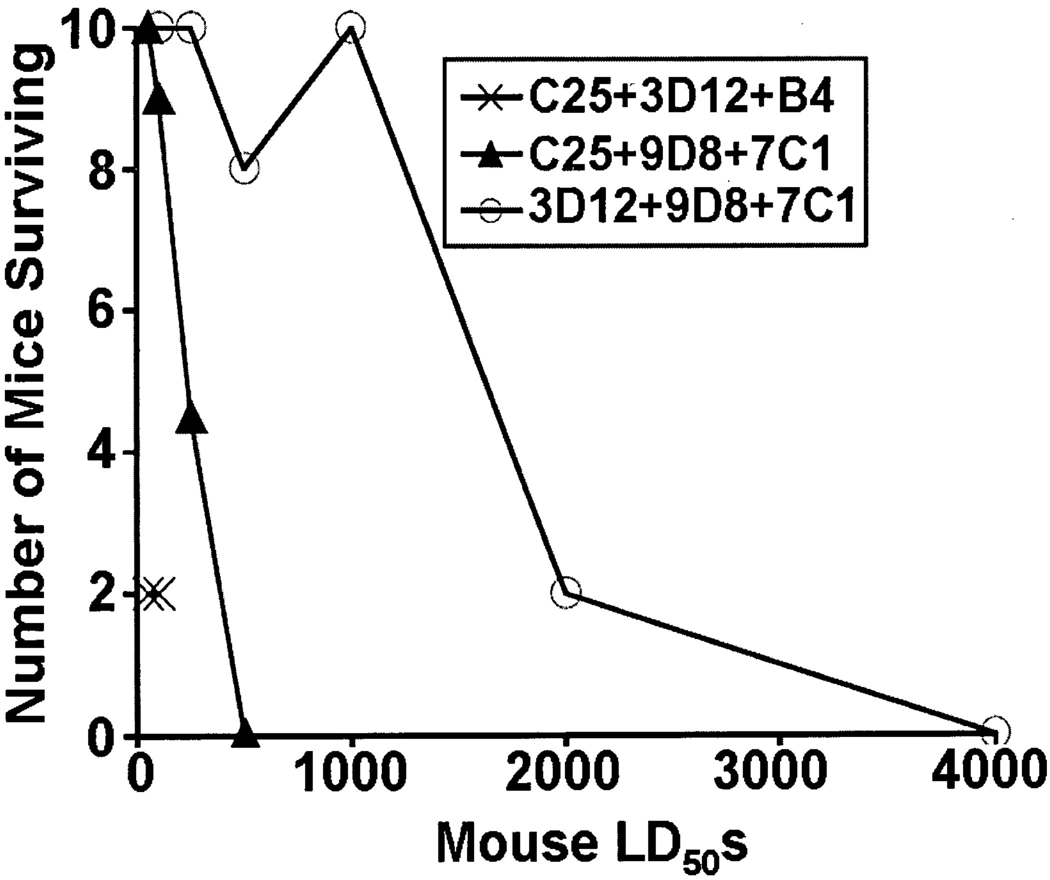

Number of Mice Surviving
10
8
6
4
2
0
0
1000
2000
3000
4000
Mouse LD50s
C25+3D12+B4
C25+9D8+7C1
3D12+9D8+7C1

Fig. 17A



Number of Mice Surviving
10
8
6
4
2
0
0
1000
2000
3000
4000
Mouse LD_{50}s
C25+3D12+B4
C25+9D8+7C1
3D12+9D8+7C1

Fig. 17B

Clone	Framework 1	CDR1	Framework 2	CDR2	Framework 3	CDR3	Framework 4
Hu-C25	QVQLQESGGGLVQPGGSLRLSCAASGFTFS	DYYMY	WVRQAPGKGLEWVA	TISDGGSYTYYPDSVKG	RFTISRDNSKNTLYLQMNSLRAEDTAMYYCSR	YRYDDAMDY	WGQGTLVTVSS
AR1	------------------------------	-----	--------------	-----------------	--------------------------I-----	---------	-----------
AR2	------------------------------	-H---	--------------	-----------------	---T----------------------I-----	---------	-----------
AR3	-----------------------------G	EH---	--------------	---------------E-	---T----------------------I-----	---------	-----------
AR4	-----------------------------E	EH---	--------------	---------------E-	---T----------------------I-----	---------	-----------
CR1	-----------------------------K	YD---	--------------	-----------S---E-	---T----------------------I-----	---------	-----------

Light Chains:

Clone	Framework 1	CDR1	Framework 2	CDR2	Framework 3	CDR3	Framework 4
ORIG	EIVLTQSPATLSLSPGERATISC	RASESVDSYGHSFMQ	WYQQKPGQAPRLLIY	RASNLEP	GIPARFSGSGSGTDFTLTISSLEPEDFAVYYC	QQSNEDPFT	FGQGTKVEIKR
AR1	-----------------------	---------------	---------------	-------	--------------------------------	--G--V---	-----------
AR2	-----------------------	---------------	---------------	-------	--------------------------------	--G--V---	-----------
AR3	-----------------------	---------------	---------------	-------	--------------------------------	--G--V---	-----------
AR4	-----------------------	---------------	---------------	-------	--------------------------------	--G--V---	-----------
CR1	-----------------------	---------------	---------------	-------	--------------------------------	--G--V---	-----------

Fig. 18

Deduced protein sequences of heavy and light chain variable regions of 3D12 and RAZ1

Heavy chain

Clone	Framework 1	CDR1	Framework 2	CDR2	Framework 3	CDR3	Framework 4
3D12	QVQLVQSGGGVVHPGRSLKLSCAGSGFTFS	DYDMH	WVRQAPGKGLEWVA	VMWFDGTEKYSAESVKG	RFTISRDNSKNTLFLQMNSLRADDTAVYYCAR	EPDWLLWGDRGALDV	WGQGTTVTVSS
RAZ1	------------------------------	-----	--------------	-----------------	--------------------------------	---------------	-----------

Light chains

Clone	Framework 1	CDR1	Framework 2	CDR2	Framework 3	CDR3	Framework 4
3D12	DIVMTQSPSTLSASVGDRVTITC	RASQSISSWLA	WYQQKPGKAPKLLMY	EASSLES	GVPSRFSGSGSGTEFTLTISSLQPDDFAAYYC	QHYNTYPYT	FGQGTKLEIKR
RAZ1	-----------------------	W-------R--	---------------	--T--G-	--------------------------------	---D-----	-----------

Fig. 19A

Deduced protein sequences of heavy and light chain variable regions of ING1, ING1Fab clones and ING2:
(A1 and A2 toxin binder)

Heavy Chain

Clone	Framework1	CDR1	Framework 2	CDR2	Framework3	CDR3	Framework4
ING1	QVQLQQSGGGLVQPGGSLRLSCAASGFTFS	NYAMT	WVRQAPGKGLEWVS	SISVGGSDTYYADSVKG	RFTVSRDNSKNTLLLQMNSLRAEDTAVYYCAK	VRTKYCSSLSCFAGFDS	WGQGTRVTVSS
1D11	------------------------------	-----	--------------	-----------------	--------------------------------	-----------------	-----------
2G11	------------------------------	-----	--------------	-----------------	--------------------------------	-----------------	-----------
5G4	------------------------------	-----	--------------	-----------------	--------------------------------	-----------------	-----------
ING2	QVQLVQSGAEVKKPGSSVKVSCKASGDTFN	RNAIA	WVRQAPGQGLEWMG	RIIPNLRTTHYAQKFQG	RVAITADKHTNTVFMELSSLRSEDTAVYYCAR	DPYYYSYMDV	WGKGTTVTVSS

Light Chain

Clone	Framework1	CDR1	Framework 2	CDR2	Framework3	CDR3	Framework4
ING1	DIVMTQSPSSLSASVGDRVTITC	RASQSISSYLN	WYQQKPGKAPKLLIYA	ASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQSYSTPRTT	FGGGTKVDIKR
1D11	E--L-------------------	----------H	----------T---SD	------	---------RF---------------------	------RAL-	-------E-R
2G11	-V---------------------	----------H	----------T---SD	---S--	---------RF---------------------	------RAL-	-------E---
5G4	E--L-------------------	----G--N--A	--------V-------	--T---	-------------------------V------	------LMCS	--Q---LE---
ING2	EIVLTQSPDSLAVSLGERATINC	KSSRSVLYSSNNNNYLA	WYQQKPGQPPKLLIYW	ASTRES	GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC	QQYYSTPFT	FGGGTKVEIKR

Fig. 19B

HuC25 KD = 8.44 x 10^{-10} M

*Library constructed by error prone PCR of whole scFv
*3 mutations, 1 VH FMW1 and 2 VL CDR3
*5 fold affinity increase

AR1 KD = 1.69 x 10^{-10} M

*Library constructed by error prone PCR of whole scFv
*1 mutation VH CDR1
*2.8 fold affinity increase

AR2 KD = 6.14 x 10^{-10} M

*VH CDR1 was diversified by spiked oliog
*3 mutations, 2 VH CDR1 and 1 VH CDR2
*2.5 fold affinity increase

AR4 KD = 2.26 x 10^{-10} M

Fig. 20A

3D12 **KD = 6.43 x 10^{-10} M**

***Library constructed by error prone PCR of whole scFv**
***5 mutations, 2 VL CDR1, 2 VL CDR2, and 1 VL CDR3**
***45 fold affinity increase**

RAZ1 **KD = 2.1 x 10^{-11} M**

Fig. 20B

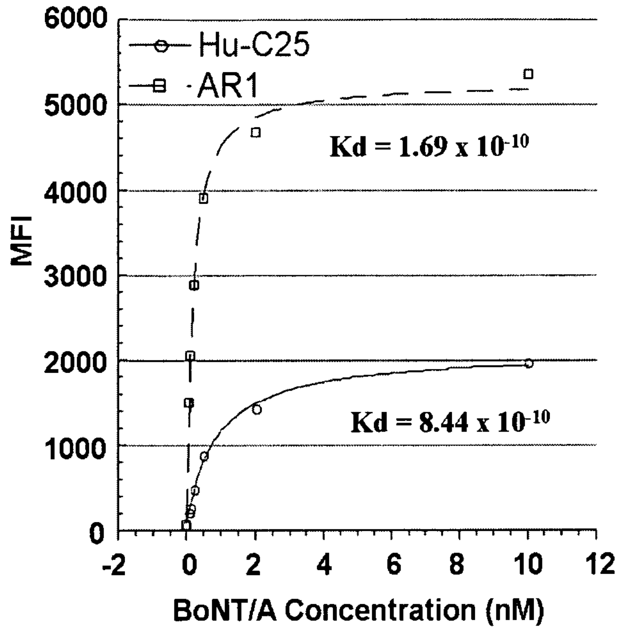


Fig. 21A

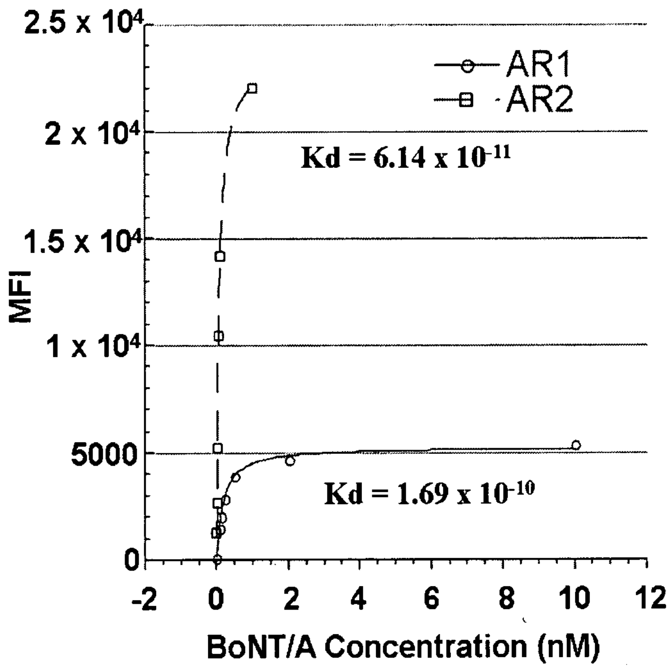


Fig. 21B

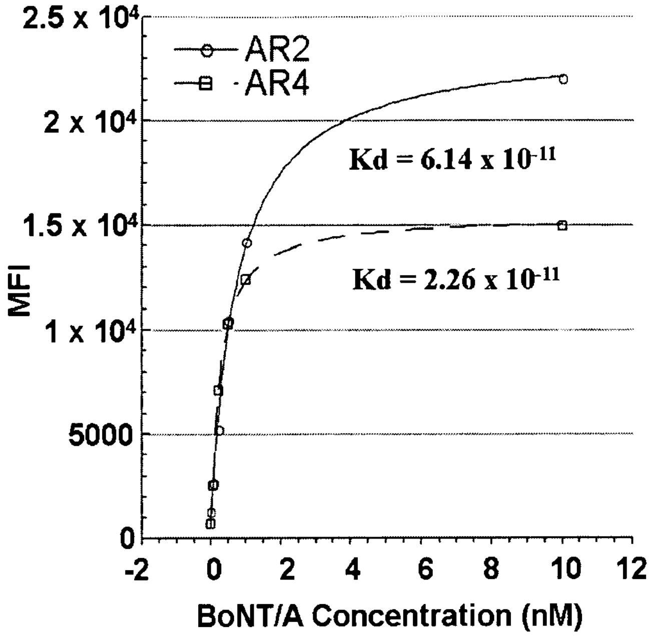


Fig. 21C

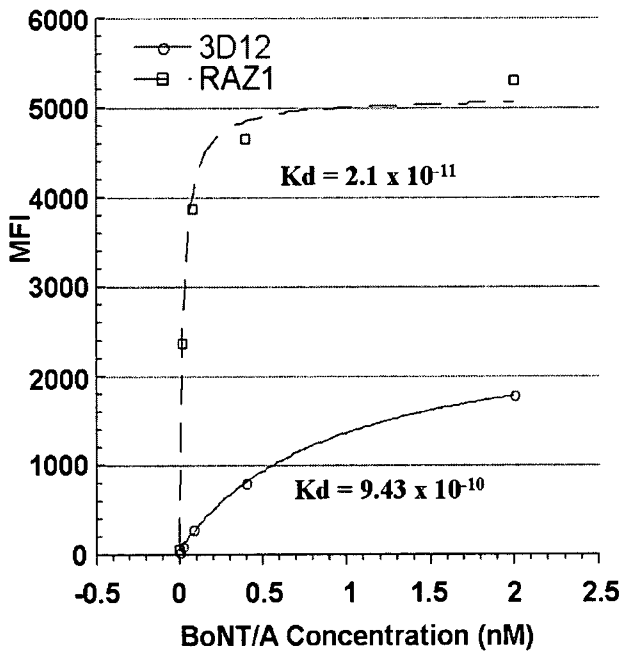


Fig. 21D

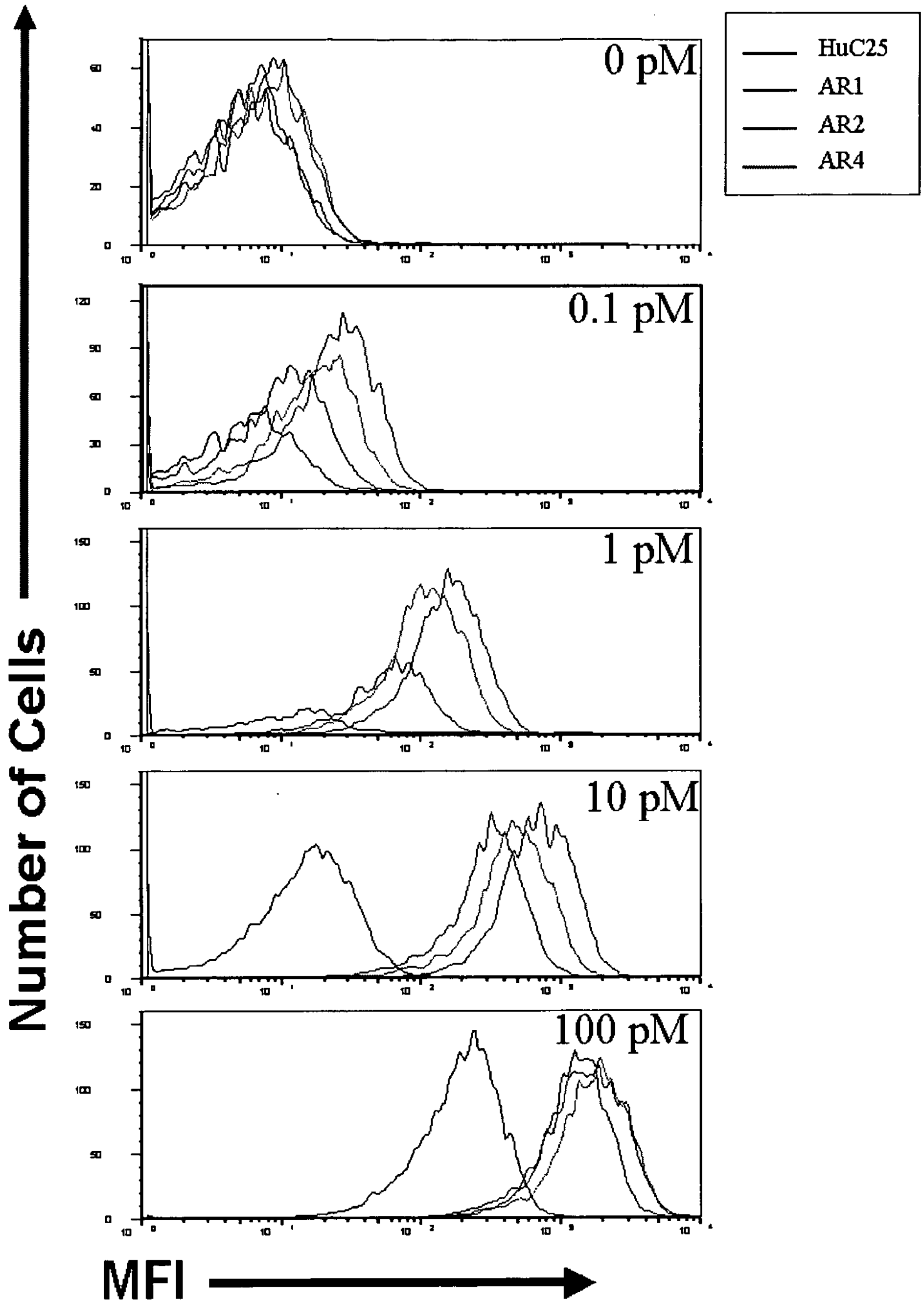


Fig. 22

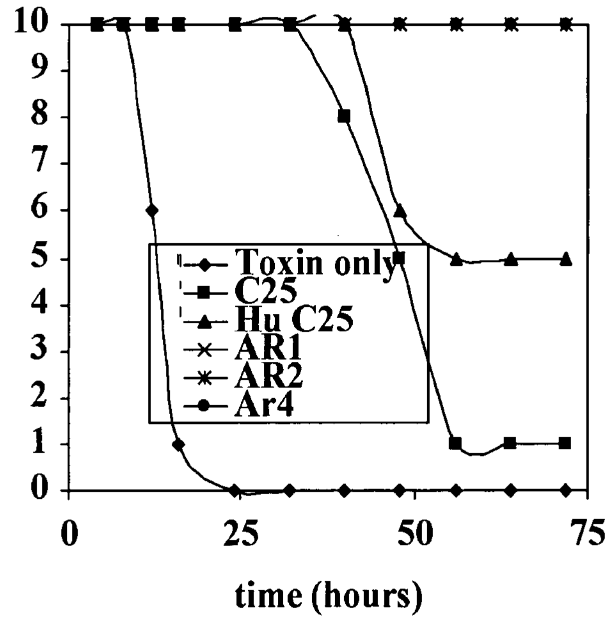


Fig. 23A

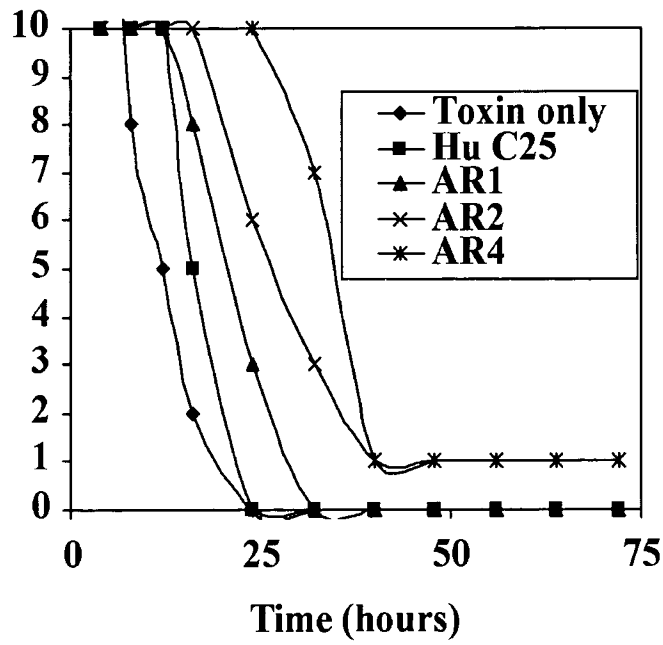


Fig. 23B

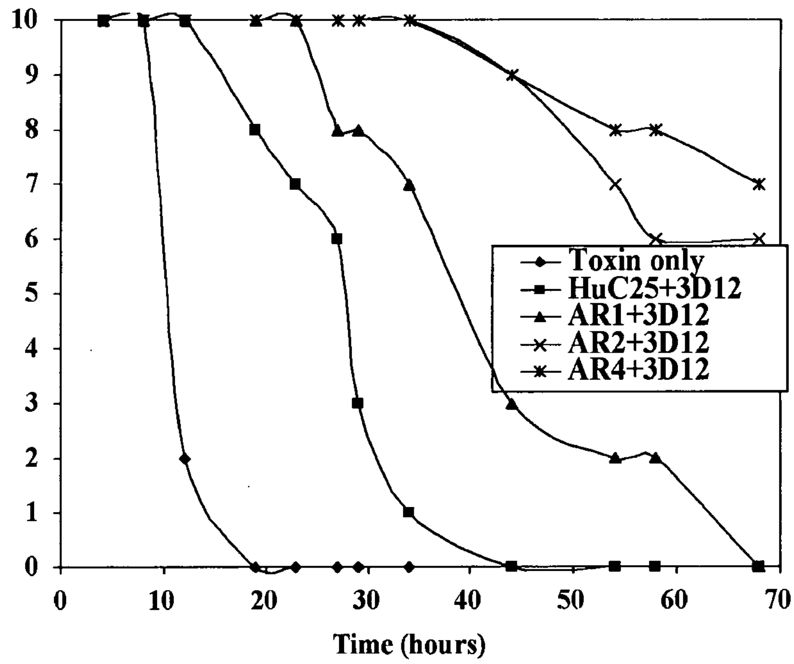


Fig. 24A

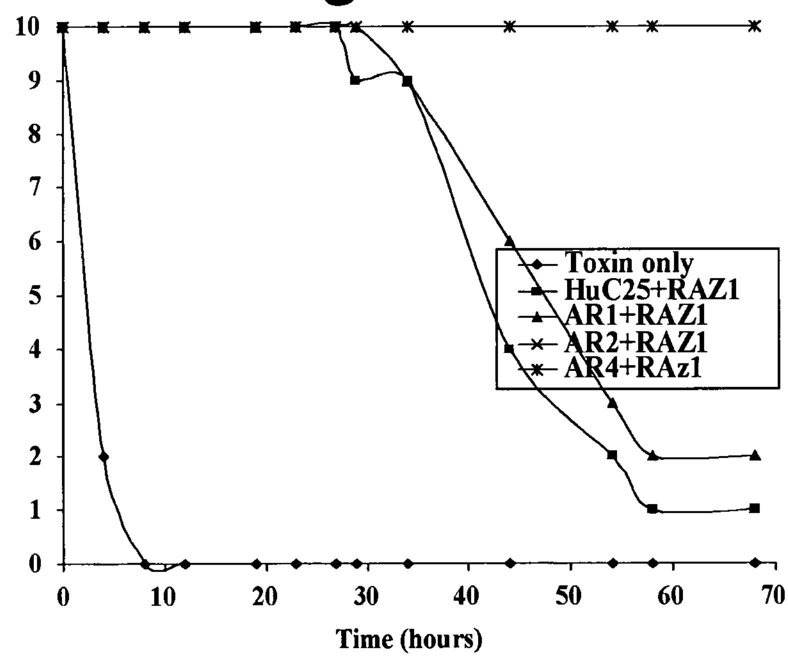


Fig. 24B

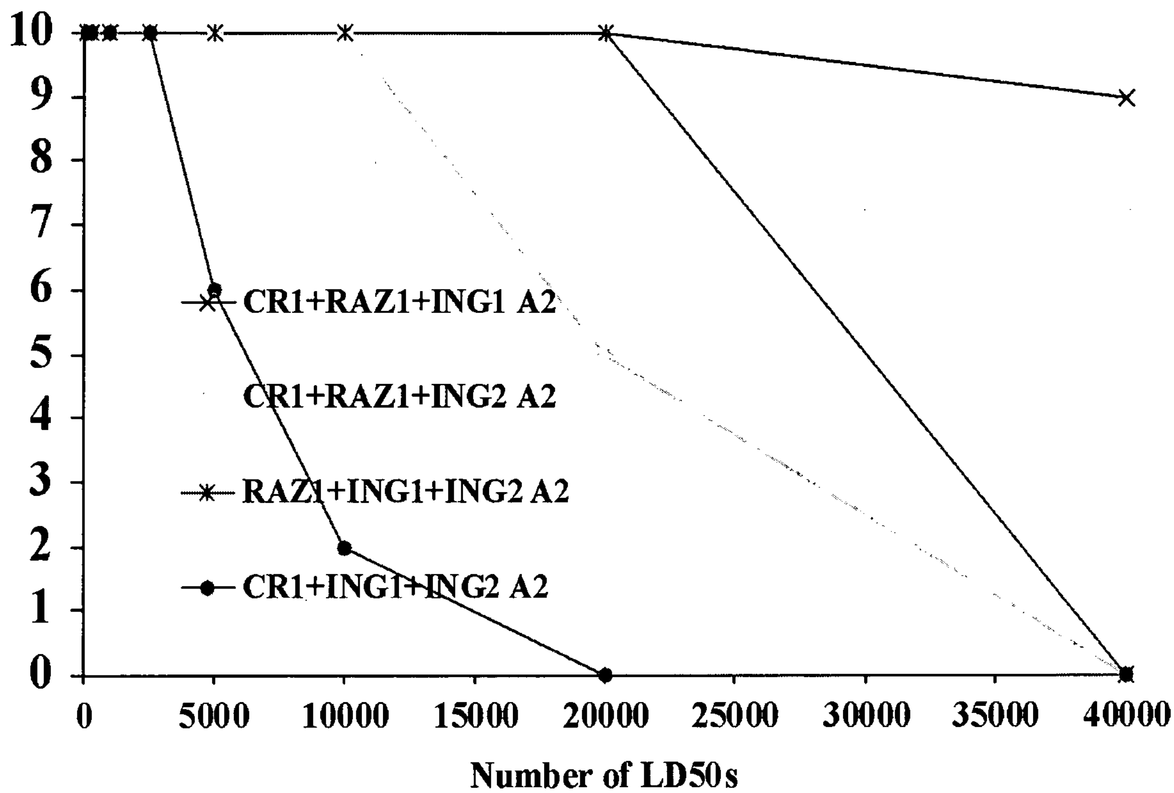

10
9
8
7
6
5
4
3
2
1
0
0
5000
10000
15000
20000
25000
30000
35000
40000
Number of LD50s
CR1+RAZ1+ING1 A2
CR1+RAZ1+ING2 A2
RAZ1+ING1+ING2 A2
CR1+ING1+ING2 A2

Fig. 25

C25 Lineage Antibodies"

Heavy Chains (VH):

Clone	Framework 1	CDR1	Framework 2	CDR2	Framework 3	CDR3	Framework 4
Hu-C25	QVQLQESGGGLVQPGGSLRLSCAAS	GFTFSDYYMY	WVRQAPGKGLEWVA	TISDGGSYTYYPDSVKG	RFTISRDNSKNTLYLQMNSLRAEDTAMYYCSR	YRYDDAMDY	WGQGTLVTVSS
AR1	-------------------------	----------	--------------	-----------------	--------------------------I-----	---------	-----------
AR2	-------------------------	------H---	--------------	-----------------	---T----------------------I-----	---------	-----------
AR3	-------------------------	----GEH---	--------------	---------------E-	---T----------------------I-----	---------	-----------
AR4	-------------------------	----EEH---	--------------	---------------E-	---T----------------------I-----	---------	-----------
CR1	-------------------------	----KYD---	--------------	-----------S---E-	---T----------------------I-----	---------	-----------
CR2	-----Q-------------------	----KYD---	-I------------	-----------S---E-	---T----------------------I-----	---------	-----------

Light Chains (VL):

Clone	Framework 1	CDR1	Framework 2	CDR2	Framework 3	CDR3	Framework 4
Hu-C25	EIVLTQSPATLSLSPGERATISC	RASESVDSYGHSFMQ	WYQQKPGQAPRLLIY	RASNLEP	GIPARFSGSGSGTDFTLTISSLEPEDFAVYYC	QQSNEDPFT	FGQGTKVEIKR
AR1	-----------------------	---------------	---------------	-------	--------------------------------	--G--V---	-----------
AR2	-----------------------	---------------	---------------	-------	--------------------------------	--G--V---	-----------
AR3	-----------------------	---------------	---------------	-------	--------------------------------	--G--V---	-----------
AR4	-----------------------	---------------	---------------	-------	--------------------------------	--G--V---	-----------
CR1	-----------------------	---------------	---------------	-------	--------------------------------	--G--V---	-----------
CR2	-----------------------	---------------	---------------	-------	--------------------------------	--G--V---	-----------

Dashes indicate conserved residues. Letters indicate mutated residues.

Fig. 26

SEQUENCE LISTING

RAZ1 VH SEQUENCE (SEQ ID NO:351 nucleic acid, SEQ ID NO:352, protein):

Sequence Range: 1 to 372

```
        10         20         30         40         50         60
CAGGTGCAGC TGGTGCAGTC TGGGGGAGGC GTAGTCCACC CTGGGAGGTC CCTGAAACTC
 Q  V  Q   L  V  Q  S   G  G  G   V  V  H   P  G  R  S   L  K  L>

        70         80         90        100        110        120
TCCTGTGCAG GGAGTGGATT CACTTTCAGT GATTATGACA TGCACTGGGT CCGCCAGGCT
 S  C  A   G  S  G  F   T  F  S   D  Y  D   M  H  W  V   R  Q  A>

       130        140        150        160        170        180
CCAGGCAAGG GCCTGGAATG GGTGGCGGTT ATGTGGTTTG ATGGAACTGA AAAATACTCT
 P  G  K   G  L  E  W   V  A  V   M  W  F   D  G  T  E   K  Y  S>

       190        200        210        220        230        240
GCAGAGTCCG TGAAGGGCCG ATTCACCATC TCCAGAGACA ATTCCAAGAA CACATTGTTT
 A  E  S   V  K  G  R   F  T  I   S  R  D   N  S  K  N   T  L  F>

       250        260        270        280        290        300
TTGCAAATGA ACAGCCTGAG AGCCGACGAC ACGGCTGTGT ATTACTGTGC GAGAGAGCCT
 L  Q  M   N  S  L  R   A  D  D   T  A  V   Y  Y  C  A   R  E  P>

       310        320        330        340        350        360
GATTGGTTAT TATGGGGGGA CAGGGGTGCT CTGGACGTCT GGGGCCAAGG GACCACGGTC
 D  W  L   L  W  G  D   R  G  A   L  D  V   W  G  Q  G   T  T  V>

       370
ACCGTCTCCT CA
 T  V  S   S>
```

RAZ1 V1 SEQUENCE (SEQ ID NO:353 nucleic acid, SEQ ID NO:354, protein):

Sequence Range: 1 to 324

```
        10         20         30         40         50         60
GACATCGTGA TGACCCAGTC TCCTTCCACT CTGTCTGCAT CTGTAGGAGA CAGAGTCACC
 D  I  V   M  T  Q  S   P  S  T   L  S  A   S  V  G  D   R  V  T>

        70         80         90        100        110        120
ATCACTTGCT GGGCCAGTCA GAGTATTAGT AGCCGGTTGG CCTGGTATCA GCAGAAACCA
 I  T  C   W  A  S  Q   S  I  S   S  R  L   A  W  Y  Q   Q  K  P>

       130        140        150        160        170        180
GGGAAAGCCC CTAAGCTCCT GATGTATGAG GCGACTAGTT TAGGAAGTGG GGTCCCATCA
 G  K  A   P  K  L  L   M  Y  E   A  T  S   L  G  S  G   V  P  S>

       190        200        210        220        230        240
AGGTTCAGCG GCAGTGGATC CGGGACAGAA TTCACTCTCA CCATCAGCAG CCTGCAGCCT
 R  F  S   G  S  G  S   G  T  E   F  T  L   T  I  S  S   L  Q  P>

       250        260        270        280        290        300
GATGATTTTG CAGCTTATTA CTGCCAACAT TATGACACTT ACCCGTACAC TTTTGGCCAG
 D  D  F   A  A  Y  Y   C  Q  H   Y  D  T   Y  P  Y  T   F  G  Q>

       310        320
GGGACCAAGC TGGAGATCAA ACGT
 G  T  K   L  E  I  K   R>
```

ING1 VH SEQ (SEQ ID NO:355 nucleic acid, SEQ ID NO:356, protein)

Sequence Range: 1 to 378

```
      5         10        15        20        25        30        35        40        45
CAG GTA CAG CTG CAG CAG TCA GGG GGA GGC CTG GTG CAG CCT GGG GGG
GTC CAT GTC GAC GTC GTC AGT CCC CCT CCG GAC CAC GTC GGA CCC CCC
 Q   V   Q   L   Q   Q   S   G   G   G   L   V   Q   P   G   G>

50        55        60        65        70        75        80        85        90        95
TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTT AGC AAC TAT
AGG GAC TCT GAG AGG ACA CGT CGG AGA CCT AAG TGG AAA TCG TTG ATA
 S   L   R   L   S   C   A   A   S   G   F   T   F   S   N   Y>

   100       105       110       115       120       125       130       135       140
GCC ATG ACC TGG GTC CGC CAG GCT CCA GGG AAG GGG CTG GAG TGG GTC
CGG TAC TGG ACC CAG GCG GTC CGA GGT CCC TTC CCC GAC CTC ACC CAG
 A   M   T   W   V   R   Q   A   P   G   K   G   L   E   W   V>

145       150       155       160       165       170       175       180       185       190
TCA TCT ATC AGT GTT GGT GGT AGT GAC ACA TAC TAC GCA GAC TCC GTG
AGT AGA TAG TCA CAA CCA CCA TCA CTG TGT ATG ATG CGT CTG AGG CAC
 S   S   I   S   V   G   G   S   D   T   Y   Y   A   D   S   V>

195       200       205       210       215       220       225       230       235       240
AAG GGC CGG TTC ACC GTC TCC AGA GAC AAT TCC AAG AAC ACG CTG CTT
TTC CCG GCC AAG TGG CAG AGG TCT CTG TTA AGG TTC TTG TGC GAC GAA
 K   G   R   F   T   V   S   R   D   N   S   K   N   T   L   L>

   245       250       255       260       265       270       275       280       285
CTG CAG ATG AAC AGC CTG AGA GCC GAG GAC ACG GCC GTA TAT TAC TGT
GAC GTC TAC TTG TCG GAC TCT CGG CTC CTG TGC CGG CAT ATA ATG ACA
 L   Q   M   N   S   L   R   A   E   D   T   A   V   Y   Y   C>

290       295       300       305       310       315       320       325       330       335
GCG AAA GTT CGC ACA AAA TAT TGT AGT AGT TTA AGT TGC TTC GCC GGA
CGC TTT CAA GCG TGT TTT ATA ACA TCA TCA AAT TCA ACG AAG CGG CCT
 A   K   V   R   T   K   Y   C   S   S   L   S   C   F   A   G>

   340       345       350       355       360       365       370       375
TTT GAC TCC TGG GGC CAG GGA ACC CGG GTC ACC GTC TCC TCA
AAA CTG AGG ACC CCG GTC CCT TGG GCC CAG TGG CAG AGG AGT
 F   D   S   W   G   Q   G   T   R   V   T   V   S   S>
```

ING1 VL Sequence (SEQ ID NO:357 nucleic acid, SEQ ID NO:358, protein)
Sequence Range: 1 to 327

```
        5        10        15        20        25        30        35        40        45
      GAC ATC GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA
      CTG TAG CAC TAC TGG GTC AGA GGT AGG AGG GAC AGA CGT AGA CAT CCT
       D   I   V   M   T   Q   S   P   S   S   L   S   A   S   V   G>

      50        55        60        65        70        75        80        85        90        95
      GAC AGA GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT AGC AGC TAT
      CTG TCT CAG TGG TAG TGA ACG GCC CGT TCA GTC TCG TAA TCG TCG ATA
       D   R   V   T   I   T   C   R   A   S   Q   S   I   S   S   Y>

       100       105       110       115       120       125       130       135       140
      TTG AAT TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC
      AAC TTA ACC ATA GTC GTC TTT GGT CCC TTT CGG GGA TTC GAG GAC TAG
       L   N   W   Y   Q   Q   K   P   G   K   A   P   K   L   L   I>

   145       150       155       160       165       170       175       180       185       190
      TAT GCT GCA TCC AGT TTG CAA AGT GGG GTC CCA TCA AGG TTC AGC GGC
      ATA CGA CGT AGG TCA AAC GTT TCA CCC CAG GGT AGT TCC AAG TCG CCG
       Y   A   A   S   S   L   Q   S   G   V   P   S   R   F   S   G>

      195       200       205       210       215       220       225       230       235       240
      AGT GGA TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGT CTG CAA CCT
      TCA CCT AGA CCC TGT CTA AAG TGA GAG TGG TAG TCG TCA GAC GTT GGA
       S   G   S   G   T   D   F   T   L   T   I   S   S   L   Q   P>

         245       250       255       260       265       270       275       280       285
      GAA GAT TTT GCA ACT TAC TAC TGT CAA CAG AGC TAC AGT ACC CCT CGC
      CTT CTA AAA CGT TGA ATG ATG ACA GTT GTC TCG ATG TCA TGG GGA GCG
       E   D   F   A   T   Y   Y   C   Q   Q   S   Y   S   T   P   R>

   290       295       300       305       310       315       320       325
      ACC ACT TTC GGC GGA GGG ACC AAA GTG GAT ATC AAA CGT
      TGG TGA AAG CCG CCT CCC TGG TTT CAC CTA TAG TTT GCA
       T   T   F   G   G   G   T   K   V   D   I   K   R>
```

ING2 VH SEQUENCE (SEQ ID NO:359 nucleic acid, SEQ ID NO:360, protein)
Sequence Range: 1 to 357

```
        10        20        30        40        50
CAGGTGCAGCTGGTGCAGTCAGGGGCTGAGGTGAAGAAGCCGGGGTCCTC
GTCCACGTCGACCACGTCAGTCCCCGACTCCACTTCTTCGGCCCCAGGAG
 Q  V  Q  L  V  Q  S  G  A  E  V  K  K  P  G  S  S>

        60        70        80        90       100
GGTGAAGGTCTCCTGCAAGGCTTCTGGAGACACCTTCAACAGGAACGCTA
CCACTTCCAGAGGACGTTCCGAAGACCTCTGTGGAAGTTGTCCTTGCGAT
  V  K  V  S  C  K  A  S  G  D  T  F  N  R  N  A>

       110       120       130       140       150
TCGCCTGGGTGCGACAGGCCCCTGGACAGGGGCTTGAGTGGATGGGACGG
AGCGGACCCACGCTGTCCGGGGACCTGTCCCCGAACTCACCTACCCTGCC
I  A  W  V  R  Q  A  P  G  Q  G  L  E  W  M  G  R>

       160       170       180       190       200
ATCATCCCTAATCTTCGAACAACACACTACGCACAGAAGTTCCAGGGCAG
TAGTAGGGATTAGAAGCTTGTTGTGTGATGCGTGTCTTCAAGGTCCCGTC
 I  I  P  N  L  R  T  T  H  Y  A  Q  K  F  Q  G  R>

       210       220       230       240       250
AGTCGCGATAACCGCGGACAAACACACGAACACAGTCTTCATGGAGCTGA
TCAGCGCTATTGGCGCCTGTTTGTGTGCTTGTGTCAGAAGTACCTCGACT
  V  A  I  T  A  D  K  H  T  N  T  V  F  M  E  L>

       260       270       280       290       300
GCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACCCT
CGTCGGACTCTAGACTCCTGTGCCGGCACATAATGACACGCTCTCTGGGA
S  S  L  R  S  E  D  T  A  V  Y  Y  C  A  R  D  P>

       310       320       330       340       350
TATTACTACTCCTACATGGACGTCTGGGGCAAAGGGACCACGGTCACCGT
ATAATGATGAGGATGTACCTGCAGACCCCGTTTCCCTGGTGCCAGTGGCA
 Y  Y  Y  S  Y  M  D  V  W  G  K  G  T  T  V  T  V>

CTCCTCA
GAGGAGT
  S  S>
```

ING2 VL SEQUENCE (SEQ ID NO:361 nucleic acid, SEQ ID NO:362, protein)
Sequence Range: 1 to 342

```
        10        20        30        40        50
GAAATTGTGCTGACTCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGA
CTTTAACACGACTGAGTCAGAGGTCTGAGGGACCGACACAGAGACCCGCT
 E  I  V  L  T  Q  S  P  D  S  L  A  V  S  L  G  E>

        60        70        80        90       100
GAGGGCCACCATCAACTGCAAGTCCAGCCGGAGTGTTTTATACAGCTCCA
CTCCCGGTGGTAGTTGACGTTCAGGTCGGCCTCACAAAATATGTCGAGGT
  R  A  T  I  N  C  K  S  S  R  S  V  L  Y  S  S>

       110       120       130       140       150
ACAATAACAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCT
TGTTATTGTTGATGAATCGAACCATGGTCGTCTTTGGTCCTGTCGGAGGA
N  N  N  N  Y  L  A  W  Y  Q  Q  K  P  G  Q  P  P>

       160       170       180       190       200
AAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCG
TTCGACGAGTAAATGACCCGTAGATGGGCCCTTAGGCCCCAGGGACTGGC
```

```
  K   L   L   I   Y   W   A   S   T   R   E   S   G   V   P   D   R>

         210           220           230           240           250
ATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCC
TAAGTCACCGTCGCCCAGACCCTGTCTAAAGTGAGAGTGGTAGTCGTCGG
   F   S   G   S   G   S   G   T   D   F   T   L   T   I   S   S>

         260           270           280           290           300
TGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT
ACGTCCGACTTCTACACCGTCAAATAATGACAGTCGTTATAATATCATGA
L   Q   A   E   D   V   A   V   Y   Y   C   Q   Q   Y   Y   S   T>

         310           320           330           340
CCTTTCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGG
GGAAAGTGAAAGCCGCCTCCCTGGTTCCACCTCTAGTTTGCC
  P   F   T   F   G   G   G   T   K   V   E   I   K   R>
```

CR1-VH (SEQ ID NO:363 nucleic acid, SEQ ID NO:364, protein)

Sequence Range: 1 to 354

```
      5        10       15       20       25       30       35       40       45
CAG GTC CAG CTG CAG GAG TCT GGG GGA GGC TTA GTG CAG CCT GGA GGG
GTC CAG GTC GAC GTC CTC AGA CCC CCT CCG AAT CAC GTC GGA CCT CCC
 Q   V   Q   L   Q   E   S   G   G   G   L   V   Q   P   G   G>

50       55       60       65       70       75       80       85       90       95
TCC CTG CGC CTC TCC TGT GCA GCC TCT GGA TTC ACG TTC AAG TAC GAC
AGG GAC GCG GAG AGG ACA CGT CGG AGA CCT AAG TGC AAG TTC ATG CTG
 S   L   R   L   S   C   A   A   S   G   F   T   F   K   Y   D>

   100      105      110      115      120      125      130      135      140
TAC ATG TAT TGG GTT CGC CAG GCT CCG GGC AAG GGC CTG GAG TGG GTC
ATG TAC ATA ACC CAA GCG GTC CGA GGC CCG TTC CCG GAC CTC ACC CAG
 Y   M   Y   W   V   R   Q   A   P   G   K   G   L   E   W   V>

145      150      155      160      165      170      175      180      185      190
 GCA ACC ATT AGT GAT GGT GGT AGT TAC ACC TAC TAT TCA GAC AGT GTG
 CGT TGG TAA TCA CTA CCA CCA TCA ATG TGG ATG ATA AGT CTG TCA CAC
  A   T   I   S   D   G   G   S   Y   T   Y   Y   S   D   S   V>

195      200      205      210      215      220      225      230      235      240
GAG GGG CGA TTC ACC ACC TCC AGA GAC AAT TCC AAG AAC ACC CTG TAT
CTC CCC GCT AAG TGG TGG AGG TCT CTG TTA AGG TTC TTG TGG GAC ATA
 E   G   R   F   T   T   S   R   D   N   S   K   N   T   L   Y>

   245      250      255      260      265      270      275      280      285
CTG CAA ATG AAC AGT CTG CGC GCT GAG GAC ACA GCC ATA TAT TAC TGT
GAC GTT TAC TTG TCA GAC GCG CGA CTC CTG TGT CGG TAT ATA ATG ACA
 L   Q   M   N   S   L   R   A   E   D   T   A   I   Y   Y   C>

290      295      300      305      310      315      320      325      330      335
TCA AGG TAT AGG TAC GAC GAT GCT ATG GAC TAC TGG GGC CAA GGC ACC
AGT TCC ATA TCC ATG CTG CTA CGA TAC CTG ATG ACC CCG GTT CCG TGG
 S   R   Y   R   Y   D   D   A   M   D   Y   W   G   Q   G   T>

   340      345      350
CTG GTC ACC GTC TCC TCA
GAC CAG TGG CAG AGG AGT
 L   V   T   V   S   S>
```

CR1 VK

Sequence Range: 1 to 336 (SEQ ID NO:365 nucleic acid, SEQ ID NO:366, protein)

5 10 15 20 25 30 35 40 45
GAG ATC GTG CTC ACT CAG TCT CCA GCT ACC TTG TCC CTG TCT CCA GGG
CTC TAG CAC GAG TGA GTC AGA GGT CGA TGG AAC AGG GAC AGA GGT CCC
E I V L T Q S P A T L S L S P G>

50 55 60 65 70 75 80 85 90 95
GAG AGG GCC ACC ATA TCC TGC AGA GCC AGT GAA AGT GTT GAT AGT TAT
CTC TCC CGG TGG TAT AGG ACG TCT CGG TCA CTT TCA CAA CTA TCA ATA
E R A T I S C R A S E S V D S Y>

100 105 110 115 120 125 130 135 140
GGC CAT AGT TTT ATG CAG TGG TAC CAG CAG AAA CCA GGA CAG GCT CCC
CCG GTA TCA AAA TAC GTC ACC ATG GTC GTC TTT GGT CCT GTC CGA GGG
G H S F M Q W Y Q Q K P G Q A P>

145 150 155 160 165 170 175 180 185 190
CGC CTC CTC ATC TAT CGT GCA TCC AAC CTA GAA CCT GGG ATC CCT GCC
GCG GAG GAG TAG ATA GCA CGT AGG TTG GAT CTT GGA CCC TAG GGA CGG
R L L I Y R A S N L E P G I P A>

195 200 205 210 215 220 225 230 235 240
AGG TTT AGT GGC AGT GGG TCT GGG ACA GAC TTC ACC CTC ACC ATT TCC
TCC AAA TCA CCG TCA CCC AGA CCC TGT CTG AAG TGG GAG TGG TAA AGG
R F S G S G S G T D F T L T I S>

245 250 255 260 265 270 275 280 285
TCC CTG GAG CCA GAG GAT TTC GCA GTG TAT TAC TGT CAG CAA GGT AAT
AGG GAC CTC GGT CTC CTA AAG CGT CAC ATA ATG ACA GTC GTT CCA TTA
S L E P E D F A V Y Y C Q Q G N>

290 295 300 305 310 315 320 325 330 335
GAG GTT CCA TTC ACG TTC GGC CAG GGG ACC AAG GTG GAA ATA AAA CGT
CTC CAA GGT AAG TGC AAG CCG GTC CCC TGG TTC CAC CTT TAT TTT GCA
E V P F T F G Q G T K V E I K R>

CR2 VH

Sequence Range: 1 to 354 (SEQ ID NO:367 nucleic acid, SEQ ID NO:368, protein)

10 20 30 40 50 60
CAGGTCCAGC TGCAGCAGTC TGGGGGAGGC TTAGTGCAGC CCGGAGGGTC CCTGCGCCTC
Q V Q L Q Q S G G G L V Q P G G S L R L>

70 80 90 100 110 120
TCCTGTGCAG CCTCTGGATT CACGTTCAAG TACGACTACA TGTATTGGAT TCGCCAGGCT
S C A A S G F T F K Y D Y M Y W I R Q A>

130 140 150 160 170 180
CCGGGCAAGG GCCTGGAGTG GGTCGCAACC ATTAGTGATG GTGGTAGTTA CACCTACTAT
P G K G L E W V A T I S D G G S Y T Y Y>

190 200 210 220 230 240
TCAGACAGTG TGGAGGGGCG ATTCACCACC TCCAGAGACA ATTCCAAGAA CACCCTGTAT
S D S V E G R F T T S R D N S K N T L Y>

250 260 270 280 290 300
CTGCAAATGA ACAGTCTGCG CGCTGAGGAC ACAGCCATAT ATTACTGTTC AAGGTACAGG
L Q M N S L R A E D T A I Y Y C S R Y R>

310 320 330 340 350
TACGACGACG CTATGGACTA CTGGGGCCAA GGCACCCTGG TCACCGTCTC CTCA
Y D D A M D Y W G Q G T L V T V S S>

CR2 VL (SEQ ID NO:369 nucleic acid, SEQ ID NO:370, protein)

Sequence Range: 1 to 336

```
        10         20         30         40         50         60
GAGATCGTCC TCACTCAGTC TCCAGCTACC TTGTCCCTGT CTCCAGGGGA GAGGGCCACC
 E  I  V  L  T  Q  S   P  A  T  L  S  L  S  P  G  E   R  A  T>

        70         80         90        100        110        120
ATATCCTGCA GAGCCAGTGA AAGTGTTGAC AGTTATGGCC ATAGTTTTAT GCAGTGGTAC
 I  S  C   R  A  S  E   S  V  D   S  Y  G   H  S  F  M   Q  W  Y>

       130        140        150        160        170        180
CAGCAGAAAC CAGGACAGGC TCCCCGCCTC CTCATCTATC GTGCATCCAA CCTAGAACCT
 Q  Q  K   P  G  Q  A   P  R  L   L  I  Y   R  A  S  N   L  E  P>

       190        200        210        220        230        240
GGGATCCCTG CCAGGTTTAG TGGCAGTGGG TCTGGGACAG ACTTCACCCT CACCATTTCC
 G  I  P   A  R  F  S   G  S  G   S  G  T   D  F  T  L   T  I  S>

       250        260        270        280        290        300
TCCCTGGAGC CAGAGGATTT CGCAGTGTAT TACTGTCAGC AAGGTAATGA GGTTCCATTC
 S  L  E   P  E  D  F   A  V  Y   Y  C  Q   Q  G  N  E   V  P  F>

       310        320        330
ACGTTCGGCC AGGGGACCAA GGTGGAAATA AAACGG
 T  F  G   Q  G  T  K   V  E  I   K  R>
```

CR2 scFv (SEQ ID NO:371 nucleic acid, SEQ ID NO:372, protein)

Sequence Range: 1 to 735

```
        10         20         30         40         50         60
CAGGTCCAGC TGCAGCAGTC TGGGGGAGGC TTAGTGCAGC CCGGAGGGTC CCTGCGCCTC
 Q  V  Q   L  Q  Q  S   G  G  G   L  V  Q   P  G  G  S   L  R  L>

        70         80         90        100        110        120
TCCTGTGCAG CCTCTGGATT CACGTTCAAG TACGACTACA TGTATTGGAT TCGCCAGGCT
 S  C  A   A  S  G  F   T  F  K   Y  D  Y   M  Y  W  I   R  Q  A>

       130        140        150        160        170        180
CCGGGCAAGG GCCTGGAGTG GGTCGCAACC ATTAGTGATG GTGGTAGTTA CACCTACTAT
 P  G  K   G  L  E  W   V  A  T   I  S  D   G  G  S  Y   T  Y  Y>

       190        200        210        220        230        240
TCAGACAGTG TGGAGGGGCG ATTCACCACC TCCAGAGACA ATTCCAAGAA CACCCTGTAT
 S  D  S   V  E  G  R   F  T  T   S  R  D   N  S  K  N   T  L  Y>

       250        260        270        280        290        300
CTGCAAATGA ACAGTCTGCG CGCTGAGGAC ACAGCCATAT ATTACTGTTC AAGGTACAGG
 L  Q  M   N  S  L  R   A  E  D   T  A  I   Y  Y  C  S   R  Y  R>

       310        320        330        340        350        360
TACGACGACG CTATGGACTA CTGGGGCCAA GGCACCCTGG TCACCGTCTC CTCAGGTGGA
 Y  D  D   A  M  D  Y   W  G  Q   G  T  L   V  T  V  S   S  G  G>

       370        380        390        400        410        420
GGCGGTTCAG GCGGAGGTGG CTCTGTCGGT GGCGGGTCGG AGATCGTCCT CACTCAGTCT
 G  G  S   G  G  G  G   S  V  G   G  G  S   E  I  V  L   T  Q  S>

       430        440        450        460        470        480
CCAGCTACCT TGTCCCTGTC TCCAGGGGAG AGGGCCACCA TATCCTGCAG AGCCAGTGAA
 P  A  T   L  S  L  S   P  G  E   R  A  T   I  S  C  R   A  S  E>
```

```
       490        500        510        520        530        540
AGTGTTGACA GTTATGGCCA TAGTTTTATG CAGTGGTACC AGCAGAAACC AGGACAGGCT
 S  V  D   S  Y  G  H   S  F  M   Q  W  Y   Q  Q  K  P   G  Q  A>

       550        560        570        580        590        600
CCCCGCCTCC TCATCTATCG TGCATCCAAC CTAGAACCTG GGATCCCTGC CAGGTTTAGT
 P  R  L   L  I  Y  R   A  S  N   L  E  P   G  I  P  A   R  F  S>

       610        620        630        640        650        660
GGCAGTGGGT CTGGGACAGA CTTCACCCTC ACCATTTCCT CCCTGGAGCC AGAGGATTTC
 G  S  G   S  G  T  D   F  T  L   T  I  S   S  L  E  P   E  D  F>

       670        680        690        700        710        720
GCAGTGTATT ACTGTCAGCA AGGTAATGAG GTTCCATTCA CGTTCGGCCA GGGGACCAAG
 A  V  Y   Y  C  Q  Q   G  N  E   V  P  F   T  F  G  Q   G  T  K>

       730
GTGGAAATAA AACGG
 V  E  I   K  R>
```