

cDNA deduced amino-acid sequences of two novel Kappa-neurotoxins from *Bungarus multicinctus*

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A cDNA library has been prepared from mRNA extracted from the venom glands of one specimen of *Bungarus multicinctus*. The cDNA sequences encoding two precursors (designated CB1 and CR1) of novel Kappa-neurotoxins are presented below. Both open reading frames encode a signal peptide (underlined) of 21 residues followed by a 66 residues polypeptide. The amino acids sequences of CB1 and CR1 are highly conserved (15 differences). The signal peptide amino acid sequence of CB1 is identical to that of short-neurotoxins (1, 2) and neurotoxin-homolog (3) and presents only one difference with that of CR1. The core sequences of CR1 and CB1 differ from that reported for Kappa-bungarotoxin (4) by 5 and 12 amino acids respectively. Both polypeptides exhibit the characteristics of κ-neurotoxins according to Grant *et al* (5). 5′ and 3′ non coding DNA sequences are very similar to the corresponding regions of short neurotoxins (1, 2) and neurotoxin-homolog (3). However a gap of 27 bases (at asterisk position) has to be introduced in the 5′ untranslated regions to obtain optimal alignment with the corresponding sequences of short-neurotoxin and neurotoxin-homolog.

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CB1

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GCAAG    ATG AAA ACT CTG CTG CTG ACC TTG GTG GTG GTG ACA ATC
         M   K   T   L   L   L   T   L   V   V   V   T   I

GTG TGC CTG GAC TTA GGA TAT ACC AAG ACA TGC CTC AAA ACA CCT
V   C   L   D   L   G   Y   T   K   T   C   L   K   T   P

TCT TCT ACC CCT CAG ACA TGT CCA CAA GGG CAG GAC ATA TGC TTT
S   S   T   P   Q   T   C   P   Q   G   Q   D   I   C   F

CTA AAG GTT TCG TGT GAG CAA TTC TGT CCC ATC AGA GGA CCT GTA
L   K   V   S   C   E   Q   F   C   P   I   R   G   P   V

ATC GAA CAA GGA TGT GCT GCT ACC TGC CCT GAA TTT AGA TCC AAT
I   E   Q   G   C   A   A   T   C   P   E   F   R   S   N

GAT AGA TCT CTT CTC TGT TGC ACA ACA GAC AAT TGC AAT CAC TAG
D   R   S   L   L   C   C   T   T   D   N   C   N   H   end

CTCTACGAGTGGCTAAATTCCTTGAGTTTTGCTCTCATCCATCATGGAC*TTTACCGGCA
GATGGTCAATCAACCCCCTCTCCCCTGCTGTCTTTGACACCTCAACATCTTTCCCTTTTC
TCTTGTTCTGTAAGTTTCCTTCTGCTAGTTCTGTAATTTGAGAATCAAATAAACCTCAGC
ATTCAAAAAAAAAAAAAAAAAAAA
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CR1

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TCCAGAGAAGATTGCAAG   ATG AAA ACT CTG TTG CTG TCC TTG GTG GTG
                     M   K   T   L   L   L   S   L   V   V

GTG ACA ATC GTG TGC CTG GAC TTA GGA TAC ACC AGG ACA TGC CTC
V   T   I   V   C   L   D   L   G   Y   T   R   T   C   L

ATA TCA CCT TCT TCT ACC CCT CAG ACA TGT CCA AAT GGG CAG GAC
I   S   P   S   S   T   P   Q   T   C   P   N   G   Q   D

ATA TGC TTT CGA AAG GCT CAG TGT GAT AAC TTC TGT CAC AGC AGA
I   C   F   R   K   A   Q   C   D   N   F   C   H   S   R

GGA CCT GTA ATC GAA CAA GGA TGT GTT GCT ACC TGC CCT CAA TTT
G   P   V   I   E   Q   G   C   V   A   T   C   P   Q   F

AGA TCC AAT TAT AGA TCT CTT CTC TGT TGC AGA ACA GAC AAT TGC
R   S   N   Y   R   S   L   L   C   C   R   T   D   N   C

AAC CAC TAG  CTCTACGAGTGGCTAAATTCCTTGAGTTTTGCTCTCATCCATCATG
N   H   end

GAC*TTTACCGGCAGATGGTCAATCAACCCCCTCTCCCCTGCTGTCTTTGACACCTCAAT
ATCTTTCCCTTTTCTCTTGTTCTGTAAGTTTCC
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