**Supplementary Table S2.** Protein sequences ofthe putative conotoxin transcripts identified from *C. generalis*. 1

|  |
| --- |
| A superfamily: CC-C-C |
| 1 MGMRMMFTVFLLVVLAINVVSVTSYRASHGR-----KDAADLSALNDNNN**CC**NHPA**C**AGKNSDL**C**G  2 --------VFLLVALATTVVPFTSDRASASRNAATDNKASELKALNARIP**CC**SYPA**C**AQSNIDL**C**GGRR 2, 3 |
| B1 superfamily(conontokin): cysteine free |
| 3 MQLYTHLYLLVPLVTFHLILGTGTLAHGDALTERRSADATALKPEPVLLQKSAARSTDDNGKDRLTQMNRILKKRGDTARGLEEDLELRLLENSKKQENEK  C superfamily(Contulakin): cysteine free  4 ---------------------------------------------MLTKFETKSARVKGLSFHPKRPWVL |
| D superfamily: C-CC-C-CC-C-C-C-C  5 MPKLEMMLLVLLILPLPYCNAAGVTTVQWGGHGDGLDRYLQRGVRDVHRP**C**QSVRPGRVWGK**CC**LTRL**C**STM**CC**ARAD**C**T**C**VYHTWRGHG**C**S**C** 2, 3  I1 superfamily: C-C-CC-CC-C-C  6 MKPSMTLLLILMILPSMTGEKSRERRLSSAAVKGFLRPAR**C**TEFGKE**C**NLPPE**CC**GRM**CC**YNSL**C**MWSSKE**C**  I2 superfamily: C-C-CC-CC-C-C; C-C-C-C-CC-C-C  7 –MVGHTAV-RFLLLSILLLHMAAMVSCD**C**DYDYGKT**C**EGGEA**C**E**C**SNHI**CC**DVLSQAKKDQ**C**VRGHDV**C**YLLNQSSRRRRAIQMQKRSRGMLRGLA  8 ------------------LGMVATVICS**C**ESGVSGET**C**DLSVEKR**C**S**C**SRHI**CC**THHALEQHK**C**MTWAK**C**MSVSLGVNGRRSIQMQDRFLRMLRAFDD  9 -------VGCFLLVIVFLNLAGVQVVLGGA**C**RLEGMF**C**IHSPE**CC**LQD**CC**SGI**C**NSGA**C**GKRAQHQRLHLRRF  10 MMFRLTSVGCFLLVIVFLNLV---VLT-DA**C**TDEGEY**C**TDDLQ**CC**KLQ**CC**RAS**C**SDI**C**RFPGKRMHGHGLLRFFGQR  I3 superfamily: C-C-CC-CC-C-C  11 MKLFLVIVLNLMLLSLSTGAETSDNRASRSATALRDRLRRPKR**C**RNRFEE**C**WEDSE**CC**EEL**CC**DGPNY**C**KDSIGR**C**H  L superfamily: C-C-C-C  12 MKLSVMFIVFLMLTMPMTGDGNNRRAANGGEVGMPAYERAAKLLALLRE-RQ**C**PAP**C**YPN**C**EE**C**  13 MKLSVTFIVVLMLTTSLTCGFSLPSNKEERAFGPRDPDAADQLVREERASRA**C**NPP**C**TGLSM**C**QAGR**C**GYIRFR  14 MKLSVTFIVVLMLTTSLTCGFSPPSNNGERAFGSHDPDAADQLVREVRASSA**C**PEP**C**AKGST**C**IGKT**C** |
| M superfamily: CC-C-C-CC; C-C-CC  15 -MMKMGAMQFTFLVLFLLVALQVDADQPAERHAENKQDLNPVERKEIIVPALRQNTNSDEED**CC**IYPW**C**DGD**C**L**CC**  16 MMFKLGVLLTICLVLFPLTALPLDGEQPVDRHAEHMQDDNSAAQNPW-VIAIRQ--------**CC**TS--**C**NFG**C**QP**CC** |
| 17 -MSKLGVALLIFIVLFPLANLQLDGDQPADRHAEERRGLLHELYKLLRRSQTRVKEPEELRVE**C**PIYY**C**PDSV**CC**KK  18 –MSKLGVVLFTILVLLPLATLLLEADQPVER----QQDLNPQRGTRGIMKHVMSKGMSRRG-**CC**TGQG**C**WNVPI**C**E**CC**V 3 |
| O1 superfamily: C-C-CC-C-C |
| 19 MKLTCVLIIAVLFLTACQLITGE-----------QKDHALRSTDKNSKLTRQ**C**SPNGGY**C**TLHIH**CC**SNH**C**IKPIGR**C**VA |
| 20 MKLTCVMIVAVLFLTACQLTTAGDSRDKEG----YRAVRSIPSMQDGIDSRE**C**RRRGQG**C**TQSTP**CC**DGLR**C**DGQRQGGM**C**VDS 2, 3 |
| 21 MKLTCVLIVAVLFLTVCQLIPADYSRDKPGYPAWKLRTKMQN-SRRSKLARS**C**KERASS**C**ETPSE**CC**SGV**C**RTRIFYL**C** |
| 22 MKLTCALIVAMLLLTACQLITTDDFRGRQQYRTARARTKMQN-YKIFRLTKR**C**DAPNAP**C**EKFDND**CC**DA**C**MLREKQQPI**C**AV 2, 3  23 MKLTCVLIITVLFLTACQLTTAVTYSRGE-----HKHRALMSTGTNYRLPKT**C**RSSGRY**C**RSPYD**CC**RRY**C**RRITDA**C**V 3  24 MKLTCVLIVVVLFLTACQLIPADYSRDTPGYPAWKLKTKMQN-SRRWKLAKR**C**KGKGAG**C**DYSHE**CC**SRQ**C**TGRIFQT**C**N 2, 3  25 MKLTCMMIVAVLFLTAWTFVTADDTRYRLENPFLKARNELQKHEASQLNERG**C**LDPGYF**C**GTPFLGAY**CC**GGI**C**LIV**C**IET 2, 3  26 MKLTCVLIITVLFLTACQLTTAVTYSRGK-----QKHRALRSTDKTSWLTKP**C**SRLMEP**C**TQHPQ**CC**SNT**C**SKFTTK**C**IS  27 MKLTCMMIIAVLFLTVWTFVANDDPRNGRQNRFSKARHGMKNRGAHRLDQRV**C**IKDGEF**C**GTPVENDPL**CC**SLI**C**DLV**C**L  28 ------------------------SRDKEG----YRAVRSRLGVRHGMRFSE**C**STRG--**C**TFSSH**CC**EGLR**C**QGTPQGGV**C**V  29 ----------------------------------KLRTKMQN-SRRSKFART**C**RERGIG**C**DDPLE**CC**SHQ**C**TFTGFST**C**  30 ---------------------------------------MQN-SRRSKLARE**C**LPKGAG**C**DEPFE**CC**SHL**C**TGRLHTT**C** |
| O2 superfamily: C-C-CC-C-C; C-C-CC-C-C-C-C |
| 31 MEKLTALILVATVLLTTQVLVQSDGERPLKRRVKEYAAKRLSALMRGSRQ**C**LPQYHP**C**IIGNEE**CC**PHLE**C**K**C**LPKP |
| 32 MEKLTTLILVATVLTTIQVLVKSDRERPPKRTVEQYAAERLLALMRGSRQ**C**KPKGDI**C**EE-DEE**CC**PSLE**C**E**C**DSLPT**C**ITNKR**C** |
| 33 MEKLTILLLVAAVLLSTQVLVQCDGEKP-KKTKLRFLKARMSSREE---P**C**KERRQP**C**ER-NEE**CC**NDS-**C**NRFY**C**  34 –QKLTILLLVAAVLISTHILGQGDGEKR-MKTKMDFFKARKHWAYKQARD**C**KGWLEE**C**EEEN--**CC**DPYE**C**IGF**C** |
| O3 superfamily: C-C-CC-C-C  35 MSGLGIMVLTLLLLVSMATNHQDG-----------RVRRLMLRNRLRQMM**C**TTDED**C**PTGQE**CC**PDNINDPQGF**C**VDD**C**IV |
| 36 MSGLGIMVLTLLLLVFMETSHQDAGEKQATQRDAINVRRRRSLTRRVVTEA**C**EES**C**EDEEKT**CC**GLENGEPV**C**ARF**C**LG  37 ---------------------------------------LMLRNRLRQMM**C**SSNED**C**PAGQE**CC**PDNLGKPEGF**C**VDD**C**II  P superfamily: C-C-C-C-C-C  38 --------------LLFALGTFVGVQLEQITRDVDNGQPTDNRHNLQSVWKQMSLLRSVVKR**C**VGS**C**DLNNP**C**SSG**C**I**C**NGDK**C**  39 -------------------GNFVGVQPGQITRDMENGQLMDNRRDLRSPWKQMSLFRSFKLV**C**GKG**C**KSRPD**C**PTE**C**F**C**YMDM**C**  S superfamily: C-C-C-C-C-C-C-C-C-C  40 ----------KVGLPFVLLLLLTSTSPKQERDVQARKRSLNSDLYRSLARSTRG**C**GGT**C**YDSQH**C**DGT**C**Y**C**PAGD**C**Y**C**GTEGPHSG**C**T**C**I**C** |
| T superfamily: CC-CC |
| 41 MRCLPVFIILLLLVPSAVSVDVQPETKNFMTLVSRDFAKKSLKGLSNK-RD**CC**QRNFL**CC**  42 MRCLPVFIILLLLIASAPSVDAQPKTKYNAPLTSLHDNAKGILQEHWN-KR**CC**PRRLA**CC**IIGRK 2  43 -------IIVLLLVPSAHGIDAEAKTKSDESHASLHDKAKGILQRLSSSRG**CC**PNHSS**CC**  44 ----------LVLIASAPGVDARPQTK-DDALASFHDSAKRHLQRLVNARK**CC**PESPP**CC**HYFGRRK 2, 3  45 --------------------------------------RILEDIVSTALAT**CC**KFQFLNF**CC**NEK 3  Con-ikot-ikot: CC-C-C-C-CC-C-C-C  46 MATNMLMTLSVFVMVVMAATVVGSTPLPEPELSRSVRDSRT**CC**IDSTLQ**C**LRGYPGEEYTYATM**C**NLEASGP**C**GLSVYQG**CC**NGYMN**C**IR  INVGNLRLEGAHNA**C**KNRR**C**  conotoxin-like: CC-C-C  47 MRCLASLVVTLLLFTATATTGASNHVNAAASGKASDSISLAARDD**CC**PNPS**C**RQNHPER**C**  Divergent MSTLGMTLL-: C-C-C-CCC-C-C-C-C  48 MSTLGMLLLIALLLPLTNPADNGDGQAKPRSRNLRSLDFMRTHRRLDKRG**C**DPTDG**C**KKAL**C**NTDTGP**CCC**QHGHN**C**QTQPSGRRA**C**VRN**C**PH  N**C**P  Unknown superfamily: C-C-C-C-C-C  49 ----------------AVCVTLVGKKPTVDV**C**SLPADPGP**C**EALDRRFFFDKVDGT**C**KPFNYGG**C**QGNGNRFDSKSR**C**ERA**C**  50 -----------------------------DV**C**ALPKVTGP**C**FAAFPRFYFDQTAGR**C**KTFTYGG**C**HGNQNNFRSLRA**C**RNT**C**A  51 -----------------------------EV**C**SLPRERGP**C**SNYEIVWYYDTAEQR**C**TRFYYGG**C**QGNGNRFANREE**C**EER**C**VR  52 -----------------------------DL**C**YQPMKVGP**C**RSKVP**C**YYFDHEYGK**C**QLFYYGG**C**RGNDNRFETKDA**C**LHT**C**  53-------------------------------**C**QLEPDTGL**C**RAAFRRFYYNWNEQQ**C**QAFIYGG**C**GGNENRFKSREE**C**EQA**C**  54-------------------------------**C**NLPKETGP**C**RALDHSFFYDVNAGQ**C**KHFIYGG**C**GGNANRFKTMAE**C**KWS**C**A  55 ----------------------------DA**C**SLPLSTGK**C**EQQQTRWHYNYRSGS**C**EKFIYTG**C**LGNANNFPTADA**C**QAR**C**  56 -----------------------------I**C**QLEADVGP**C**SGTFPRWFYNSGMRK**C**QLFDYGG**C**RGNENRFDTEEE**C**MEL**C**  57 -------------------------DFVSI**C**EMPEDPGP**C**RGRLPRWFYDPLDRQ**C**RAFYWSG**C**QGNENNFLSVQE**C**QQT**C**M  58 -----------------------------V**C**SLAPETGN**C**RANIPRWYYDAQFGQ**C**RQFVYGG**C**RGNSNNFETEQD**C**LNY**C**RR  59 -------------------------DFVSI**C**EMPEDPGP**C**RGRLPRWFYDPLDRQ**C**RAFYWSG**C**QGNENNFLSVQE**C**QQT**C**M  60 -----------------------------L**C**RLPAVPGP**C**RSRQPRYFYNYKVGK**C**QRFNYGG**C**KGNTNRFLTLGE**C**QSR**C**  61 ----------------------------DI**C**RMPKVVGP**C**RAGITRYYYDSASAA**C**RQFIYGG**C**QGNLNNFGTLEA**C**QGK**C**ARH |

1Signal regions are shown in red, mature regions are shown in green, and cysteine residues are marked in bold black. The sequences isolated and identified previously are highlighted in grey shading. 2Mature peptides in the sequences were aligned with previously recorded conotoxins in ConoServer. 3Mature peptides in the sequences were aligned with previously recorded conotoxins in GenBank.