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The venom gland transcriptome of the Desert Massasauga Rattlesnake (*Sistrurus catenatus edwardsii*): towards an understanding of venom composition among advanced snakes (Superfamily Colubroidea)

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Abstract

Background: In the eukaryotic genome, the presence of protein-coding genes and pseudogenes is a common feature. The identification of novel genes is a challenging task due to the presence of introns and the complexity of the genome.

Results: The conserved cDNA library of the eukaryotic genome was sequenced. The results demonstrate the presence of several protein-coding genes and pseudogenes. The analysis of the cDNA library revealed the presence of three finger domains and no other possible genes. The results also showed the presence of several pseudogenes. The analysis of the cDNA library revealed the presence of several pseudogenes. The analysis of the cDNA library revealed the presence of several pseudogenes. The analysis of the cDNA library revealed the presence of several pseudogenes.

Conclusion: The three finger domains are characteristic of the eukaryotic genome. The results also showed the presence of several pseudogenes. The analysis of the cDNA library revealed the presence of several pseudogenes. The analysis of the cDNA library revealed the presence of several pseudogenes.

o ser ed .n h s nd o her s .d.es .nd.c es gre er co pos .on s . r. y of eno s
ho gh po ency . d.ffer ong d nced sn es h n h s een pre .o s y
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en eno .on y sn es .n he gen s *Atractaspis* c n .nc de socons r.c .on res .ng
.nc rd. c rres , Desp. e o er s . r. y .nc .nc sy p o s e h . ed fer

Homo sapiens ce s nd . s proposed o h e q . y con ro ro e . n rRNA
 degr d . on . h . s . s pre . n ry repor sho ng he poss . . y of
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Identification of toxin families

Serine proteinase: The serine proteases in the venom gland of *S. c. edwardsii*
 re expressed in the highest mRNA abundance of E . s . Figure and
 elongo c . sers , M . p e c ones ppe red . n c . sers h e ere s . ng e ons
 Add . on d f e , One represen . e E from e ch c . ser s co p e e y
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 serine protease from *Bothrops jararaca* venom gland ,

Mos sn e eno serine proteases Ps o d e re s . ng e po y pep . de ch . ns
 e cep for o f r . no y . c enzy es fro he eno of ore n . per *Agkistrodon*
blomhoffi brevicaudus re . n se A and s on se AF , n o h c ses
 f rds rdno prec . sors os . e y ce d o d , he p . , s e

.n.nogen nd p ee receptors , o e Pse h . ore h n one c . y, For
 e p e .n dd .on o he.r hro .n . e c . y o hro .n cro se nd LM▲L
 .nd, ce p ee ggreg .on .n.n re e se nd gyr ory c . .es respec . e y , e
 cons r, c ed ne.gh or o.n.ng N phy ogene .c ree . h ne y.den.f.ed P
 .sofor s fro *S. c. edwardsii*, o ss.gn p . e f,nc .ons nd o e .ne rends .n he
 e o .on of ne .sofor s F.g.re , ▲he phy ogene .c ree sho ed sc ered
 d.s r .on of r.o.s .sofor s . h d.fferen ph r co og.c c . .es fro se er
 spec.es of p .pers, ▲h.s p ern.nd.c es h Ps d.erged f er sn e .ne ges
 spec. ed, M ny Ps re co on y considered s hro .n . e enzy es ▲LEs
 ec se hey . .c he f .r.nogeno y.c f,nc .on of hro .n pro o.ng ood
 co g .on, ▲herefore .n os c ses on y f .r.nogeno y.c f,nc .on of Ps .s es ed
 nd he P.s c egor.zed s ▲LE, o e er so e hro .n . e enzy es .n
 dd .on o re e s.ng f .r.no pep .de A nd or B fro f .r.nogen so c . e pro e.n C
 co p e en C nd p e e s , ▲herefore . o d e.n eres.ng o
 de er .ne he spec.f.c ph r co og.c proper.es of r.o.s P.s ofor s . h.n e ch
 gro,p nd p hese on he.r e o .on ry re onsh.ps,

P genes e ong o . gene f . y nd he pro e.n cod.ng reg.ons h e een
 sho n o e e per.enc.ng cce er ed e o .on . h.n he eno g nds of p .pers
 , ch cce er ed e o .on co d e d o he ch nges .n s,r f ce oops s,rro nd.ng
 he s,r s r e .nd.ng s.e res .ng .n he r .on of s,r s r e recogn .on nd hence he
 f,nc .on of he pro e.n, ▲he r .o e een nonsynony o.s nd synony o.s s,r s .on
 d_N/d_S of he pro e.n cod.ng seq,nces of ser.ne pro e.n se .sofor s of h.s spec.es s
 fo,nd o e , .nd.c .ng rend o rd cce er ed e o .on nd herefore
 d.ergence .n ph r co og.c f,nc .on d,r.ng eno .on,

Metalloproteinase and Disintegrin: A total of 10 EGF-like domains are found in the signal sequence of pro-peptides. Figure 1. Addition of the EGF-like domain. One representative EGF-like domain is sequenced. DQ1, the only metalloproteinase MP precursors are classified into four groups according to size and domain composition. P1 metalloproteinase domain only. P2 metalloproteinase domain and P3 metalloproteinase domain and P4 metalloproteinase domain and P5 metalloproteinase domain and P6 metalloproteinase domain and P7 metalloproteinase domain and P8 metalloproteinase domain and P9 metalloproteinase domain and P10 metalloproteinase domain. None of the EGF-like domains encode P-type MPs.

The P1 domain from *S. c. edwardsii* DQ1 has been identified as the

mono- and dimeric receptors are arranged in a dimeric structure. The receptors are synthesized primarily from the genes of *S. miliaris barbouri* and *S. c. tergeminus* respectively.

The dimeric receptor binding of dimeric receptors R₁D₁s found on the surface of the epithelial cell, the function of the dimeric receptors is to bind to R₁M₁D₁ and MLD₁M₁D₁ or R₁ on the surface of the cell confers specificity of the receptors e.g., receptor of R₁h₁ in R₁D₁ of dimeric receptors. The specificity increases the sensitivity for α β for the dimeric receptor. The binding of α β ₁ for the dimeric receptor or α β ₃ for the dimeric receptor. Additionally the receptors are encoded by the R₁D₁ gene so the specificity and affinity for dimeric receptors. For example dimeric receptors in R₁D₁ and R₁DNP have the specificity higher affinity for α β and α β respectively. The R₁DNP containing dimeric receptors are found in the epithelial cells containing dimeric receptors. The binding of the dimeric receptors is mediated by α β . The primary structure of dimeric receptors from *S. c. edwardsii* has R₁DNP compared to R₁D₁ and R₁D₁ in the dimeric receptors and receptors respectively. Therefore further studies of the physiological reference of the dimeric receptor specificity of dimeric receptors from the same genes are necessary for the

The presence of MP receptors are determined by the epithelial cells.

edwardsii eno hough sn e eno PLA .s one of he os r p.d y e o .ng enzy e
 f . .es, n os spec.es se er .sofor s of PLA re o ser ed .n cDNA . r r.es nd
 eno s nd hese h e cq .red d. erse phys. o og.c f .nc .ons , h.s
 o ser .on .s so s.ppor ed y pro eo .c n .ys.s of *S. c. edwardsii* eno h. e
 eno s fro .nd .d .s of o her spec.es of *Sistrurus* con .n .p e PLA .sofor s

Phosphodiesterase eq .nce of p r . s.ng e on E r nscr.p .nd nce ,
 Add .on d f. e F.g .re DQ sho s .den . y o he C er .n
 reg.on of he phosphod.es er se gene fro ch. p nzee XP , h.s.s he f.r.s
 cDNA seq .nce for phosphod.es er se fro sn e eno , Phosphod.es er se c . . y h s
 een o ser ed .n eno s of E p.d e .per.d e nd Co .rd e sn es .
 ho e er he ro e of h.s enzy e .n eno .on .s no ye ce r, eno
 phosphod.es er ses hydro yze , phosphod.es er nd pyrophosph e onds .n n.c eo .des
 nd n.c e.c .ds nd re e se , d.phosph es , onophosph es nd p.r.nes , Free
 p.r.nes re so presen .n sn e eno s nd hey y con r .e o en eno .on
 seq .e e for de .s see

L-amino acid oxidase:

C-type lectin: The primary CLP cDNA for ppro... e y , and hence the one c...er DQ and os.ng e ons DQ and DQ. Addition d f e F.g.re , On BLA...P se rch hey ch...h he β s...n. of sh.g.n Q Y...den.y C B P...den.y and he A ch.n of F c or X F c or X nd.ng pro.e.n X X p...A...den.y respec.e y, M sh.g.n C B nd X X p re he erod. er.c. ho e er .n o...r...ry e.d.d no f.nd ny ch o E...s encod.ng he correspond.ng co p e en ry s...n. s, therefore...y e.n eres.ng o e...ne he CLP re ed pro.e.n.s.n h.s eno nd de er .ne he.r .o og.c proper.es,

Growth factors: The o...ned one c...er r nscr.p...nd nce encod.ng sc...r endo he...gro h f c or E F Addition d f e F.g.re , eq...ng of cones fro h.s c...er sho ed here re o.sofor s DQ and DQ...h on y o...no c.d res.d.e n.c eo.d e d fferences pos. ons Q CA E A nd AA E A...e so seq...ed s.ng e on DQ encod.ng ner e gro h f c or N F, Ano her s.ng e on DQ ched...h he C er...ns of connec. e...s gro h f c or re ed pro.e.n C...F, h.s.s he f rs repor of C...F re ed pro.e.n.n eno cDNA...r ry, s or.g.n.n he eno g nd .ns e d of o her s...rro.nd.ng...s es needs o e er.f.ed,

Cysteine-rich secretory protein: The o...ned one c...er r nscr.p...nd nce Addition d f e F.g.re for CR P DQ...h.ch ches...h C r.n AAO...den.y fro *C. atrox* eno , CR Ps re .de y d.s.r...ed .n s rep.es ph...ns r hropods ne odes cone sn .s nd p ns nd hey e h...d. erse .o og.c f...nc.ons , they re s.ng e ch.n M of -...D

d.s.f.de r.dge.s.n oop Figure , A.sofor sh e he po en. N.g ycosy .on
o.f N X. Figure ,

Es were though o e found on y.n e p.d hydroph.d eno s though he or.g.n of
recre.en o he e p.d hydroph.d eno pro eo e.s no ce r , A po y pep.de
o.n D h.ch crossre cs . h α ng ro o.n nd .nds . h h.gh ff.n. y o
n.co.n.c ce y cho .ne recep or d of M.n co pe .on . h α ng ro o.n
s.so ed fro he eno of *A. halys* p. .per , o e er no sequence
nfor .on of h.s pro e.n.s . e, Recen y hree c ones DY DY
nd DY were o .ned fro cDNA . r ry of *L. muta* eno g nd h.ch
po en. y encode po y pep .des s. r d. E fo d pro e.ns , o e er on y one
c one DY h s he s r nd s op codons co p e e ORF . he o her o do no ,
hese sequences do no h e ny ho oogy e. her he n.c eo .de or pro e.n e e s o
hose o .ned fro *S. c. edwardsii* h.s s dy ,

Phy o gene .c n y.s.s of Es from hree f .es of sn es E p.d e Co r.d e nd
.per.d e s ch.e ed.s ng PA P , ,rees o .ned.s ng Ne gh or
o.n.ng oo s r pp.ng or P rs. ony An y.s s r.c consens.s ree.s no sho n ere
so e h d.fferen or opo og c fe res ere re .ned Figure , One
r nscr.p fro *S. c. edwardsii* DQ does no c.s er . h he o her fo r f s
. h.n sep r e c de con .n.ng *Naja* nd *Bungarus* o he p.ds Es, Fo r o her
r nscr.p s of *S. c. edwardsii* for onophy e.c c de . h.n n e c.s. eye p.d
c de, neres .ng y o h e hods p ce *L. muta* .per.d c ones DY nd
DY nd *Coelognathus radiatus* co r.d. Es s s o o her Es

sugges .ng co on or.g.n fo o ed yd. ers.f.c .on of E s ong d nced

pro e.n.s.r.ch.n Cys res.d.es s. . r o ny o her sn e eno o ns, s N er .n
 do .n ches . h n. z BP o ns .den. y nd he .dd e do .n
 ches . h pr.ns .den. y nd he no e r nscr.p h s n e ended C
 er .ns F.g.re ,Bo h n. z BP nd pr.ns re fo.nd sep r e y
 s s.ng e do .n pro e.n.s.n sn e eno s, o of he Cys res.d.es h.ch for one of
 he fo.r d.s.f.de onds.n pr.ns re .s.ng.n he ne r nscr.p F.g.re , R
 PCR .s.ng fresh RNA o her h n.sed o e cDNA . r ry s e p e nd
 seq. enc.ng e per. en s sho he presence of h.s f.sed r nscr.p .n he eno g nd
 nd hence .s no n r.f.c d.e o e p e s . ch.ng y he Re rse.r nscr.p se .sed
 for .ng he cDNA . r ry , A ho gh n er of cDNA seq. ences of
 n. z BP fro sn e eno s h e een co p e ed none of he h e he pr.n
 do .n nd he C er .n e ens.on, C.rren y cDNA seq. ences of pr.ns re no
 no n, o e er h.s.s he f.r.s e per. en e .dence for he presence of pr.n
 do .n ho gh f.sed . h no her o .n .n .per.d eno ,

he onger ORF h .ng n. z BP nd pr.n do .ns oge her co.d e d.e o he
 f.s.on of o.nd .d genes encod.ng n. z BP nd pr.n, ene f.s.on ed. ed
 y e on sh.ff.ng .n ron ed. ed reco .n .on or re ro r nspos .on h s een
 es .shed s n essen. gene.c ech.n.s for he or.g.n of ne genes .n
 .n ere r es ere r es nd p ns , Recen y ne gene.c process
 r nscr.p.on nd.ced ch. er.s C .n c ses of nde y oc ed gene p.r.s h s een
 sho n o e respons. e for gene f.s.on .n he h n geno e prod.c.ng ch. er.c

no e o n h o d s n c d o n s n d h n g n e o o g c f n c o n h s
 een o ser ed h n e genes of en g e r s e o n e o o g c f n c o n s d r e n y
 d p e D r n n s e c o n , h e e c h n s o f f n s o n o f h e s e p p r e n y
 n d e n d e n g e n s h e e o n r y r e c o r y o f h s f n s e d g e n e n d h e p o e n e n e
 o c f n c o n o f h e c h e r c p r o e n r e r e s f o r f n r e n e s g o n ,

Iron-binding protein For E s Add on d f e F g r e d E

CE YPO r n s c r p n d n c e , s h o e d h o o o g y h n r o n n d n g
 p r o e n h p o e n s g n p e p d e , A h o g h o s r o n n d n g p r o e n s r e
 g e n e r y c e g o r z e d s s o r g e p r o e n s o e o f h e s c h s o o r n s f e r r n n d
 c o f e r r n h e n c r o c e s , s n o c e r h e h e r o n o h s
 p r o e n s f o n d n h e e n o , o e e r o p r n e e r o f h e p r n p r o e n
 f y n d h e C e r n r e g o n o f y o o c P L A e r e o h s h o n o h e
 n c r o c e y ,

Identification of cellular transcripts

e o n e d c s e r s r n s c r p n d n c e s e q u e n c e s h c h r e n o e d
 n r o s c e r f n c o n s n c d n g r n s c r p o n n d r n s o n s e c r e o n p o s
 r n s o n o d f c o n g e n e r e o s n d o h e r f n c o n s A d d o n d f e
 F g r e , r h o s e e e p n g p r o e n p r o d c s h e e e n o s e r e d n o h e r s n e
 e n o g n d s , O n e o f h e E s C E c h e s c c n d
 n e g r n n d n g p r o e n h c h s s s p e e s p r e d n g , A h o g h o d o n o f
 p e e n d n e g r n f n c o n s s e y c e y o f s e e r s n e e n o c o p o n e n s e
 d o n o e e e h h s p r o e n s p r e s e n n e n o s c s h e s g n p e p d e ,

recruitment ensues and increases in the specific of non-indigenous
factors decreasing the composition specific factors long-term effects, other
differences in composition of specific components of the other expressed protein of
effects does not distinguish differences in composition between species,

A central theme in the evolution of the systems is competition of
genes followed by accelerated evolution which forms nonsynonymous
substitution orders of nucleotide sequence. Modification of selected surface
of proteins is responsible for producing the functional diversity in
species and subgroups. Other species in the gene families, other one
portion of series in the present reports the occurrence of non-enzymatic
nucleic acid generated by fusion of non-coding genes in zBP and protein
in the endogenous, although the mechanism for creation of hybrid gene needs to be
studied further. It carries out other genetic processes gene shuffling or
recombination in the endogenous to create non-coding genes, genes originating
other genetic processes such as gene shuffling recombination and therefore the addition
of hybrid non-coding protein of the endogenous proteins perhaps not. A hybrid gene
is a product of specific hybridization of order organization of differences of
MPs which appears to be the result of gene fusion and deletion of genetic
process other than gene duplication. MPs are very abundant and carry out
protein production in endogenous system and therefore studies of their genetic
organization and organization of genes of green algae. Current evidence of
speculation for the generation of serine proteinase for the endogenous of *V. lebetina*
has been presented. It opens up the show that the evolution of gene
duplication recombination corrected evolution by mechanisms. According to P

ne o .ns nd pro .des ech n.s.c e p n .ons for he.r e o .on nd d.ers.f.c .on,
 An nreso ed q.es .on.n o es he re .onsh.p e een he eno g nd r nscr.p o e
 nd ho h.s.s . e y r ns ed o he f.n pro eo e, h.s r. e pro eo .c
 co .pos. .on.n rn de er .nes he co p e nd of en d.ff.c .o reso e seq.e e h.ch
 frequen y de e op fo o .ng en eno .on y he dfferen spec.es of eno o.s sn es,

Methods

Venom extraction and collection of venom glands

pec. ens of *Sistrurus c. edwardsii* Deser. M ss s .g ere co ec ed .n L.nc o n
 Co n y Co or do A .nder per .s gr n ed y he Co or do D .s.on of . d.fe o
 PM per .s P ., eno s e r c ed fro d .sn es .s.ng s nd rd
 n .e hods . eno s ere hen cen r.f.ged o re o e p r.c .es frozen nd
 yoph .zed, Pr.or o g nd re o sn es ere e r c ed of eno , Fo rd y s er
 hen RNA e e s re pres .ed . o sn es ere nes he .zed . h
 .sof .or ne nd hen s cr.f.ced y dec p .on, nds ere hen r p d y d.ssec ed fro

.nco p e e cDNAs ere re o ed y p ss.ng he . r ry hrogh C ROMA P N
 co n, he . r ry s p c ged s.ng .g p c go d p c g nge r c r gene
 Ced r Cree e s A, nd .d c ones ere resc ed fro r ndo y se ec ed
 h. e p q es nd gro n.n L.r. ro h, p.c. n ed, P s ds ere p.r.f.ed
 s.ng he Q Aprep sp.n .n prep . Q. gen .den er ny, P.r.f.ed p s ds ere
 sequenced y cyc e sequenc.ng re c.ons s.ng he B.gDye er n or, . App.ed
 B.osys e Fos er C. y C .forn. A nd n o ed DNA sequencer Mode
 A App.ed B.osys e Fos er C. y C .forn. A,

RT-PCR

R PCR s perfor ed n order o se rch for sofor s of E sequences n he eno
 g nd, n r.ef o RNA s.so ed fro eno g nds s o e nd s sed s
 e p e, he fo o ng pr. ers ere sed for p.f.c on for rd pr. er, A A
 AAAC C C N ACC N, N A C .re erse pr. er, AAAA
 ACCA CC AAA C, Re erse r nscr.p.on nd s sequen p.f.c on
 re c.ons ere done s.ng he one sep R PCR pro oco of Q. gen .den er ny,
 he p.f.ed prod c s coned n o pDr. e ec or Q. gen .den er ny nd
 r ndo c ones ere sequenced, R PCR s so perfor ed o conf.r he presence of
 f sed o n r nscr.p.n he eno s.ng s e proced re h he fo o ng pr. ers
 for rd pr. er, A C C A C C C, .re erse pr. er, CCA
 ACA AA AA C C A,

Bioinformatic analysis

C s er.ng of he E s s perfor ed s.ng he CAP progr f er re o ng
 poor q . y sequences nd ec or sequences s.ng ec creen fro NCB, e oo ed
 for f A B recogn .on sequences n he E s nd n y re o ed ps re nd

do not re-sequences of these sequences. As a result, the sequences from the ends, and the other part of the protein. In the other part, there are several criteria for the construction. As a result, the sequences of BLA, BLA-N, and BLA-X are required. The non-redundant database of NCB is used, and the good coverage of the sequences is pursued. In addition, the presence of signal peptides is predicted. The analysis of the sequences of the protein is done in the Epsys, and the protein is done using the programs C and DNAMAN. Lynn Corporation, Doron, Quec, and the other non-synonymous d_N and synonymous d_S are calculated using the NAP program. The program NAP has been developed based on the method of the incorporation of the sequence analysis developed by

Phylogenetic analysis

Phylogenetic analysis is carried out using the program MEGA. The protein positions corrected distances and trees are constructed using the program PA-P, which is used for bootstrap neighborhood and parsimony analyses. For the Bayesian inferences of phylogeny, the posterior probability distribution of the trees is obtained using the MrBayes program. The analysis is run for 100 generations for each tree and sampled every 100 generations. The log-likelihood score of each tree is reported. The number of generations of the tree is chosen such that the log-likelihood scores of the analysis reached the stationary state.

pos er or pro ... es for he c des ere es shed y cons r,c ng consens s ree of
rees gener ed fer he co p e on of he r n n ph se,

... e nc ded he fo o ng seq ences fro hree f es of sn es n o r n yses he
ne y den f ed E sequences o of h s s dy fro S. c. edwardsii per. d e
enB n DQ DQ DQ DQ nd DQ L. muta
per. d e enB n DY DY α co r. o n ss Pro P
fro Coelognathus radiatus Co r. d e nd non con en on E sequences
ss Pro P O nd P E e sequences ss Pro Q
P P P P P P P P
Q nd Z nd F sequences ss Pro P P P
Q Y C P Q Y P P P nd P fro
E p. d e, A hese seq ences e ong o he shor ch n E f y, A BLA P se rch
s ng enB n DY fro L. muta eno fo nd h r pep. de seq ence
enB n AA sho ed he h ghes ho o gy o Ly n gen h ch h s een

List of abbreviations

E₃ expressed sequence tag, ORF open reading frame, PLA phospholipase A₂, E₃ three finger domain, CRP cysine rich secretory protein, CLP C type lectins, BPP rdy domain containing peptidase, CNP C type natriuretic peptidase, LAO Lipoic acid oxidase, BP₁ bone pincer cryptosporin, E₃ F₁ secretory endohelical growth factors, N₁ F₁ nerve growth factor, P₁ snail endoserine proteinase, LE₁ hromolipase enzymes, CRD cysine rich domain, N₁ neophorin, C₁ rnscription induced chemokines,

Authors' contributions

Ph designed and coordinated the experiments and developed the concept and wrote the manuscript, PM has coordinated the endogenous peptide, RM and PM have edited the manuscript, prosequy, PM has participated in phylogenetic analysis of E₃ sequences, All the authors have approved the final form of the manuscript,

Acknowledgments

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FIGURE LEGENDS

Figure 1

The rnsr.p o e prof. e of the eno g nd of *S. c. edwardsii*. A nd nce of o ns
nd o n . e r nscr.p c sers nd ce r pro e.ns nd hypo he.c sequences
c sers, Percen ge of o E s for e ch c egory re sho n,

Figure 2

Phy o gene.c N tree of Ps, eq uences co p e e ORF e fro o her p.
.pers nd .sofor s DQ DQ fro h.s s dy f. ed c.rc e ere
sed, s s e . re.n P .s sed s o, gro p, the n ers on he r nches
nd.c e he oo s r p s ppor es for nodes nd he hor. zon r represen s n er
of s s . ons per s. e, LE hro .n . e enzy es. N .n.nogen se, PA
p s .nogen c. or, PA p e e ggreg .on nd cer, BCD ood c o d.s pers.on, X
c. . y n no n, E per. en y er.f.ed c. . es re sh ded,

Figure 3

Phy o gene.c N tree for c ss P e o pro e.n ses of .per.d eno s, D se
co p e e ORF sed fro .n dd .on o one .sofor DQ o .ned.n h.s
s dy f. ed c.rc e, ADAM fro *Danio rerio* Q PE nd ADAM fro *Mus
musculus* ere sed s o, gro p, A gn en of he d.s.n egr.n do .n of c ss P
MPs sho ng C C C nd C r ed.n grey h.ch re proposed o e
.n o ed.n he for .on of o h ono er.c M nd d. er.c D d.s.n egr.n s.n he
eno , On y re e n por .ons of he sequences re sho n,

Figure 4

A gn en of .no c.d sequences of the p . e prec rsors of E s, Cys res.d es
h.ch re sh ded.n grey re co on y presen .n shor ch .n E nd for d.s.f.de

ranges so.d c .nes , Cys res.d es sh ded .n c poss. y for he dd .on
d.s.f.de r.dge do ed c .ne presen .n he non con en .on E f .y,
Po en . N g ycosy .on s. es re nder .ned,

Figure 5

Ne.gh or o.n.ng c dogr of E sequences, N ers preced.ng e ch spec.es n e
refer o en n ccess.on n ers nd n ers efore os nodes.nd.c e oo s r p
es rep.c es ,

Figure 6

A.gn en of he no e o .n . e r nscr.p . h sn e eno n.z BP pro e.ns nd
pr.ns, ABD *Daboia russellii russellii*). Q e .n.n *Pseudonaja textilis*
textilis .P C.c.d.n *Dendroaspis angusticeps* .P Dendro o .n
Dendroaspis polylepis polylepis nd BP fro Bo .ne, P O pr.n *Oxyuranus*
microlepidotus). P N pr.n *Naja nigricollis*), he presence of conser ed
d.s.f.de onds re.nd.c ed y so.d c .nes, he d.s.f.de ond h.ch.s .ss.ng.n
he no e o .n conser ed.n pr.ns.s.nd.c ed y do ed .nes, he e ended C
er .ns of he no e o .n.s nder .ned,

Table 1. Distribution of ESTs sequenced from *S. c. edwardsii* genomic DNA and non-coding regions. The number of ESTs, number of clusters, redundancy, and representation over total clones and matching clones are shown.

Transcripts category	Number of ESTs	Number of clusters	Redundancy (clones/cluster)	Representation over total clones (%)	Representation over matching clones (%)
Toxin	360	76	4.74	69.40	77
Cellular	107	106	1.04	20.65	23
Mitochondrial	9	9	1.00	1.73	-
Hypothetical	42	42	1.00	8.10	-

The results presented here are preliminary and should be confirmed by sequencing the genomic DNA of single clones.

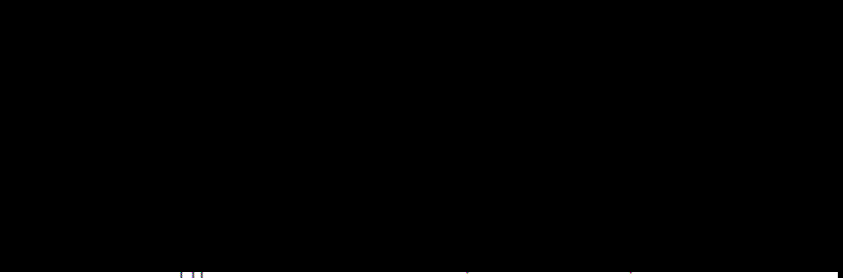
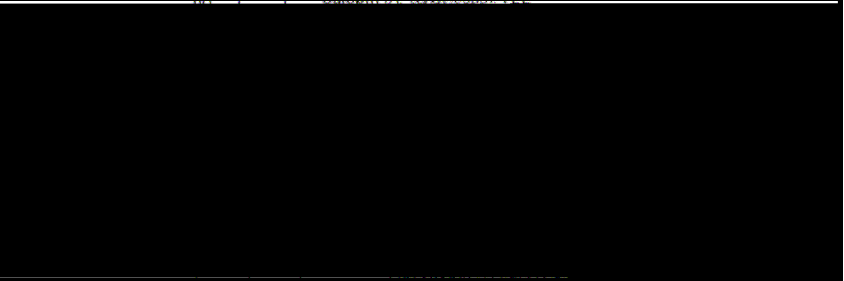
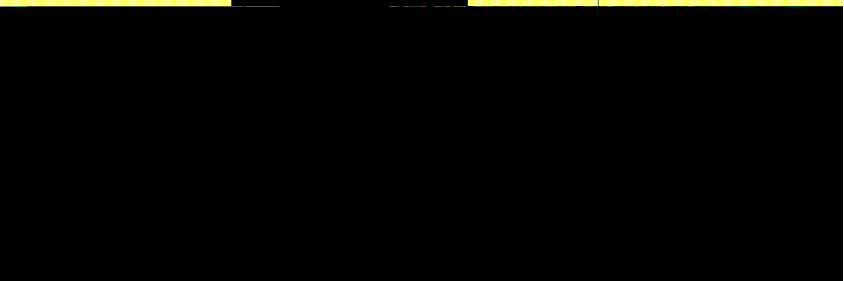
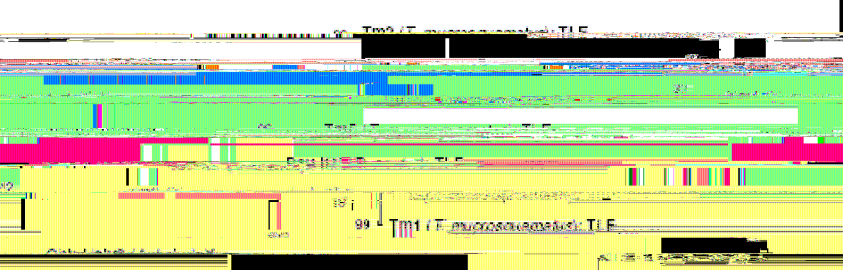
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Additional data file 6

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pos er.or c de pro . . y, E sequences fro *S. c. edwardsii* nd *L. muta* . r r.es
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Figure 1



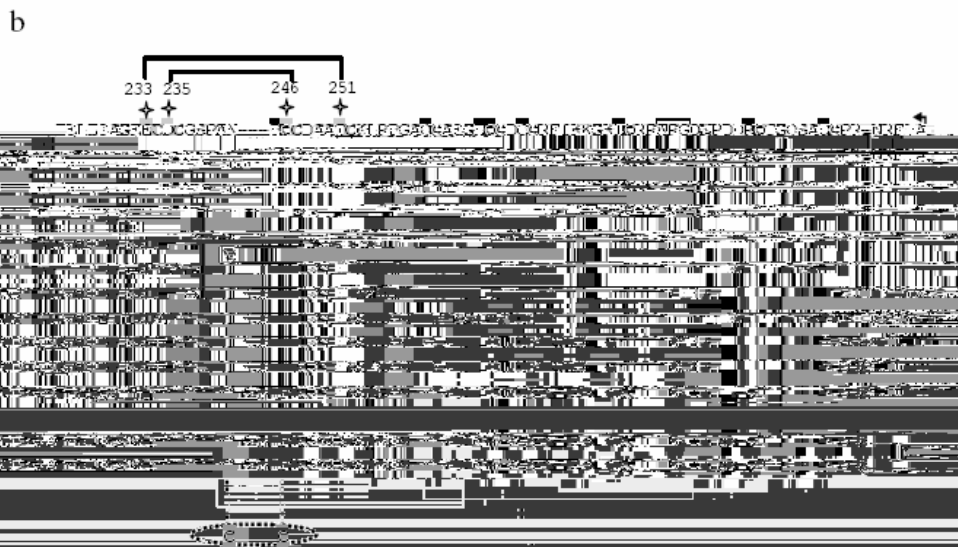
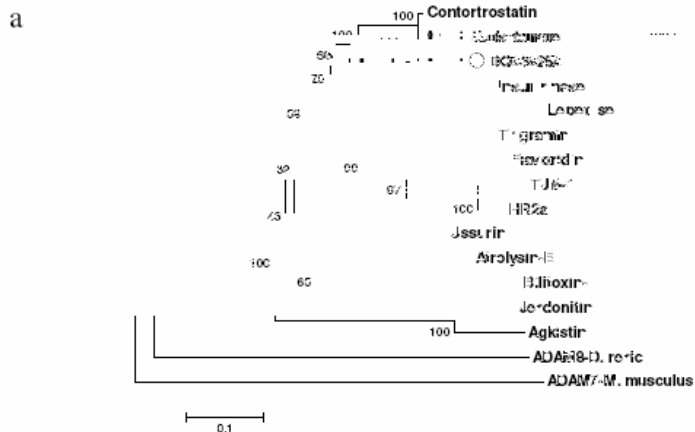


Figure 3



Figure 4

Figure 6

Additional files provided with this submission:

Additional file 1: additional data file 1.pdf, 23K
