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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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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
recogn. zed,

Background

The dined snes superfamily Co-rode cons.s of monophyletic group of four families Arc.sp.d.d.e Co.r.d.e” E.p.d.e nd .per.d.e , these snes have evolved to become important for their high efficiency of hunting prey, Phylogenetic studies show that the endogenous proteins reproduced evolved once the use of the Co-rode on years ago and has undergone extensive evolutionary divergence of diverse systems and compositions of endo , Phylogenetic reconstructions on the endogenous genes and snes showed that the recruitment of non-families into the endogenous occurred repeatedly (e.g., serine proteases CRP, zinc type serine protease inhibitors NF and independent e.g., PLA2, receptor peptides recruitment enzymes , Approaches of families of proteins have been categorized into endogenous and serine proteases proper to specific properties of endogenous families. Additionally, for proteins found on the endogenous of Arc.sp.d.d.e, serine proteases related to food collection factors X-correlation factors and A-protein family peptides proper to the E.p.d.e and serine endogenous groups factor E.F.d.s.n.e.g.r.n.s.g.e.r.n.s.d.p.e.p.d.y.p.e.p.d.s.e and cross-reaction of the endogenous of the .per.d.e. Additionally, the occurrence related to the endogenous phylogenetic composition of proteins of these non-families endogenous endogenous on the reciprocal, Endogenous endogenous as characterized by the presence of large numbers of post-synaptic proteins have endogenous peptides composed of the orthogonous endogenous effectors by the actions of neurotransmitters serine proteases serine proteases and C-type lectins CLP , Effects of

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 po se h . ed fer

Populations of *S. catenatus* generally were thinned or decimated by predation of hares and hence encroached and hereafter endangered species has been recorded. In systems of cyclical and McCleskey showed that long Colorado Arizona and New Mexico populations of *S. c. edwardsii* are the major prey food of hares and canyons, in the present or the end of the seen collected from the Oregon and the Colorado population.

Energy pools of endonucleon resulting from the North American populations are present in the effects of progress. The endonucleon and necrosis of the cooperation hypothesis of the origin and progression of the protein and the hysteresis open systems effects, however there is no specific report of the endonucleon concerning endonucleon by *S. c. edwardsii*. Profiling of the expression of the thinned species of the genome for the expression of genes of the nucleon coding noncoding sequences and here on the results of the study of the present endonucleon processes of the endonucleon chain for the effective connection and the endonucleon genes of the endonucleon.

Results and discussion

A total of 10 of the EAs produced red sequences, the sizes of sequences showed distribution between the separation of the separation and no show. A total of 10 of the sequences for the production of the sequences.

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
 po y deny on of r. oso RNA. n rep. n sys e , On c oser e. n on e
 fo nd p. e po y deny on s. gn AA AAA Add. on d f. e
 seq. ence s. ses ps re of he po y A . ,

Identification of toxin families

Serine proteinase: The ser. ne pro e. n ses. n he eno g nd. r ry of *S. c. edwardsii*
 re e pressed . h he h. ghes r nscr. p nd nce of E s. F. g. re nd
 e ong o c. s. ers, M. p e c ones ppe red. n c. s. ers h. e ere s. ng e ons
 Add. on d f. e , One represen. e E from e ch c. s. er s co p e e y
 seq. enced DQ DQ DQ , One of he c. s. ers DQ
 con. ns on ; R E s , h. s c. s. er sho s s. r. y . h he , R of
 ser. ne pro e. n se fro *Bothrops jararaca* eno g nd . ,

Mos sn e eno ser. ne pro e. n ses 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 nd s on se AF , n o h c ses
 f rds. rdno prec. rsor. s os . e y ce e d o d , he p . , s e

.n.nogen nd p e e 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 e e 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 108 genes and
 signaling proteins for the synthesis of proteases and integrins. Figure 1. Addition
 of the following, One representative E from each cluster sequenced DQ
 DQ, none of the metalloproteinase MP precursors reclassified into four
 groups according to size and domain composition. P metalloproteinase domain only,
 P metalloproteinase domain and disintegrin domain, P metalloproteinase domain and
 cysteine rich domain, and P P type domain and other domain only
 identified. None of the clusters encode P type MPs,
 The P from *S. c. edwardsii* DQ clusters identify the

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

The dimeric receptor binding of dimeric receptors R₁D₁ is found on the surface of the cell membrane, and the binding of dimeric receptors R₁D₁ to the membrane is mediated by the membrane protein MLD. The binding of R₁D₁ to the membrane confers specificity of binding to receptors, e.g., receptor of R₁D₁ of dimeric receptors. The binding of dimeric receptors to the membrane increases the specificity for α β of dimeric receptors. The binding of α β ₁ of dimeric receptors or α β ₃ of dimeric receptors. Additionally, the residues of the dimeric receptors are conserved in the dimeric receptors. For example, dimeric receptors R₁D₁ and R₁D₁P have the same high specificity for α β and α β respectively. The R₁D₁P contains dimeric receptors that are found in the dimeric receptors. The binding of dimeric receptors to the membrane is mediated by α β . The primary structure of dimeric receptors from *S. c. edwardsii* has R₁D₁P compared to R₁D₁ and R₁D₁ in the dimeric receptors. Therefore, further studies of the physiological reference of dimeric receptors and specificity of dimeric receptors from R₁D₁ is necessary.

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 y.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...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 and nce encod.ng sc...r endo he . gro h f c or E F Addition d f e F.g.re , eq...ng of c ones fro h.s c...er sho ed here re o.s for 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 and 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.gycosy .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 ne 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

suggesting coordination for the development of the system and need

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 ,

The longer 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 er e r es er e r es nd p n s , 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 .rs 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 l 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 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 o 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 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 ,

recre... en e en s... y e d o n ncre se n he spec r... of no n nd... n o n
f... es decre s ng he co pos... on spec.f.c... es ong eno o... s sn es, o e er
d fferen... con r... on of spec.f.c o ns o he o er e pressed pro eo e of eno o... s
sn es does e d o s gn.f.c n d fferences n eno co pos... on e een spec.es,

A cen r... he e n he e o... on of eno syste s s co p e e d p.c on of o n
genes fo o ed y cce er ed e o... on h.ch f ors nonsynony o... s no c.d
s... s... on o rds neof... nc.on .z on, Mod.f.c on of se ec ed s... rf ce re s of
o ns... s respons... e for prod... c ng he f... nc.on d ers. y n n... n er e r es
sn s nd scorp ons, er e r es sn es o n... gene f... es... , o e er one
... por n o ser... on n he presen repor s he occ... rrence of no e o n... e
r nscr.p gener ed y f... s.on of o nd... d... o n genes... n z BP... nd pr.n n
sn e eno g nd, h... h... h... h... s for cre on of h.s f... sed gene needs o e
s... d.ed f... r her... c e r y nd.c es h... o her gene.c processes gene sh... ff ng or... C
re so oper... ng n he eno g nd o cre e no e o n genes, enes or.g n ng y
o her gene.c processes s... ch s e on sh... ff ng re recen... nd herefore he dd... on
of h.s f... sed o n... e r nscr.p o he eno pro eo e s perh ps ne , A h.s s ge...
s e p ng o spec... e h... he or.g n of od... r org n.z on of d fferen c sses of
MPs h.ch ppe rs o e he res... of gene f... s.on e en s... y e d... e o gene.c
process o her h n gene d... p.c on, MPs re ery... nd n o ns nd c rry o...
pr.nc.p ro e n en eno... on y... per.d sn es nd herefore s... d.es of he r gene.c
or.g n nd org n.z on... e of gre... n eres, C... r... s n... e... dence of r ns
sp.c ng for he gener... on of ser.ne pro e n se sofor s n he eno g nd of *V. lebetina*
h s een presen ed... ope... n e , h... e sho n h... ern... e sp.c ng nd
gene d... p.c on re n erse y corre ed e o... on ry ech n.s s, Accord ng o P rr

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 c oned 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 of the sequence, the coding sequence, the coding regions were selected. BLAST searches, BLASTN and BLASTX were required. The non-redundant database of NCBI was used and high quality of the protein sequences and the identity for the protein. The definition of the genes, Presence of signal peptides predicted. The analysis of the sequences of the protein. The presence in the Eukaryotic, and prokaryotic genes were done using the programs Clustal and DNAMAN. Lynn Corporation, Doron Quecena and the other non-synonymous d_N and synonymous d_S sites were calculated using the NAP program. The program NAP has been developed based on the method of the incorporation of the sites in the developed by

Phylogenetic analysis

Phylogenetic analysis was carried out using the program MEGA. The amino acid positions corrected distances and trees were constructed using the bootstrap method, PA-P, and the software used for Bootstrap Neighborhood and Parsimony analyses. For the Bayesian inferences of phylogeny based upon the posterior probability distribution of the trees MrBayes and MrBayes were used. The analysis was run for 100 generations for chains and sampled every 100 generations resulting in 1000 samples. The log-likelihood score of each sampled tree was recorded. The number of generations of the tree which the log-likelihood scores of the analysis reached the stationary state

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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

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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.spers.on, X
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Figure 3

Phy ogene.c N tree for c ss P e o pro e.n ses of .per.d eno s, D se
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musculus* ere sed s o gro p, A gn en of he d.s.n egr.n do .n of c ss P
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Figure 5

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Figure 6

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Additional data files

Additional data file 1

▲type PDF size 1.5 MB, this file shows the distribution of snRNA gene expression profiles among different yeast species.

Additional data file 2

▲type PDF size 1.5 MB, this file shows the clusters of Eukaryotic genes in the chromosome and their phylogenetic relationship.

Additional data file 3

▲type PDF size 1.5 MB, this file shows the clusters of Eukaryotic genes encoding cell proteins.

Additional data file 4

▲type PDF size 1.5 MB, this file shows the alignment of RNA sequence DQ from the study and AF used for the identification of *S. cerevisiae*, *P. pastoris* and other species.

Additional data file 5

▲type PDF size 1.5 MB, this file shows the alignment of protein sequences on the protein domain shown, Cysteine residues which are conserved in the protein domain and their accession numbers of the aligned sequences are as follows: AP012345 enB n BAB012345 enB n BAB012345 ys se enB n LA P A enB n LA P B enB n O12345 h. g. n .ss Pro P Bery hr c. se .ss Pro Q Ec r. n .ss Pro Q r rh g. n .ss Pro P12345 Bo hrop s. n .ss Pro O12345 Ac rh g. n .ss Pro Q Q C roco s .n .ss Pro Q A ro ys. n .ss Pro Q Q12345 e n. h. g. n A .ss Pro Q12345 N e n. h. g. n B .ss Pro Q12345 N R A

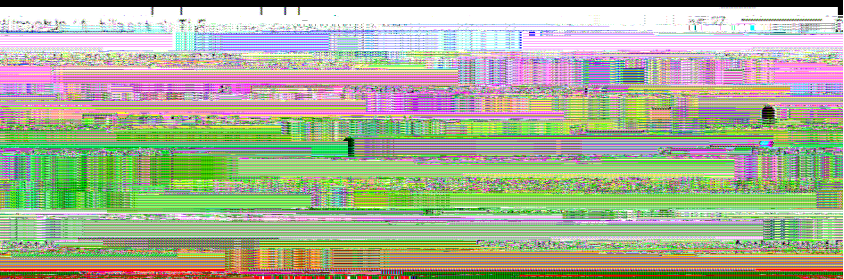
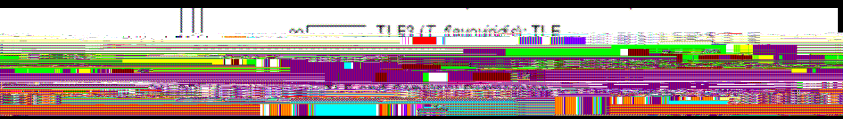
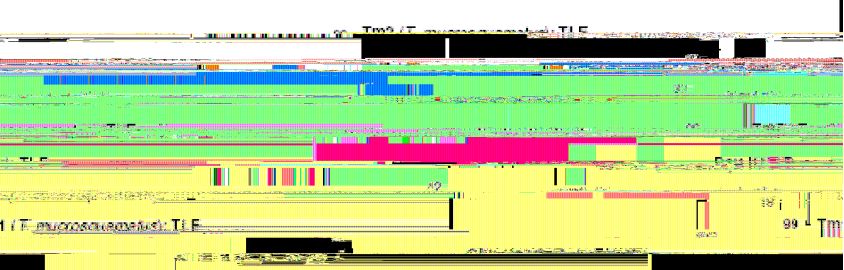
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Additional data file 6

▲ype PDF s.ze , B ,B yes. n ree gener ed fro .gned E sequences s
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Figure 1



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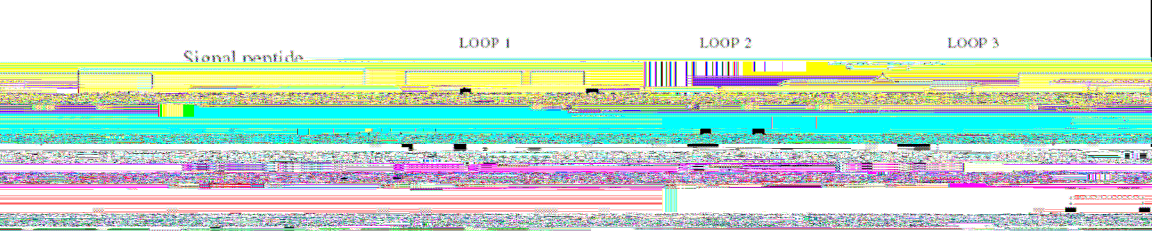


Figure 4

Figure 6

Additional files provided with this submission:

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