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## Molecular characterization and evolutionary analysis of carnivore zona pellucida

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| Complete List of Authors: | Moros Nicolás, Carla; Universidad de Murcia, Cell Biology and Histology. <br> Faculty of Medicine. <br> Leza, Andrea; Universidad de Murcia, Cell Biology and Histology. Faculty of <br> Medicine. <br> Chevret, Pascale; Université Claude Bernard Lyon 1 <br> Guillén Martinez, Ascensión; Universidad de Murcia - Campus de Espinardo, <br> Cell Biology and Histology <br> González Brusi, Leopoldo; Universidad de Murcia, Cell Biology and <br> Histology. Faculty of Medicine. <br> Boué, Franck; ANSES - French Agency for Food, Environmental and <br> Occupational Health \& Safety, Nancy Laboratory for Rabies and Wildlife <br> López Béjar, Manel; Universitat Autonoma de Barcelona, Department of <br> Animal Health and Anatomy <br> Ballesta, José; Universidad de Murcia, Cell Biology and Histology <br> Avilez-Sanchez, Manuel ; Universidad de Murcia, Cell Biology and <br> Histology <br> Izquierdo-Rico, María José ; Cell Biology and Histology |
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## Molecular characterization and evolutionary analysis of carnivore zona pellucida

Moros-Nicolás $\mathbf{C}^{\mathbf{1}^{*}}$, Leza $\mathbf{A}^{1}$, Chevret $\mathbf{P}^{\mathbf{2}}$, Guillén $\mathbf{A}^{\mathbf{1}}$, González-Brusi $\mathbf{L}^{1}$, Boué $\mathbf{F}^{\mathbf{3}}$, LópezBejar $\mathbf{M}^{4}$, Ballesta $\mathbf{J}^{\mathbf{1}}$, Avilés $\mathbf{M}^{\mathbf{1}}$, Izquierdo-Rico $\mathbf{M J} \mathbf{I}^{\mathbf{*}}$.

${ }^{1}$ Department of Cell Biology and Histology, Faculty of Medicine, Biomedical Research Institute of Murcia (IMIB-Arrixaca-UMU), University of Murcia. 30100, Murcia, Spain. ${ }^{2}$ Laboratoire de Biométrie et Biologie Evolutive, UMR5558, CNRS, Université de Lyon, Université Claude Bernard Lyon 1, Villeurbanne, France. ${ }^{3}$ Laboratory for Rabies and Wildlife. French Agency for Food, Environmental and Occupational Health and Safety (ANSES), Nancy, France. ${ }^{4}$ Department of Animal Health and Anatomy, Universitat Autònoma de Barcelona, Barcelona, Spain.
*Corresponding authors: Carla Moros Nicolás (carla.moros@um.es) and María José Izquierdo Rico (mjoseir@um.es).

## ABSTRACT

The zona pellucida (ZP) is an extracellular envelope that surround mammalian oocytes. This coat participates in the interaction between gametes, induction of the acrosome reaction, block to polyspermy and protection of the oviductal embryo. Previous studies suggested that carnivore ZP was formed by three glycoproteins (ZP2, ZP3 and ZP4), being ZP1 a pseudogene. However, a recent study showed the expression of four proteins in the cat.

In this study, in silico and molecular analyses were performed in several carnivores to clarify the ZP composition in this order of mammals. The in silico analysis demonstrated the presence of the $Z P 1$ gene in five carnivores: cheetah, panda, polar bear, tiger and walrus, whilst in the Antarctic fur seal and the Weddell seal there are evidences of pseudogenization. The molecular analysis showed the presence of four ZP transcripts in
ferret ovaries $(Z P 1, Z P 2, Z P 3$ and $Z P 4)$ and three in fox ovaries $(Z P 2, Z P 3$ and $Z P 4)$. The analysis of fox ZP1 gene showed the presence of a stop codon.

The results of this study strongly suggest that four ZP genes are expressed in most carnivores, whilst $Z P 1$ pseudogenization has affected independently three families (Canidae, Otariidae and Phocidae) of the carnivore tree.

## INTRODUCTION

The zona pellucida ( ZP ) is a translucent, glycoproteic and acellular matrix that surrounds mammalian oocytes. Other vertebrates have a similar structure, which is called the vitelline envelope in amphibians, chorion in fishes and the perivitelline envelope in birds (Wassarman, 1988; Tian et al. 1997; Hyllner et al. 2001; Sasanami et al. 2002; Monné and Jovine, 2011). The ZP functions are related with important events in oocyte formation and different steps during fertilization; being involved in folliculogenesis, the organization and differentiation of granulosa cells, recognition and binding to spermatozoa, the induction of the acrosome reaction (AR), the block to polyspermy and the protection of the oocyte and the oviductal embryo (Modliński 1970 ; Bleil and Wassarman 1980b; Florman and Storey 1982; Berger et al. 1989; Liu et al. 1996; Rankin et al. 1996, 1999, 2001; Benoff 1997; Fazeli et al. 1997; Dean 2004; Gupta and Bhandari 2011; Gupta et al. 2012; Tanihara et al. 2013; Cao et al. 2016).

Recently, the genome availability in some species and the development of different techniques; such as mass spectrometry, have allowed to study in depth the ZP
composition in different species. The number of the analyzed species is growing fast; however, the information in carnivores is still scarce.

According to its ZP composition, placental mammals can be classified into three different categories. 1) species with a ZP formed by three proteins ZP1, ZP2 and ZP3, where $Z P 4$ is a pseudogene (to date, only the house mouse) (Bleil and Wassarman 1980a; Lefièvre et al. 2004; Evsikov et al. 2006; Goudet et al. 2008); 2) species showing three proteins, where $Z P 1$ is a pseudogene (pig, cow, dog, common marmoset, dolphin and tarsier) (Hedrick and Wardrip 1987; Noguchi et al. 1994; Goudet et al. 2008; Stetson et al. 2012) and 3) species with four proteins (ZP1, ZP2, ZP3 and ZP4), for instance, cat, hamster, human, rabbit, and rat (Hughes and Barratt, 1999; Lefièvre et al. 2004; Hoodbhoy et al. 2005; Izquierdo-Rico et al. 2009; Jiménez-Movilla et al. 2009; Stetson et al. 2012, 2015).

Carnivores are classified in two suborders (Caniformia and Feliformia); the divergence between these two suborders is dated around 60-65 Ma (Nyakatura and Bininda-Emonds, 2012; Zhang et al. 2013). Caniformia comprises 9 families: Canidae (foxes, wolves, dogs), Odobenidae (walrus), Otariidae (sea wolves), Phocidae (seals), Mephitidae (polecats), Procyonidae (racoons, coatis), Mustelidae (weasels, otters), Ailuridae (red panda) and Ursidae (bears), whereas Feliformia comprises 6 families: Hyaenidae (hyenas), Eupleridae (fossa, mongooses), Herpestidae (mongooses), Viverridae (genets, civets, binturong) Prionodontidae (linsangs) and Felidae (cats) whilst the family Nandiniidae (African palm civet) is a sister of the feliformians (Agnarsson et al. 2010; Nyakatura and Bininda-Emonds, 2012).

Focusing on the ZP composition in carnivores, previous studies have reported a ZP1 pseudogenization in the dog with three stop codons at positions 151 (exon 3), 279 (exon 5) and 421 (exon 8) (Goudet et al. 2008). This finding lead some authors to believe that $Z P 1$ was a pseudogene in other carnivores, such as the cat. In fact, the presence of ZP1 had never been reported in a carnivore until 2015 when our research group described this protein in the cat zona pellucida by molecular and proteomic analyses (Stetson et al. 2015).

In GenBank database there are sequences submitted from five species: the cat (Felis catus): where sequences from the 4 glycoproteins have been submitted; the dog (Canis lupus familiaris): with completed sequences from ZP2 and ZP3 and a partial sequence of ZP4; the ferret (Mustela putorius furo): with only ZP3 submitted; the fox (Vulpes vulpes): with ZP2 and ZP3 sequences available and the stoat (Mustela erminea): with a partial sequence of ZP2 and complete sequences of ZP3 and ZP4 (see Table 1).

Thus, taking into account the bibliography available until now, two different ZP models are possible in carnivores: 1) carnivores with 4 proteins in their ZP: ZP1, ZP2, ZP3 and ZP4, such us the cat (Stetson et al. 2015); and 2) carnivores with 3 proteins in their ZP: ZP2, ZP3 and ZP4, being ZP1 a pseudogen, like the dog (Goudet et al. 2008). For that reason, the aim of this study was to decipher the ZP composition in other carnivore families. In silico analyses were performed in the species were the genome is available (Antartic fur seal, cheetah, ferret, panda, polar bear, tiger, walrus and Weddell seal) and a gene expression analysis using RT-PCR was performed from ferret and fox ovaries; this allowed us to covered 8 different families of the carnivore tree (see Fig. 1).

## MATERIALS AND METHODS

## In silico analyses

## Phylogenetic analysis of $\boldsymbol{Z P 1}$

ZP1 sequences from seven species: cheetah (Acinonyx jubatus), ferret (Mustela putorius furo), panda (Ailuropoda melanoleuca), polar bear (Ursus maritimus), tiger (Panthera tigris altaica), walrus (Odobenus rosmarus divergens) and Weddell seal (Leptonychotes weddellii) were retrieved from GenBank and/or Ensembl databases (Table 2). All these predictions were checked manually to detect annotation errors especially close to splicing sites. Similarity searches were performed using BLAST and BLAT against the assembled genome of dog (Canis lupus familiaris) in ENSEMBL (http://ensembl.org) and against the draft genome assembly of Antarctic fur seal (Arctocephalus gazella) recently published by Humble et al. 2016 downloaded from Dryad (doi:10.5061/dryad. 8 kn 8 c ). The sequence obtained was aligned to the other carnivoran sequences with Muscle implemented in Seaview (Gouy et al. 2010) and verified visually to predict exons missing from the ENSEMBL predictions. Only the exonic portions were kept for the phylogenetic analysis. It was also checked that the new sequence corresponded to a syntenic region of the corresponding chromosome. We added to the alignment our partial sequences of fox (Vulpes vulpes) and sequences of 2 species each of Perissodactyla (Ceratotherium simum simum and Equus caballus) and Chiroptera (Pteropus alecto and Miniopterus natalensis) that were used as outgroups. The appropriate model of evolution (GTR+G) was determined using Akaike information criterion (AIC) and jModeltest software (Posada and Crandall, 1998). Phylogenetic trees were reconstructed using maximum likelihood with PhymL
(Guindon et al. 2010) and the robustness of the nodes was estimated with bootstrap support ( $\mathrm{n}=1000$ ).

## Bioinformatic analysis

Sequences were analyzed to determine the degree of similarity with other known sequences using "BLAST program" (Basic Local Alignment Search Tool) (http://www.ncbi.nlm.nih.gov/blast/). Direct comparison between two sequences was made with "ALIGN program", and the multiple sequence alignment were carried out using "Clustal Omega" (http://www.ebi.ac.uk/Tools/msa/clustalo/).

The amino acid sequences were analyzed to predict the signal peptide and different domains with the following software packages: "signalP" (www.cbs.dtu.dk/services/SignalP/) and "smart genome" (www.smart.emblheidelberg.de). The programs "NetOGlyc" (www.cbs.dtu.dk/services/NetOGlyc) and "NetNglyc" (www.cbs.dtu.dk/services/NetNGlyc) were used to predict potential Olinked and N -linked glycosylation sites, respectively. The theoretical protein molecular weight and mature protein molecular weight were calculated with "PeptideMass" from "ExPASy" (http://web.expasy.org/peptide_mass/).

## Molecular analyses

## Ovaries collection

Ferret ovaries were obtained from two females subjected to ovariectomy in "Veterinary Clinic Huellas" (Murcia, Spain); dog ovaries from two females were donated from "Veterinary Clinic La Alcayna" (Murcia, Spain) and ovaries from three females were donated by the Laboratory for Rabies and Wildlife (Nancy, France). The
ovaries were immediately immersed in RNAlater (Sigma-Aldrich, USA) and kept at $80^{\circ} \mathrm{C}$ until use.

## DNA isolation

Total DNA was extracted from ovaries of two foxes and two bitches using a QIAamp DNA Mini Kit (Qiagen, Germany) following manufacturer's recommendations.

## Purification of ovarian RNA, cDNA synthesis and polymerase chain reaction amplification

Total RNA was isolated from ovaries of two ferrets, two foxes and two bitches using RNAqueous® kit (Ambion, USA) according to the manufacturer's instructions. The first-strand cDNA was synthesized with the SuperScript First-Strand Synthesis System kit for RT-PCR (Invitrogen-Life Technologies, USA), according to the supplier's protocol.

Ferret and fox ZP genes ( $Z P 1, Z P 2, Z P 3$ and $Z P 4$ ) and $\operatorname{dog} Z P 1$ gene were amplified using polymerase chain reaction (PCR) by means of specific primers. Ferret primers were designed according to the cDNA sequences obtained from GenBank and Ensembl databases with the following accession numbers: ENSMPUT000000014555 for ZP1, XM_004780136 for ZP2, NM_001310185 for ZP3 and XM_004774783 for ZP4; AF038150 for $\beta$-actin was used as positive control.
$Z P 2$ and $Z P 3$ fox primers were designed from the sequences of this species, which are available at the GenBank database with accession numbers AY598031 and

AY598032 respectively. To amplify $Z P 1$ and $Z P 4$, primers were designed according to the predicted cDNA sequences of the dog, its closest relative in the GenBank database with accession numbers XM_014120952 for ZP1 and XM_536329 for ZP4. To amplify $\operatorname{dog} Z P 1$, primers were designed according to the predicted sequence XM_014120952.

PCR amplifications were performed using $2 \mu \mathrm{l}$ of target cDNA, $0.5 \mu \mathrm{~g}$ of each primer, $200 \mu \mathrm{M}$ of each dNTP, and 1 IU of Taq DNA Polymerase (Fermentas, USA). PCR was carried out using an initial denaturation cycle of 3 min at $95^{\circ} \mathrm{C}$, and then 30 cycles of 1 min at $95^{\circ} \mathrm{C}, 1 \mathrm{~min}$ at annealing temperature (depending on the primers) and then 1 min at $72^{\circ} \mathrm{C}$. The final extension time was 10 min at $72^{\circ} \mathrm{C}$. PCR products were analyzed by electrophoresis on $1.5 \%$ agarose gels; four microliters of the PCR reaction mixture were mixed with loading buffer (Fermentas, USA) and separated for 60 min at 90 V . The gel was immersed in ethidium bromide (Sigma-Aldrich, USA) and visualized under UV light.

When multiple bands were obtained, amplicons of the expected size were carefully excised from the agarose gels and purified with the QIAquick Gel Extraction Kit Protocol (Quiagen, Germany) according to the manufacturer's protocol. When only one band was obtained, it was directly purified with the DNA Clean \& ConcentratorTM-5 (Zymo, USA) according to the kit instructions. After that, the amplicons were automatically sequenced using 3500 Genetic Analyzer (Applied Biosystem, USA).

## Amplification of the exon 8 of ZP1 in fox and dog

Considering that three stop codons were described in exons 3,5 and 8 of dog ZP1 inducing the pseudogenization (Goudet et al. 2008); exon 8 was amplified in the fox. Furthermore, as a control of our results the same experiment was conducted in the dog. Primers and the conditions for the PCR amplification were identical to that used in the fox cDNA (as explained in the previous section).

Amplifications by PCR were performed using 100 ng of target DNA, $0.5 \mu \mathrm{~g}$ of each primer, $200 \mu \mathrm{M}$ of each dNTP, and 1 IU of Taq DNA Polymerase (Fermentas, USA). PCR amplifications, sample purification and sequencing were carried out as explained above.

## RESULTS

## In silico analysis

Taking into account that $Z P 1$ is a pseudogen in the $\operatorname{dog}$ (Goudet et al. 2008) this event could have affected other species of carnivores. To explore this possibility an in silico analysis was made using the $Z P 1$ sequences from Antartic fur seal, cheetah, tiger, ferret, panda, polar bear, walrus and Weddell Seal corresponding to 6 different families (Otariidae, Felidae, Mustelidae, Ursidae, Odobenidae and Phocidae) which are available in GenBank, Ensembl or Dryad databases. The ORF of ZP1 from six of these species, have an initial ATG and a terminal stop codon, not showing evidences of pseudogenization. The alignment among the species shows a high degree of similarity, presenting the typical architecture of the ZP proteins, with a signal peptide, a trefoil domain (present in ZP1 and ZP4 proteins), the ZP domain, a furin cleavage-site (Arg-Gln-Arg-Arg) conserved in all the species and the transmembrane domain (Fig. 2). In
the different species analyzed there are two putative N-glycosylation sites; Asn75, which is conserved in the seven species aligned, and Asn362, conserved in all of them, with the exception of the polar bear. The comparative analysis of this sequence revealed high similarity with ZP1 from other species. The amino acid sequence of ferret ZP1 is $79 \%$ identical to walrus ZP1, $78 \%$ to tiger, $76 \%$ to cheetah, cat and panda and $75 \%$ to polar bear.

On the other hand, the genome analysis made in the Antarctic fur seal and the Weddell seal showed evidences of pseudogenization. In the Antarctic fur seal, there are two indels present in exon 3 and exon 4 that lead to the presence of stop codons. In the Weddell seal, the initial ATG is replaced by ACG, furthermore, it revealed the presence of different indels: two deletions in exon 3 , one deletion in exon 8 and one deletion in exon 12, and the insertion of a " $G$ " in exon 4 and a " $T$ " in exon 12. These indels of 1 base pair disrupt the open reading frame of the gene and lead to the presence of several stop codons. Moreover, a mutation at the splicing site at the end of exons 7 and 9 was found (Fig. 3).

## Molecular analyses

## Ferret $Z P 1, Z P 2, Z P 3$ and $Z P 4$ mRNA amplification

Ferret ZP1 mRNA was totally amplified. Furthermore, partial amplifications of $Z P 2, Z P 3$ and ZP4 mRNA were made to confirm the presence of four transcripts in ferret ovaries.

ZP1 mRNA contains an ORF of 1878 nucleotides. This sequence was submitted to GenBank database with accession number KX583606. The ATG initiation codon predicted with the Pedersen and Nielsen algorithm (Pedersen and Nielsen, 1997) was found to be associated with vertebrate initiator codons (Kozak, 1991). The sequence contains a stop codon (TAA) in positions 1879-1881. The ORF of ZP1 codifies for a polypeptide 626 amino acids long with a theoretical molecular weight of 67.34 kDa . The sequence contains a signal peptide of 24 aminoacids long between Thr24 and Gln25, predicted by the Bendtsen algorithm (Bendtsen et al. 2004) and a furine cleavage site in Gln537 (Duckert et al. 2004), being 55.79 kDa the expected molecular weight of the mature protein (Fig. 4).

This ZP protein shares domains with other proteins of the same family, the archetypal 'ZP domain', a signature domain comprising 272 amino acid residues (Gln262-Gly533) with ten Cys residues. The trefoil domain, characteristic of ZP1 and ZP4 is also present; this part contains 44 residues (Glu217-Thr260) with 6 Cys residues. The last domain is the transmembrane domain (TMD) between Leu586 and Leu608 with 23 amino acids; followed by a cytoplasmic tail. A basic amino acid domain (Arg536-Gln-Arg-Arg539) upstream of the TMD may serve as a consensus furin cleavage site (Fig. 4) (Boja et al. 2003, 2005; Duckert et al. 2004).

A total of 89 potential O-glycosylation sites were predicted in the ZP4 protein and two potential N -glycosylation sites (Asn-X-Ser/Thr) are present in the mature protein at the position (Asn75 and Asn362) (Fig. 4).

## Fox $Z P 1, Z P 2, Z P 3$ and $Z P 4$ mRNA amplification

The mRNA of fox ZP4 was totally amplified. Although the ORFs corresponding to fox ZP2 and ZP3 were previously characterized (Harris et al. 1994; Okazaki et al. 1995; Okazaki and Sugimoto, 1995), partial amplifications of each transcript were made to confirm the above results (Fig. 5).

Full-length fox ZP4 mRNA contains an ORF of 1704 nucleotides; containing a stop codon (TAG) in positions 1705-1707. This sequence was submitted to GenBank database with accession number KF956365. The ORF of ZP4 codifies for a polypeptide 568 amino acids long with a theoretical molecular weight of 63.26 kDa . The signal peptide is 16 aminoacids long between Ala16 and Leu17, which was predicted by the Bendtsen algorithm (Bendtsen et al. 2004) and a furin cleavage site in Gln499 (Duckert et al. 2004). The expected molecular weight of the mature protein is 53.87 kDa (Fig. 6).

The ZP domain comprises 274 amino acid residues (His224-Ala497) with ten Cys residues. The trefoil domain contains 45 residues (Asp178-Thr222) with 6 Cys residues; and the transmembrane domain (TMD) between Thr544 and Ile566 is 23 amino acids long; is followed by a cytoplasmic tail. A basic amino acid domain (Arg498-Gln-Arg-Arg501) upstream of the TMD may serve as a consensus furin cleavage site (Fig. 6) (Boja et al. 2003, 2005; Duckert et al. 2004).

A total of 89 potential O-glycosylation sites were predicted in the mature protein and two potential N -glycosylation sites (Asn-X-Ser/Thr) are present in the mature protein at the positions Asn44 and Asn68 respectively (Fig. 6).

On the other hand, the presence of $Z P 1$ mRNA in fox ovary was studied in this work, using PCR amplifications from cDNA. However, none of them had success. Thus, parallel experiments using cDNA and gDNA were conducted using the same primers. An amplicon of ZP1 was obtained only from gDNA (see Fig. 5), suggesting that there is not expression of this gene in fox ovaries. Furthermore, as a control, same amplifications, with identic primers were conducted in the dog using cDNA and gDNA, like in the fox a PCR amplification was only obtained when gDNA was used.

Considering that Goudet et al. in 2008 described the presence of three stop codons in the exons 3,5 and 8 of $\operatorname{dog} \mathrm{ZP} 1$, an amplification of exon 8 was performed in both species (fox and dog). The sequences shown a high degree of similarity between both sequences and the presence of a stop codon conserved in both of them (Fig. 7). This event could be the reason of the pseudogenization in fox $Z P 1$, not allowing the expression of the mRNA in its ovaries.

## Phylogenetic analysis

The phylogenetic tree reconstructed with all the $Z P 1$ sequences found in databases and with our new ones is presented in figure 8. The phylogeny of ZP1 is congruent with phylogenies obtained in previous studies (e.g. (Nyakatura and BinindaEmonds, 2012) (Fig.1). Four species in the phylogeny presented in this work are affected by the pseudogenization, the dog and the fox, both belonging to the Canidae family, the Antartic fur seal, belonging to the Otariidae family and the Weddell seal, belonging to the Phocidae family. Whereas, the walrus, belonging to the family Odobenidae, does not present evidences of pseudogenization. These results indicate that there was at least three pseudogenisation events in the Carnivora order, one that took
place in the lineage leading to dogs and foxes, a second one in the lineage leading to the Weddell seal and the third one in the lineage leading to the Antarctic fur seal (Fig. 8).

## DISCUSSION

## Zona pellucida composition in carnivores

The ZP is an extracellular matrix surrounding the oocyte and the early embryo and it is involved in important steps during fertilization. The ZP composition is different among the species, being formed by 3 or 4 proteins. The differences in composition are mainly due to a pseudogenization process or death of genes (Goudet et al. 2008). Previous studies showed that the ZP pseudogenization has affected different mammalian orders, such us the pseudogenization of ZP4 in the house mouse (Bleil and Wassarman 1980a; Lefièvre et al. 2004; Evsikov et al. 2006); or the pseudogenization of ZP1 in the pig, cow, dog, common marmoset, dolphin and tarsier (Hedrick and Wardrip 1987; Noguchi et al. 1994; Goudet et al. 2008; Stetson et al. 2012). In the case of carnivores, the pseudogenization of ZP1 was expected, at least in Caniformia, according to the data described in the dog (Goudet et al. 2008).

Different authors have submitted sequences from ZP2, ZP3 and ZP4 corresponding to different species; for instance the stoat (Jackson and Beaton, 2004), ferret (Jackson and Beaton, 2004), dog (Harris et al. 1994; Okazaki et al. 1995; Okazaki and Sugimoto, 1995; Srivastava et al. 2002; Blackmore et al. 2004; McLaughlin et al. 2004) and fox (Beaton and Bradley, 2004; Reubel et al. 2005), but as far as we are concern ZP1 was never reported in those species (see table 1). In the cat, the protein sequences submitted to the gene database until 2013, like in the rest of carnivores were ZP2, ZP3 and ZP4 (Harris et al. 1994, 1995; Okazaki and Sugimoto, 1995; Jewgenow
and Fickel, 1999; Okazaki et al. 2007; Eade et al. 2009); however in 2015, our group confirmed the presence of ZP1 on this species by means of molecular and proteomic analyses, being the first carnivore with 4 ZP proteins described (Stetson et al. 2015). Thus, we considered that the reanalysis of the ZP composition in this group of mammals was necessary to shed light on the carnivore ZP composition.

## Zona pellucida pseudogenization in carnivores

Carnivores are classified in two suborders (Caniformia and Feliformia); thus, the presence of a functional ZP1 in the cat indicated that the pseudogenization could have affected only the suborder Caniformia; after the divergence between these two suborders, event dated around 60-65 Ma (Nyakatura and Bininda-Emonds, 2012; Zhang et al. 2013). This hypothesis is reinforced in this work by the fact that a functional ZP1 gene was evidenced in tiger and cheetah, two other Feliformia species (Fig. 1).

The analysis of the genomic data of several species of Caniformia led us to discover that ferret, panda, polar bear and walrus present a sequence corresponding to $Z P 1$, which seems to be functional. However, different events in the sequence of the Antarctic fur seal and the Weddell seal indicate that $Z P 1$ is not a functional gene in these species; suggesting that $Z P 1$ pseudogenization occurred in the Otariidae and Phocidae families. Nevertheless, none of these events were found in the walrus (Odobenidae family), all of them belong to the same superfamily Pinnipedia; thus, it would indicate that the pseudogenization of the ZP1 gene in the lineage of the Antarctic fur seal and the Weddell seal was produced after the separation of these two families, event estimated around 22 Ma (Nyakatura and Bininda-Emonds, 2012). As there are more indels and defective mutations in the Weddell seal than in the Antarctic fur seal

ZP1 sequence, we could hypothesized that the pseudogenisation is more ancient in the Weddell seal lineage.

Additional sequence data of other Otariidae and Phocidae would be necessary in order to determine more precisely when the pseudogenisation took place.

Apart from the in silico analyses, the presence of the mRNA codifying for the different ZP proteins has been explored in two species; the ferret and the fox. These species were chosen due to its interest to control their populations. In ferret, only the protein ZP3 was previously described (Jackson and Beaton, 2004). In this work, ZP1 was totally amplified and fragments from $Z P 2, Z P 3$ and $Z P 4$ genes were amplified and automatically sequenced, demonstrating the presence of four transcripts in ferret's ovaries.

Considering the results obtained in ferret, the expression of $Z P 1$ was explored in the fox too. In this species, only ZP3 protein was previously described (Reubel et al. 2005). In this study, the mRNA of different ZPs was amplified from fox ovaries. The open reading frame of red fox $Z P 4$, present in all carnivores studied until this date, was completely amplified, moreover partial sequences of the open reading frame of ZP2 and ZP3 were also obtained. To ascertain whether ZP1 pseudogenization also affected the foxes, the exon 8 of $\operatorname{dog}$ ZP1 was amplified in $\operatorname{dog}$ and fox, as a stop codon was previously described in the dog (Goudet et al. 2008). Our results indicated that this stop codon was conserved in both species. These results confirm that the ZP1 pseudogenization also affected the fox branch. Thus, this event probably occurred after the separation of the Canidae from the other carnivorous families and as this event
affected both subfamilies (Canini and Vulpini), it probably took place between 15-60 Ma (Nyakatura and Bininda-Emonds, 2012).

These results indicate that, the pseudogenization of $Z P 1$ has been produced several times along mammalian evolution, affecting other orders than Carnivora. For instance, it was documented also in the cow (Goudet et al. 2008), common marmoset, dolphin, pig and tarsier (Stetson et al. 2012). In this work, the pseudogenization of ZP1 has been reported in three more species, the fox, the Antarctic fur seal and the Weddell seal. On the other hand, other studies reported the pseudogenization of ZP4 in mammals; for instance in the house mouse (Bleil and Wassarman 1980a; Lefièvre et al. 2004; Evsikov et al. 2006; Goudet et al. 2008); whereas, ZP2 and ZP3 proteins are present in all the species described to this date, meaning that the functions developed by these proteins are essential (Liu et al. 1996; Rankin et al. 1996, 2001; Dean, 2004; Goudet et al. 2008; Baibakov et al. 2012; Avella et al. 2014, 2016).

Thus, during the evolution of vertebrates the pseudogenization of $Z P 1$ or $Z P 4$ genes has been a common event. These two genes, come from the duplication of a common ancestral gene (Bausek et al. 2000; Goudet et al. 2008); some species maintain both copies (ZP1 and ZP4), whilst others only one (ZP1 or ZP4).

On the other hand, it is not the first time that a gene is loosed several times during the evolution affecting different evolutionary lineages; for instance, the pseudogenization of the olfactory receptor genes was previously reported in primates, coinciding with the acquisition of the trichromatic vision (Gilad et al. 2004). The
pseudogenization of $Z P 1$ or $Z P 4$ in several lineages of mammals remains unclear, further investigations are needed to clarify this aspect.

## Zona pellucida contraception

For years ZP proteins have been used to develop contraceptive vaccines in mammals; such us cats (for a review see Levy, 2011), dogs (for a review see Gupta et al. 2011; Maenhoudt et al. 2014), elephants (Delsink et al. 2007), feral horses (Joonè et al. 2015), kangaroos (Kitchener et al. 2009a), koalas (Kitchener et al. 2009b), whitetailed deers (Rutberg et al. 2013), etc. The description of ZP1 in ferret could be important for developing contraceptive vaccines to control the population size of this species. This could be relevant in countries like New Zealand, where the number of these predators is out of control (McLennan JA et al. 1996; Wilson PR et al. 1998; Jackson RJ et al. 2007; D Prada et al. 2014). Vaccines with native ZP from mink and ferret were produced and tested in the cat; animals responded to immunization with an antibody production; however, no reactivity was observed after an immunohistochemistry analysis and all the cats were pregnant after a breeding trial (Levy et al. 2005). Nevertheless, as far as we are concern, none of these vaccines have been tested in the Mustelidae population.

A recent study revealed that a homozygote mutation in human ZP1 induces infertility in women (Huang et al. 2014) and it was demonstrated that ZP1 binds to the spermatozoa and induces the acrosome reaction in humans (Ganguly et al. 2010a, 2010b). Thus, considering that the ZP composition is similar in humans, ferrets and cats, the development of a contraceptive vaccine including ZP1 as an antigen could be beneficial to induce contraception in these carnivores.

Like in the ferret, several authors point out the need to control the fox population; as it is a predator of native and endangered species and a reservoir of zoonotic diseases, like the rabies (Bradley 1994; Robinson and Holland 1995; Artois 1997; Suppo et al. 2000; Smith and Wilkinson 2003). As far as we are concern, in the fox, only the recombinant porcine and fox ZP3 proteins have been tested to induce contraception, but no immune response was obtained with either of them (Reubel et al. 2005).

It should be considered that, previous studies demonstrated that the use of native porcine ZP to induce contraception in seals (grey seals, harp seals and hooded seals), produces a good and a long response to a single dose administration (Brown et al. 1997a, 1997b). Antarctic fur seals, Weddell seals and pigs present only three proteins in their ZP, with a high homology (71\% for ZP2, 74\% for ZP3, 68\% and 70\% for Weddell seal ZP4 isoforms X1 and X2 respectively); the fox presents the same composition model, thus it may be indicated to test these three proteins (porcine and fox) to induce contraception in the fox. However, the use of porcine ZP in bitches induces side effects (Mahi-Brown et al. 1982, 1985, 1988), whilst recent studies indicate that recombinant dog ZP3 could be a promising candidate to induce contraception in dogs (Gupta et al. 2011). Further studies are necessary to develop an efficient vaccine to control the wildlife population and for the management of street cats and dogs.

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## REFERENCES

Agnarsson, I., Kuntner, M., and May-Collado, L.J. (2010). Dogs, cats, and kin: a molecular species-level phylogeny of Carnivora. Mol. Phylogenet. Evol. 54, 726-745.

Artois M. (1997). Managing problem wildlife in the 'Old World': a veterinary perspective. Reprod. Fertil. Dev. 9, 17-25.

Avella, M.A., Baibakov, B., and Dean, J. (2014). A single domain of the ZP2 zona pellucida protein mediates gamete recognition in mice and humans. J. Cell Biol. 205, 801-809.

Avella, M.A., Baibakov, B.A., Jiménez-Movilla, M., Sadusky, A.B., Dean, J. (2016). ZP2 peptide beads select human sperm in vitro, decoy mouse sperm in vivo, and provide reversible contraception. Sci Transl Med. 8, 336ra60.

Baibakov, B., Boggs, N.A., Yauger, B., Baibakov, G., and Dean, J. (2012). Human sperm bind to the N-terminal domain of ZP2 in humanized zonae pellucidae in transgenic mice. J. Cell. Biol. 197, 897-905.

Bausek, N., Waclawek, M., Schneider, W.J., and Wohlrab, F. (2000). The major chicken egg envelope protein ZP1 is different from ZPB and is synthesized in the liver. J. Biol. Chem. 275, 28866-28872.

Bendtsen, J.D., Nielsen, H., von Heijne, G., and Brunak, S. (2004). Improved prediction of signal peptides: SignalP 3.0. J. Mol. Biol. 340, 783-795.

Benoff S. (1997). Carbohydrates and fertilization: an overview. Mol. Hum. Reprod. 3, 599-637.

Berger T, Turner KO, Meizel S, Hedrick JL. (1989). Zona pellucida-induced acrosome reaction in boar sperm. Biol. Reprod. 40, 525-30.

Berta, and Churchill (2012). Pinniped taxonomy: review of currently recognized species and subspecies, and evidence used for their description. Mammal Rev. 42, 207-234.

Blackmore, D.G., Baillie, L.R., Holt, J.E., Dierkx, L., Aitken, R.J., and McLaughlin, E.A. (2004). Biosynthesis of the canine zona pellucida requires the integrated participation of both oocytes and granulosa cells. Biol. Reprod. 71, 661-668.

Bleil JD, Wassarman PM. (1980a). Structure and function of the zona pellucida: identification and characterization of the proteins of the mouse oocyte's zona pellucida. Dev. Biol. 76, 185-202.

Bleil JD, Wassarman PM. (1980b). Mammalian sperm-egg interaction: identification of a glycoprotein in mouse egg zonae pellucidae possessing receptor activity for sperm. Cell 20, 873-82.

Boja, E.S., Hoodbhoy, T., Fales, H.M., and Dean, J. (2003). Structural characterization of native mouse zona pellucida proteins using mass spectrometry. J. Biol. Chem. 278, 34189-34202.

Boja, E.S., Hoodbhoy, T., Garfield, M., and Fales, H.M. (2005). Structural conservation of mouse and rat zona pellucida glycoproteins. Probing the native rat zona pellucida proteome by mass spectrometry. Biochemistry 44, 16445-16460.

Bradley MP. (1994). Experimental strategies for the development of an immunocontraceptive vaccine for the European red fox, Vulpes vulpes. Reprod. Fertil. Dev. 6, 307-317.

Brown, R.G., Bowen, W.D., Eddington, J.D., Kimmins, W.C., Mezei, M., Parsons, J.L., and Pohajdak, B. (1997a). Evidence for a long-lasting single administration contraceptive vaccine in wild grey seals. J. Reprod. Immunol. 35, 43-51.

Brown, R.G., Bowen, W.D., Eddington, J.D., Kimmins, W.C., Mezei, M., Parsons, J.L., and Pohajdak, B. (1997b). Temporal trends in antibody production in captive grey, harp and hooded seals to a single administration immunocontraceptive vaccine. J. Reprod. Immunol. 35, 53-64.

Cao, L., Huang, Q., Wu, Z., Cao, D.-D., Ma, Z., Xu, Q., Hu, P., Fu, Y., Shen, Y., Chan, J., et al. (2016). Neofunctionalization of zona pellucida proteins enhances freezeprevention in the eggs of Antarctic notothenioids. Nat. Commun. 7, 12987.

D Prada, A Veale, J Duckworth, E Murphy, S Treadgold, R Howitt, S Hunter, and D Gleeson. (2014). Unwelcome visitors: employing forensic methodologies to inform the stoat (Mustela erminea) incursion response plan on Kapiti Island. N. Z. J. Zool. 41, 1-9.

Dean, J. (2004). Reassessing the molecular biology of sperm-egg recognition with mouse genetics. Bioessays 26, 29-38.

Delsink AK, van Altena JJ, Grobler D, Bertschinger HJ, Kirkpatrick JF, Slotow R. (2007). Implementing immunocontraception in free-ranging African elephants at Makalali conservancy. J. S. Afr. Vet. Assoc. 78, 25-30.

Duckert, P., Brunak, S., and Blom, N. (2004). Prediction of proprotein convertase cleavage sites. Protein Eng. Des. Sel. 17, 107-112.

Eade, J.A., Roberston, I.D., and James, C.M. (2009). Contraceptive potential of porcine and feline zona pellucida A, B and C subunits in domestic cats. Reprod. 137, 913-922.

Evsikov AV, Graber JH, Brockman JM, Hampl A, Holbrook AE, Singh P, Eppig JJ, Solter D, Knowles BB. (2006). Cracking the egg: molecular dynamics and evolutionary aspects of the transition from the fully grown oocyte to embryo. Genes Dev. 20, 27132727.

Fazeli A, Hage WJ, Cheng FP, Voorhout WF, Marks A, Bevers MM, Colenbrander B. (1997). Acrosome-intact boar spermatozoa initiate binding to the homologous zona pellucida in vitro. Biol. Reprod. 56, 430-438.

Florman HM, Storey BT. (1982). Mouse gamete interactions: the zona pellucida is the site of the acrosome reaction leading to fertilization in vitro. Dev. Biol. 91, 121-130.

Ganguly A, Bukovsky A, Sharma RK, Bansal P, Bhandari B, Gupta SK. (2010a). In humans, zona pellucida glycoprotein-1 binds to spermatozoa and induces acrosomal exocytosis. Hum. Reprod. 25, 1643-1656.

Ganguly A, Bansal P, Gupta T, Gupta SK. (2010b) 'ZP domain' of human zona pellucida glycoprotein-1 binds to human spermatozoa and induces acrosomal exocytosis. Reprod. Biol. Endocrinol. 8, 110.

Gilad Y, Przeworski M, Lancet D. (2004). Loss of olfactory receptor genes coincides with the acquisition of full trichromatic vision in primates. PLoS Biol. 2.

Goudet, G., Mugnier, S., Callebaut, I., and Monget, P. (2008). Phylogenetic analysis and identification of pseudogenes reveal a progressive loss of zona pellucida genes during evolution of vertebrates. Biol. Reprod. 78, 796-806.

Gouy M, Guindon S, Gascuel O. (2010). SeaView version 4: A multiplatform graphical user interface for sequence alignment and phylogenetic tree building. Mol. Biol. Evol. 27, 221-224.

Guindon, S., Dufayard, J.-F., Lefort, V., Anisimova, M., Hordijk, W., and Gascuel, O. (2010). New algorithms and methods to estimate maximum-likelihood phylogenies: assessing the performance of PhyML 3.0. Syst. Biol. 59, 307-321.

Gupta SK, Bhandari B. (2011). Acrosome reaction: relevance of zona pellucida glycoproteins. Asian J. Androl. 13, 97-105.

Gupta, S.K., Srinivasan, V.A., Suman, P., Rajan, S., Nagendrakumar, S.B., Gupta, N., Shrestha, A., Joshi, P., and Panda, A.K. (2011). Contraceptive vaccines based on the zona pellucida glycoproteins for dogs and other wildlife population management. Am. J. Reprod. Immunol. 66, 51-62.

Gupta SK, Bhandari B, Shrestha A, Biswal BK, Palaniappan C, Malhotra SS, Gupta N. (2012). Mammalian zona pellucida glycoproteins: structure and function during fertilization. Cell Tissue Res. 349, 665-78.

Harris, J.D., Hibler, D.W., Fontenot, G.K., Hsu, K.T., Yurewicz, E.C., and Sacco, A.G. (1994). Cloning and characterization of zona pellucida genes and cDNAs from a variety of mammalian species: the ZPA, ZPB and ZPC gene families. DNA Seq. 4, 361-393.

Hedrick JL, Wardrip NJ. (1987). On the macromolecular composition of the zona pellucida from porcine oocytes. Dev. Biol. 121, 478-88.

Hoodbhoy, T., Joshi, S., Boja, E.S., Williams, S.A., Stanley, P., and Dean, J. (2005). Human sperm do not bind to rat zonae pellucidae despite the presence of four homologous glycoproteins. J. Biol. Chem. 280, 12721-12731.

Huang, H.-L., Lv, C., Zhao, Y.-C., Li, W., He, X.-M., Li, P., Sha, A.-G., Tian, X., Papasian, C.J., Deng, H.-W., et al. (2014). Mutant ZP1 in familial infertility. N. Engl. J. Med. 370, 1220-1226.

Hughes, D.C., and Barratt, C.L. (1999). Identification of the true human orthologue of the mouse $\mathrm{Zp1}$ gene: evidence for greater complexity in the mammalian zona pellucida? Biochim. Biophys. Acta 1447, 303-306.

Humble, E., Martinez-Barrio, A., Forcada, J., Trathan, P. N., Thorne, M. A. S., Hoffmann, M., Wolf, J. B. W. and Hoffman, J. I. (2016), A draft fur seal genome provides insights into factors affecting SNP validation and how to mitigate them. Mol. Ecol. Resour. 16, 909-921.

Hyllner, S.J., Westerlund, L., Olsson, P.E., and Schopen, A. (2001). Cloning of rainbow trout egg envelope proteins: members of a unique group of structural proteins. Biol. Reprod. 64, 805-811.

Izquierdo-Rico, M.J., Jimenez-Movilla, M., Llop, E., Perez-Oliva, A.B., Ballesta, J., Gutierrez-Gallego, R., Jimenez-Cervantes, C., and Aviles, M. (2009). Hamster zona pellucida is formed by four glycoproteins: ZP1, ZP2, ZP3, and ZP4. J. Proteome Res. 8, 926-941.

Jackson R.J., Beaton S., and Dall D.J. (2007). "Stoat zona pellucida genes with potential for immunocontraceptive biocontrol in New Zealand". Wellington, N.Z.: Science \& Technical Pub., Dept. of Conservation.

Jewgenow, K., and Fickel, J. (1999). Sequential expression of zona pellucida protein genes during the oogenesis of domestic cats. Biol. Reprod. 60, 522-526.

Jiménez-Movilla, M., Martínez-Alonso, E., Castells, M.T., Izquierdo-Rico, M.J., Saavedra, M.D., Gutiérrez-Gallego, R., Fayrer-Hosken, R., Ballesta, J., and Avilés, M. (2009). Cytochemical and biochemical evidences for a complex tridimensional structure of the hamster zona pellucida. Histol. Histopathol. 24, 599-609.

Joonè, C.J., Bertschinger, H.J., Gupta, S.K., Fosgate, G.T., Arukha, A.P., Minhas, V., Dieterman, E., and Schulman, M.L. (2015). Ovarian function and pregnancy outcome in pony mares following immunocontraception with native and recombinant porcine zona pellucida vaccines. Equine Vet. $J$.

Kitchener, A.L., Harman, A., Kay, D.J., McCartney, C.A., Mate, K.E., and Rodger, J.C. (2009a). Immunocontraception of Eastern Grey kangaroos (Macropus giganteus) with recombinant brushtail possum (Trichosurus vulpecula) ZP3 protein. J. Reprod. Imтипоl. 79, 156-162.

Kitchener, A.L., Kay, D.J., Walters, B., Menkhorst, P., McCartney, C.A., Buist, J.A., Mate, K.E., and Rodger, J.C. (2009b). The immune response and fertility of koalas
(Phascolarctos cinereus) immunised with porcine zonae pellucidae or recombinant brushtail possum ZP3 protein. J. Reprod. Immunol. 82, 40-47.

Kozak, M. (1991). Structural features in eukaryotic mRNAs that modulate the initiation of translation. J. Biol. Chem. 266, 19867-19870.

Lefièvre, L., Conner, S.J., Salpekar, A., Olufowobi, O., Ashton, P., Pavlovic, B., Lenton, W., Afnan, M., Brewis, I.A., Monk, M., et al. (2004). Four zona pellucida glycoproteins are expressed in the human. Hum. Reprod. 19, 1580-1586.

Levy, J.K., Mansour, M., Crawford, P.C., Pohajdak, B., and Brown, R.G. (2005). Survey of zona pellucida antigens for immunocontraception of cats. Theriogenology 63, 1334-1341.

Levy, J.K. (2011). Contraceptive vaccines for the humane control of community cat populations. Am. J. Reprod. Immunol. 66, 63-70.

Liu, C., Litscher, E.S., Mortillo, S., Sakai, Y., Kinloch, R.A., Stewart, C.L., and Wassarman, P.M. (1996). Targeted disruption of the mZP3 gene results in production of eggs lacking a zona pellucida and infertility in female mice. Proc. Natl. Acad. Sci. U. S. A. 93, 5431-5436.

Mahi-Brown, C.A., Huang, T.T., and Yanagimachi, R. (1982). Infertility in bitches induced by active immunization with porcine zonae pellucidae. J. Exp. Zool. 222, 8995.

Mahi-Brown, C.A., Yanagimachi, R., Hoffman, J.C., and Huang, T.T. (1985). Fertility control in the bitch by active immunization with porcine zonae pellucidae: use of
different adjuvants and patterns of estradiol and progesterone levels in estrous cycles. Biol. Reprod. 32, 761-772.

Mahi-Brown, C.A., Yanagimachi, R., Nelson, M.L., Yanagimachi, H., and Palumbo, N. (1988). Ovarian histopathology of bitches immunized with porcine zonae pellucidae. Am. J. Reprod. Immunol. Microbiol. 18, 94-103.

McLennan, J.A., Potter, M.A., Robertson, H.A., Wake, G.C., Colbourne, R., Dew, L., Joyce, L., McCann, A.J., Miles, J., Miller, P.J., et al. (1996). Role of predation in the decline of the kiwi, Apteryx spp., in New Zealand. N. Z. J. Ecol. 20, 27-35.

Modliński, J.A. (1970). The role of the zona pellucida in the development of mouse eggs in vivo. J Embryol Exp Morphol. 23, 539-47.

Maenhoudt, C., Santos, N.R., Fontbonne, A. (2014). Suppression of fertility in adult dogs. Reprod. Domest. Anim. 49 Suppl 2, 58-63.

Monné, M., and Jovine, L. (2011). A structural view of egg coat architecture and function in fertilization. Biol. Reprod. 85, 661-669.

Noguchi, S., Yonezawa, N., Katsumata, T., Hashizume, K., Kuwayama, M., Hamano, S., Watanabe, S., Nakano, M. (1994). Characterization of the zona pellucida glycoproteins from bovine ovarian and fertilized eggs. Biochim. Biophys. Acta. 1201, 714.

Nyakatura, K., and Bininda-Emonds, O.R.P. (2012). Updating the evolutionary history of Carnivora (Mammalia): a new species-level supertree complete with divergence time estimates. BMC Biol. 10, 12.

Pedersen, A.G., and Nielsen, H. (1997). Neural network prediction of translation initiation sites in eukaryotes: perspectives for EST and genome analysis. Proc. Int. Conf. Intell. Syst. Mol. Biol. 5, 226-233.

Posada, D., and Crandall, K.A. (1998). MODELTEST: testing the model of DNA substitution. Bioinforma. 14, 817-818.

Rankin, T., Familari, M., Lee, E., Ginsberg, A., Dwyer, N., Blanchette-Mackie, J., Drago, J., Westphal, H., and Dean, J. (1996). Mice homozygous for an insertional mutation in the Zp 3 gene lack a zona pellucida and are infertile. Dev. Camb. Engl. 122, 2903-2910.

Rankin T, Talbot P, Lee E, Dean J. (1999). Abnormal zonae pellucidae in mice lacking ZP1 result in early embryonic loss. Development 126, 3847-55.

Rankin, T.L., O'Brien, M., Lee, E., Wigglesworth, K., Eppig, J., and Dean, J. (2001). Defective zonae pellucidae in Zp 2 -null mice disrupt folliculogenesis, fertility and development. Dev. 128, 1119-1126.

Reubel, G.H., Beaton, S., Venables, D., Pekin, J., Wright, J., French, N., and Hardy, C.M. (2005). Experimental inoculation of European red foxes with recombinant vaccinia virus expressing zona pellucida C proteins. Vaccine 23, 4417-4426.

Robinson, A.J., Holland, M.K. (1995). Testing the concept of virally vectored immunosterilisation for the control of wild rabbit and fox populations in Australia. Aust. Vet. J. 72, 65-68.

Rutberg, A.T., Naugle, R.E., and Verret, F. (2013). Single-treatment porcine zona pellucida immunocontraception associated with reduction of a population of whitetailed deer (Odocoileus virginianus). J. Zoo Wildl. Med. 44, 75-83.

Sasanami, T., Pan, J., Doi, Y., Hisada, M., Kohsaka, T., and Toriyama, M. (2002). Secretion of egg envelope protein ZPC after C-terminal proteolytic processing in quail granulosa cells. Eur. J. Biochem. 269, 2223-2231.

Smith, G.C., Wilkinson, D. (2003). Modeling control of rabies outbreaks in red fox populations to evaluate culling, vaccination, and vaccination combined with fertility control. J. Wildl. Dis. 39, 278-286.

Srivastava, N., Santhanam, R., Sheela, P., Mukund, S., Thakral, S.S., Malik, B.S., and Gupta, S.K. (2002). Evaluation of the immunocontraceptive potential of Escherichia coli-expressed recombinant dog ZP2 and ZP3 in a homologous animal model. Reprod. 123, 847-857.

Stetson, I., Izquierdo-Rico, M.J., Moros, C., Chevret, P., Lorenzo, P.L., Ballesta, J., Rebollar, P.G., Gutiérrez-Gallego, R., and Avilés, M. (2012). Rabbit zona pellucida composition: a molecular, proteomic and phylogenetic approach. J. Proteomics 75, 5920-5935.

Stetson, I., Avilés, M., Moros, C., García-Vázquez, F.A., Gimeno, L., Torrecillas, A., Aliaga, C., Bernardo-Pisa, M.V., Ballesta, J., and Izquierdo-Rico, M.J. (2015). Four glycoproteins are expressed in the cat zona pellucida. Theriogenology $83,1162-1173$.

Suppo, C., Naulin J.M., Langlais, M., Artois, M. (2000). A modelling approach to vaccination and contraception programmes for rabies control in fox populations. Proc. Biol. Sci. 267, 1575-1582.

Tanihara, F., Nakai, M., Kaneko, H., Noguchi, J., Otoi, T., Kikuchi, K. (2013). Evaluation of zona pellucida function for sperm penetration during in vitro fertilization in pigs. J. Reprod. Dev. 59, 385-92.

Tian, J., Gong, H., Thomsen, G.H., and Lennarz, W.J. (1997). Gamete interactions in Xenopus laevis: identification of sperm binding glycoproteins in the egg vitelline envelope. J. Cell Biol. 136, 1099-1108.

Wassarman, P.M. (1988). Fertilization in mammals. Sci. Am. 259, 78-84.

Wilson PR, Karl BJ, Toft RJ, Beggs JR, and Taylor RH (1998). The role of introduced predators and competitors in the decline of kaka (Nestor meridionalis) populations in New Zealand. Biol. Conserv. 175-185.

Zhang, G., Cowled, C., Shi, Z., Huang, Z., Bishop-Lilly, K.A., Fang, X., Wynne, J.W., Xiong, Z., Baker, M.L., Zhao, W., et al. (2013). Comparative analysis of bat genomes provides insight into the evolution of flight and immunity. Science 339, 456-460.

Figure 1. Phylogeny and divergence-time estimates for the taxa involved in our study. For each taxon the family name is indicated within brackets. Horse and cow are used as outgroups. The ages of the nodes are from Nyakatura and Bininda-Edmonds, 2012.

Figure 2. Comparison of ZP1 amino acid sequences from tiger, cheetah, cat, panda, polar bear, ferret and walrus. The accession numbers of the sequences used are: tiger (XP_007092072), cheetah (XP_014930922), cat (AEI98737), panda (XP_002928701), polar bear (XP_008705767), ferret (KX583606) and walrus (XP_012421243). Identical amino acids are marked by an asterisk (*), colon (:)
represents conserved residues and dot (.) represents semi-conserved residues. The signal peptide is marked in pink. The trefoil domain is shown in blue. The zona domain is shown in red. The consensus furin cleavage-site is underlined. The transmembrane domain is marked in orange. The cystein residues are marked in green. The potential N glycosylation sites are shown in purple.

Figure 3. Comparison of Antarctic fur seal, Weddell seal and walrus ZP1 sequences. The first ACG codon, the indels and the stop codons (*), which are indicative of $Z P 1$ pseudogenization in the Antarctic fur seal and the Weddell seal are shown in bold on gray background.

Figure 4. Nucleotide and deduced amino acid sequence of ferret ZP1. The initial and final codons are in pink. The signal peptide is marked with green colour. Trefoil domain is shown in blue. The zona domain is shown in red. The consensus furin cleavage-site is underlined. The transmembrane domain is marked in orange. The putative N -glycosylation sites (Asn75 and Asn362) are indicated in violet. In capital letters and bold: two polymorphisms (positions: $885(\mathrm{Y})$ and $1296(\mathrm{Y})$ ).

Figure 5. Analysis of $Z P 1, Z P 2, Z P 3$ and $Z P 4$ gene expression in fox ovary by PCR. Amplicons corresponding to each gene are shown. In line 1 a fragment of $Z P 1$ amplified from gDNA is shown. In line $2 Z P 1$ was not amplified from cDNA. Lines 3,4 and 5 show fragments of $Z P 2, Z P 3$ and $Z P 4$ genes amplified from cDNA.

Figure 6. Nucleotide and deduced amino acid sequence of fox ZP4. The initial and final codons are in pink. The signal peptide is marked with green colour. Trefoil domain is shown in blue. The zona domain is shown in red. The consensus furin cleavage-site is underlined. The transmembrane domain is marked in orange. The putative N glycosylation sites (Asn44 and Asn68) are indicated in violet.

Figure 7. Comparison of ZP1 amino acid sequences (exon 8) from dog and fox. Identical amino acids are marked by an asterisk $\left(^{*}\right)$ and colon (:) represents conserved residues. The stop codon in both species is signaled by an arrow ( $\downarrow$ ). This stop codon along with others stop codons or modifications could be responsible of the ZP1 pseudogenization.

Figure 8. Phylogenetic relationship of the $Z P 1$ gene in carnivores. Bootstrap support is indicated for each node. Species with ZP1 pseudogenised (dog, fox, Antarctic fur seal and Weddell seal) are indicated in gray background.

Figure 1


## Figure 2

Tiger
Cat
Cheetah
Panda
Polar bear
Ferret
Walrus

Tiger
Cat
Cat
Cheetah
Panda
Polar bear
Ferret
Walrus

Tiger
cat
Cheetah
Panda
Polar bear
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Tiger
Cat
Cheetah
Panda
Polar bear
Ferret
Walrus

Tiger AYAPTRCSPTQDTGSFVVFQFPLTHCGTTVQVVGNQLLYENQLVSDIDVQMGPQGSITRD 359
MVAVVYLTTRALAMVWDGCVALLLLLLVAALGLGQRPHPEPGLRGLRHSSDCGIKGMQLL MVAVVYLMTRASAMVWDGCVALLL-LLVAALGLGQRPHPEPGLRGLRHSSDCGIKGMQLL MVAVVYLMTRASAMVWNGCLELLL-LLVAALGLGPQPHPEPGLRGLRHSSDCGIKGMQLL -------MAGASARVWGCCVALL--LLLAALGLGQRPHPEPGLAGLWHRYDCGVKGMQLQ ---MVCLMAGASAGVWCRCMALL---LLAALGLGQRPHPAPGLTGLWHHYDCGVKGMQLR -------MAGISARLRDGCVALL---LVAALGLTQRPHTEPGPSGLWHGYDCGVKGMQLW -------MAGASAGVWDCHVALL---LVTALGLGQRLHPKPGLSSLGYSYDCGVKGLQLR

VFPRPGQTVRFKVVDEFGNQFEVHNCSVCYHWVTARPLGPAVFSADYRGCHVLEKDGRFH 120 VFPRPGQTVRFKVVDEFGNQFEVHNCSVCYHWVTARPLGPAVFSADYRGCHVLEKGGRFH 119 VFPRPGQTVRFKVVDEFGNQFEVHNCSVCYHWVTARPLGPAVFSADYRGCHVLEKDGRFH 119 VFPRPGQMIRFKVVDEFGNQFEVNNCSACYHWVTTKPLGPAVFSAGYKGCHVLEKDGRSH 111 VFPQPGQTIRFKVVDEFGNQFEVNNCSACYHWVTTKPLGPAVFSAGYKGCHVLEKDGRSH 114 AFPGPGQTIRFKVVDEFGNQFEVNNCSACYHWVTTKPPGHAVFSAGYKGCHVLEKDGRSH 110 VLPQSGQMVRFKVVDEFGNQFEVNNCSACYHWVSTKPQAPAVFSAGYKGCHMLEKDGRSH 110

LRVFVEAVLRDGRVDAAGEVTLICPKPGHTWTPESHLASRTGFSLPTPHTRPLRPTREHS 180 LRVFVEAVLRDGRVDAAGEVTLICPKPGHTWTPESHLASRTGFSLPTPHTRPLRPTQEHS 179 LRVFVEAMLRDGRVDAAGEVTLICPKPGHTWTPESHLASRTGFSLPTPHTRPLRPTQEHS 179 LRVFIEVVLPDGRVDATRDVTLICPKPGHTWTPDTHLAPHTGFSLPTPQARPLHPTPERG 171 LRVFIEAVLPDGRVDATRDVTLICPKPGHTWTPDAHLAPHTGFSLPTPQARPLHPTPEHG 174 LKVIIEAVLPNGQVEATGDVTLICPKPAHTWTPDPHLAPRTGFSRPTPQAWSLRPNPEHS 170 LTVFIEAVGPDGRVDATRDVTLICPKPGHAWTPASRPEPPVGFSLPTPQARPLRPIPEHG 170 * *: : . : : * : : * : : ********.*:*** : .*** ***: : * * *: .

FTRPTPALLPLRPGA-TRPTLTPPPWDILEHWGVDEPLHPGAPLTWEQCQVPSGHIPCVV 239 FTRPTPALLPLRPGA-THPTLTLPQWDILEHWGVDEPLHPGAPLTWEQCQVPSGHIPCVV 238 FTRPTPALLPLRPGA-TRPTLTLPQWDILEHWGVDEPLHPGAPLTWEQCQVPSGHIPCVV 238 LVHATPTLLSLRPGPTTHPTQAPPQWGTLEHWGGSEPPYPGAHLPRERCQVPSGPIPCGV 231 LVRATPTLPSLRPGPTTHPTQAPPQWGTLEHWGGSEPPYPGAHLPREQCQVPSGPIPCGV 234 FVHATPALPSLGPGPTSHATQAPPQGGTLRPWGVDEPPYSGAPLTPELCQVPSRAISCGV 230 FVRATPALPSLEPGPTTHPTQAQPQWGTLEHGGVDKPPYPGMRLTPGRCQVSSRPIPCGV 230


RRGSKEACQKAGCCYDNRRGVPCYYGNTATVQCERNGHFVLVVSQETALAHGITLANIHV 299 RRGSKEACQKAGCCYDNSRAVPCYYGNTATVQCERNGHFVLVVSQETALAHGITLANIHV 298 RRGSKEACQKAGS----SSAVPCYYGNTATVQCERNGHFVLVVSQETALAHGITLANIHV 294 RRGSKEACQRAGCCYDNSREVPCYYGNTATVQCERNGHFVLVVSREIALAHGITLASIHL 291 RRGSKEACQRAGCCYDNSREVPCYYGNTATVQCERNGHFVLVVSRETALAHGITLANIHL 294 GRSSKEACQQAGCCYDNSRAIPCYYGNTATVQCERNGHFVLVVSQETALAHGITLANLHM 290 R-SSEEACLRAGCCYDNSREVPCYYGNTATVQCERNGHFVLVVSRETALAHGITLANIHM 290
$. *: * * *: * * . \quad: * * * * * * * * * * * * * * * * * * * * * *: * * * * * * * * * *: ~ *: ~$

AYAPTSCSPTQDTGSFVVFQFPLTHCGTTVQVVGNQLLYENQLVSDIDVRMGPQGSITRD 358 AYAPTSCSPTQDTGSFVVFQFPLTHCGTTVQVVGNQLLYENQLVSDIDVRMGPQGSITRD 354 AYAPTSCSPTQETRSFVVFRFPFSHCGTTVQVAGDQLIYENQLVSDIEAQTGPQGSITRD 351 AYAPTSCSPTQETRSFVVFRFPFSHCGTTVQVAGNQLIYENQLVSEIEARTGPQGSITRD 354 AYAPTGCSPTQETGSFVVFRFPLSHCGTTAQVAGNQLVYENQLVSDIEARTGPQGSITRD 350 AYAPTSCSPAQKTGSFVVFRFPFSHCGTTVQVAGNQLIYENQLVSDIEAQTGPQGSITRD 350 $\star * * * * * * *: * . * * * * * *: * *:: * * * * * . * * . *: * *: * * * * * * *: *: .: * * * * * * * * *$

GTFRLHVR------CIVNASDFLPLRASIFPPPSPAPVIQSG------------PLRFQL 401
GAFRLHVR------CTVNASDFLPLQASIFSPPSPVPVIQSG--------------PLREQL 400
GAFRLHVR------CTINASDFLPLRASIFPRPSPAPVIQSG-------------PLRFQL 396 GTFRLQAR------CVENASDFLPLRASVSPRPSPAPVTQSXXXXXAPPPPPPSPPRLRA 405 GTFRTWLVPGPVSGCSTSSWSTRPRLESSLPEVKGEPLGAGGKG-------GWGQLSLQN 407 GTFRLHMR------CIFNASDFLPLQASIFPPPSPAPVTQSG-------------PLHLQL 392 GTFRLHVR------CVFNTSDFLPLQASIFLPPSPAPVTQSG--------------PLQLQL 392 * . . * * . * :

RIATDETFRSFYEEGDYPIVRLLREPVSVEVRLLDRTDPGLVLLLHRCWATPSASPFQQP 461 RIATDETFRSFYEEGDYPIVRLLREPVSVEVRLLDRTDPGLVLLLHQCWATPGVSPFQQP 460 RIATDETFRSFYEEGDYPIVRLLREPVSVEVRLLDRTDPGLVLLLHRCWATPSVSPFQQP 456 PLPADETFRSFYGPGDYPIVRLLREPAAVEVRLLQRADPGLVLLLHQCWATPGASPFQQP 465 MGCRAWTFRSYYEAGDYPIVRLLPEPVPVEVRLLQRADPGLVLLLHQCWATPGASPFQQP 467 RIAKDETFRSFYEEGDYPLVRLLREPVPVEVRLLHRTDPGLVLLLHQCWATPGASPFQQP 452 RIAKDESFRSYYEEGDYPLVRLLRQPVPVEVRLLERTDPSLVLLLHQCWATPGANPFQQP 452


## Figure 3

Walrus
Weddell seal
Antarctic fur seal

Walrus
Weddell seal
Antarctic fur seal

Walrus
Weddell seal
Antarctic fur seal

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Walrus
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Antarctic fur seal

ATGGCAGGAGCCTCGGCCGGGGTCTGGGATTGCCACGTGGCCCTGCTGCTGGTGACCGCTCTGGGGCTGGGGCAGCGGCTACACCCCAAGCCTGGTCTCT 100
 ACGGCAGGAGCCTCGGCCGGGGTCTGGGATTGCCACGTGGCCCTGCTGCTGATGAGCGCTCTGGGGCTGGGGCAGCAGCTACTCCCCGAGCCTTATCTCT 100
 ATGGCAGGAGCCTCGGCCGGGGTCTGGGATTGCCACGTGGCCCTGCTGCTGGTGACTGCTCTGGGGCTGGGGCAGCGGCTACACCCCAAGCCTGGTCTCT 100


CCAGCCTGGGGTACAGCTATGACTGTGGGGTCAAGGGCCTGCAGCTACGGGTGCTCCCCCAGTCAGGCCAGATGGTCCGCTTCAAGGTGGTAGATGAATT 200
 CCGGCCTGGGGTACAGCTATGACTGTGGGGTCAAGAGTTTGCAGCTACGAGTGCTCCCCCGGTCAGGCCAGACAGTCCACTTCAAGGTGGTAGATGAATT 200



EXON 2
TGGGAACCAATTTGAGGTGAACAACTGCTCTGCTTGCTACCACTGGGTCAGCACCAAGCCCCAGGCACCCGCTGTCTTCTCTGCAGGTTACAAAGGCTGC 300
 TGGGAACCGGTTTGAGGTAAACAACTGCTCTGCTTGTTACCACTGGGTCAGCACCAAGCCCCGGGCACCTGCTGTCTTCTCTGTGGGTTACAAAGGCTGC 300 $\begin{array}{llllllllllllllllllllllllllllllllll}G & \mathrm{~N} & \mathrm{~N} & \mathrm{~F} & \mathrm{E} & \mathrm{V} & \mathrm{N} & \mathrm{N} & \mathrm{C} & \mathrm{S} & \mathrm{A} & \mathrm{C} & \mathrm{Y} & \mathrm{H} & \mathrm{W} & \mathrm{V} & \mathrm{S} & \mathrm{T} & \mathrm{K} & \mathrm{P} & \mathrm{R} & \mathrm{A} & \mathrm{P} & \mathrm{A} & \mathrm{V} & \mathrm{F} & \mathrm{S} & \mathrm{V} & \mathrm{G} & \mathrm{Y} & \mathrm{K} & \mathrm{G} & \mathrm{C}\end{array}$ TGGGAACCAATTTGAGGTGAACAACTGCTCTGCTTGCTACCACTGGGTCAGCACCAAGCCCTGGGCACCCGCTGTCTTCTCTGCAGGTTACAAAGGCTAC 300


EXON 3
CACATGCTGGAGAAGGACGGGCGCTCCCACCTAACGGTGTTCATTGAAGCCGTGGGGCCCGATGGTCGAGTTGATGCAACCCGAGATGTCACTCTGATTT 400
 CACATGCTGGAGAAGGATGGGCGCTCCCACCTGAGGGTGCTCATCGAAGCCGTGCTGCCCGATGGTCGAGTTGATGCAACACAAGATGTCACTCTGATTT 400 H M ,


GTCCTAAACCTGGCCACGCCTGGACTCCGGCCTCCCGTCCGGAACCACCCGTGGGCTTCTCCCTTCCCACGCCTCAGGCCCGGCCCCTCCGCCCCATCCC 500

 GTCCTAAACCTGGCCACGGCTGGACTCCGGCCTCCCATCCGGAACCACCCGTGGGCTTCTCCCTTCCCACGCCTCAGGCCCAGCCCCTCCGCCCCATCCC 500


AGAGCACGGCTTTGTCCGTGCAACCCCTGCCTTGCCGTCCCTCGAACCTGGACCCACCACCCATCCCACCCAGGCTCAACCCCAGTGGGGCACCCTGGAA 600
 AGAGCACGGCTTTGTCTGTGCACCCCCTGCCTTGCTGTCCCTCGGACCTGGACCCACCGCCCATCCCA----GGTTAAACCCCAGTGGGGCACCCTGGAA 595
 AGAGCACAGCTTTGTCCGTGCAACCCCTGCTTTGCCGTCCCTCGGACCTGGACCCGCCACCCATCCCACCCAGGCTCAACCCCAGTGGGGCACCCTGGAA 600



AAGAAGCCTGTCTGCGGGCAGGCTGCTGCTATGACAAC-AGCAGAGAGGTTCCCTGTTACTATGGCAACACAGCAACTGTCCAGTGCTTCAGAAATGGCC 799
 AGGAAGCCTGTCTGCAGGCGGGCTGCTGCTTTGACAACGGGCGGAGAGATTCCCTGTTACTATGGCAACACAGCAACTGTCCAGTGCTTCAGAAATGGCC 795
 AGGAAGCCTGTCTGCCGGC-GGCTGCTGCTATGACAAC-GGCAGAGAGGTTCCCTGTTACTATGGCAACACAGCAACTGTCCAGTGCTTCAGAAATGGCC 797


EXON 5
ACTTTGTCCTGGTGGTGTCCCGAGAAACAGCCTTGGCACATGGGATCACACTGGCCAACATCCACATGGCCTATGCCCCCACCAGCTGCTCCCCAGCCCA 899
 ACTTTGTCCTGGTGGTGTCCGGAGAAACAGCCTTGGCACGTGGGATCACACTGGCCAACATCCACACGGCCTGTGCCCCCACCAGCTGCTCCCCAGCCCA 895
 ACTTTGTCCTGGTGGTGTCCCGAGAAACAGCCTTGGCACATGGGATCACACTGGCCAACATCCACATGGCCTATGCCCCCACCAGCTGCTCCCCGGCCCA 897


GAAGACCGGGTCCTTCGTGGTCTTTCGCTTCCCTTTCTCCCACTGTGGGACCACGGTCCAGGTGGCTGGCAACCAGCTCATCTATGAGAATCAGCTGGTG 999
 GGAGACCGGGTCCTTCGTGGTCTTTCGCTGCCCTTTCTCCCACTGTGGGACCACGGTCCAGGTGGCCGGCAACCAGCTCATCTATGAGAATCAGCTGGTG 995
 GCAGACCGGGTCCTTCGTGGTCTTTCGCTTCCCTTTCTCCCACTGTGGGACCACGGTCCAGGTGGCTGGCAACCAGCTCATCTATGAGAATCAGCTGGTG 997


EXON 6
TCTGACATTGAGGCCCAAACGGGGCCACAGGGCTCCATCACGCGGGACGGCACCTTCCGGCTTCACGTGCGCTGCGTCTTTAACACCAGTGACTTCCTGC 1099
 TCTGACTTCGAGGCCCAAACGGGGCCACAGGGCTCCATCACGCGGGATGGCACCTTCTGGCTTCACGTGTGCTGCGTCTTCAACACTGGTGATTTCCTGC 1095



EXON 7

Walrus
Weddell seal
Antarctic fur seal

Walrus
Weddell seal
Antarctic fur seal

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Weddell seal
Antarctic fur seal

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Weddell seal
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Walrus
Weddell seal
Antarctic fur seal

Walrus AGTCGGTGTTTTCGTGCGCCTGAGCCGAGCCCAGCACAGGAACTCCAG-GAAGGCAATGGCGGGTGAAGGGGCTCAATAA 1878

GGTCAGTGTTTTCATGCGCCTGAGCCGAGCCCAGCGCAGGAGTTCCAGTGAAGGCAACGGAGGGTGAAGGGGCTCAATAA 1871
$G \quad Q \quad C \quad F \quad H \quad A \quad P \quad E \quad P \quad S \quad P \quad A \quad Q \quad E \quad F \quad Q \quad * \quad R \quad Q \quad R \quad R \quad V \quad K \quad G \quad L \quad N$
GGTCGGTGTTTTCGTGCGCCTGAGCCGAGCCCAGCACAGGAGCTCCAG-GAAGGCAATGGAGGGTGAAGGGGCTCAATAA 1876

## Figure 4

```
atggcagggatctcggccaggctccgggacggttgcgtggcgctgctgctggtggctgct
    M A G I S A R L R D G C V A A L I L L V A A
ctggggctgacgcagcggccacacaccgaacctggtccctcaggcctgtggcacggctat
L G L T Q R P P H T F E P P
gactgtggggtcaagggcatgcagctatgggccttcccggggccaggccagacaatccgc
    D Clllllllllllllllllllllllll
ttcaaggtggtagatgaatttgggaaccaatttgaggtaaacaactgttctgcctgctac
    F
cactgggtcaccaccaagcccccgggacacgcggtcttctctgctggttacaaaggctgc
    H
cacgtgctggagaaggacgggcgctcccacctgaaggtgatcatcgaagccgtgctgccc
    H
aacggtcaagttgaggcaacaggagatgtcactctgatttgtcctaaacctgcccacacc
    N G Q V E A T T G D V V T L L I Clllllllllll
tggactccggacccacacctggcaccacgcacaggcttctcccgccccaccccccaggcc
```



```
tggtccctccgccccaacccagagcacagcttcgtccatgcgaccoctgccttgccgtcc
W
ctcggacctggacccacctcccatgccacccaggccccaccccaggggggcaccctgaga
    L G P G P T S H A T T Q A A P
ccctggggggttgacgagccaccatactcaggtgcacctctgactccagagctgtgccag
P W W G V D E P P P Y S S G A P P L T T P
gtgccctcaagggccatctcctgtggagtgggaagaagctcgaaggaagcctgccagcag
V P S R A I S C G V G R S S S K K E A Clllllll
gctggctgctgctatgacaacagcagagcgattccctgttactatggcaacacagcaact
A G C C Y D N S R A I P C C Y Y Y G N T A T
gtccagtgcttcagaaatggccactttgtcctggtggtgtcccaagaaactgccttggcg
```



```
cacgggatcacgctggccaacctccacatggcctatgcccccacYggctgctcccccacc
H G I T L A N L L H M M A P
caggagaccgggtccttcgtggtcttccgcttccccctctcccactgtgggaccacagcc
Q E T G S F V V F F R F F P L L S F H
caggtggctggcaaccagctcgtctatgagaatcagctggtgtctgacatcgaggctcgg
    Q V A G N Q L V Y E N Q L L V S S D I I E A R
acggggccacagggctccatcacaagggacggcaccttccggcttcacatgcgctgcatc
T G P Q G S I T R D D G T F F R R L F H
ttcaacgccagtgacttcctgccgctccaggcatccatcttcccgccaccctctccagcc
    F N A S D F F L P L L Q A S S I F F P
cctgtgacccagtccgggcccctgcatctccagcttcggatcgccaaagatgagactttc
    P V T Q S G P L H L Q Q L R I I A A K D D E N T F
cgctccttctacgaggaaggggactaccccctcgtgaggctgctgcgtgagcctgtccca
    R S F F Y E E G D I Y P
gtggaggtccggctcctgcacaggacagaccccggYctggtcctgctgctgcaccagtgc
    V E V V R L L L H
tgggccactcccggggccagccctttccagcagcctcagtggcccattctgtctgaaggg
    W A T P G A S P F F Q Q P P Q W P P I I L S S E E
tgtccttttgatggcgacagctacaggacccaactggtagccttggacggggcagagctt
```



```
tccttcccatcccactaccggcgcttcaccgtggccaccttcgccctcctgcaccctggc
    S
tcccagagggccctcaggggatgggtttacttcttctgcagtgcctctgcctgttcccct
    S Q R A L R G W V Y F F F Cllllllllllll
tcggggctggagacctgccccactatgtgcagctctgggccctcgagacagcgacgatcc
```



```
tctgctgcccgcagcactgctgctgggccccagaaccttgtgagctctccagggcccgtg
S A A R S S T A A A G P Q N N L V V S S S P
ggctttgaggattcttacaggcaggagcctgcgctggggcccacaggctcccccaggaac
```



```
1 7 4 1 ~ g t c a a c c a g a g g c c t c t c c t c t g g g t g g t c c t t c t g c t g g c g g c t g t t g c c c t g g t c c t a ~
    V N Q R P L I W V V V I I I A A A V N A I V V I
1 8 0 1 ~ g g g g t c g g t g t t t t c g t g g g c c t g c a c c a a g c c a a g c a c g g a a g c t c c a g g a a g g c c a c a
    601 G V G V F V G I H Q A K H G S S S R K A T
1861 gagggcgaaggggctcaataa
    621 E G E G A Q -
```

Figure 5


## Figure 6

```
atgcggcagctgcagatcatcttgctctgttttcccttgtctcttgcgttgaggggccac
    M R Q L Q I I L L C F P L S L A A L R G H
cctgagcctgaggcaccagattatctgggtgagctccactgtgggctccggagtcttcgg
    P E E P E A P P D Y L L G E L L H
ttcaccgtaaacctgagccaggggacagcgactcctacgctaatagcttgggatgaccac
    F
gggctgccacgcaggctgcagaatgactctggctgtggtacctgggtgacggagggccca
    G L P P R R R L Q N N D S S G Cllllllllllll
ggaagctccatggtgttagaagcctcttatgatggctgctatgtcaccgagtgggtgagg
```



```
acgactcgatcaccagaaatgccaaggccccgtgcgtcaccatcagggggtgtctccccag
    T
gacccccactatatcatgatggttggagttgaaggagcagatgtggctggatgcaacatg
```



```
gttaccaagacacagctgctcaggtgtcctatggatcccccagacccaactttgttatct
V Tlllllllllllllllllllllll
agcttgagttactctcctgatcaaaacagagccctagatgtcccaaatgctgatctgtgt
S L S Y Y S P D Q N N R A L L D V V P
gactttgtcccagtgtgggacaggctgccatgtgttccttcacccatcactgaaggagac
    D F V V P V W I D R L P C C V P P S S P
tgcaagaagattggttgctgctacaattcggaggtgaatttctgttattatggaaacaca
C K K I G C C Y N S E V N F C C Y Y M N N T
gtgacctcacactgtacccaagatggctacttctacatcactgtgtctcgggatgtgacc
V T S H C T Q D G Y F Y Y I T T V S R R D N T
tcgcccccacttctcttgaattctgtgcgcttggccttcgggaatgatgtggaatgtacc
    S P P L L L L N N S V R L L A F F G N N D V V E C T
cctgcgatggcaacacacacttttgccctattctggtttccatttaactcctgtggtacc
    P
acaagacggatcactggagaccaggcagtatatgaaaatgagctggttgcagctagagat
    T R R I T G D Q A V Y E N E L V A A A R D
gttagaacttggagccatggttctatcacccgtgacagtattttcaggctccgagttagc
```



```
tgcagctactctataagtagcaatgccttcccagttaatgtccacgtgtttacatttcca
C S F S I S S N A F F P V V N V F H
ccaccgcattctgagacccagcctggacccctcactctggaactcaagattgccaaggat
P
aagcactatggttccttctacactgttggtgactacccagtggtgaagctacttcgggat
    K H Y G S F Y T V G D Y P V V V K L L L R D
cccatttatgtggaggtctctatccgccacagaacagacccccacctggggctgctcctc
    P I Y V V E V S S I R R H
1 2 0 1 ~ c a t t a c t g t t g g g c c a c a c c c a g c a g a a a c c c a c a g c a t c a g c c c c a g t g g c t c a t g c t a ~
    H Y C W A T P S R R N P Q Q H
1 2 6 1 \text { gtgaaagggtgcccctacactggagacaactatcagacgcagctgattcctgtccagaaa}
    421 V K G C P Y T G D N Y Q T Q L I P V Q K
1 3 2 1 ~ g t c c t g g a t c c t c c a t t t c c a t c t t a c t a c c a g c g c t t c a g c a t t t t t a c c t t c a g c t t t ~
V L D P P P F P S S Y Y Q R R F S S I I F F T F F
atagactcggtgacaaagtgggcactcaggggaccggtgtatctgcactgtagtgcatcc
    I D S V T K W A L R G F P V Y I L H C S S A S
gtctgccagcctgctggaacaccgtcctgtatgataacctgtcctgttgccaggcaaaga
V C Q P A G T P S C C M I T C C P V F A R Q R
agaaactctaacatccattttcacaaccatactgctagcatttctagcaagggtcccatg
R N N S N I I H F H
attctactccaagccactaaagactcaggaaagctccataaatactcaagttttcctgta
I L L L Q A Tllllllllllllllllllll
1 6 2 1 ~ g a c t c t c a a a c t c t g t g g a t g g c a g g c c t t t c t g g g a c c t t a a t c g t t g g a g c c t t g t t a ~
541 D S Q
1 6 8 1 ~ g t g t c c t a c t t a g c t a t c a g g a a a t a g
5 6 1
```


## Figure 7

| Dog | QVSISPRPPPAPVSPSGPCGSSSNHQGYGAPRPAEETFCSY*EERDYPNIR |
| :---: | :---: |
| Fox | FNASSLLLLQVSIFPQPPPAPVSPSGPCGSSSNHRGYGAPRATDETFCSY*EERDYPNIR |
| Dog | LPCKPVPVGVRLLRAQTPVWSCCCTSAGPLPVPAPSSSLSGPSYQTDEWQGMFLLPQGVT |
| Fox | LPCKPVPVGVRLLRAQTPVWSCCCTSAGPLLVPAPSSSLSGPSYQTDEWQGMFLLPQGVT <br>  |
| Dog | PPTSPIPLLPTWPLSFPGVLLTG- |
| Fox | PPTSPIPLLPTWPHSFPGVLLTGTATGPKWYPWTEVSFSSHCQCFTVTTFALPDPGSQRT |

Figure 8


Table 1. Accession numbers for the different carnivore ZP sequences.

| Species | ZP1 | ZP2 | ZP3 | ZP4 |
| :---: | :---: | :---: | :---: | :---: |
| Cat | HQ702466 (Stetson et al. 2015) | U05776, D45067, NM_001009875 (Harris et al. 1994; Jewgenow and Fickel, 1999; Okazaki et al. 2007; Eade et al. 2009) | U05778, D45068, NM_001009330 <br> (Harris et al. 1994, 1995; Okazaki and Sugimoto, 1995; Jewgenow and Fickel, 1999; Eade et al. 2009) | U05777, NM_001009260 (Harris et al. 1994; Jewgenow and Fickel, 1999; Eade et al. 2009) |
| Dog | pseudogene <br> (Goudet et al. 2008) | U05779, NM_001003304, D45069 (Harris et al. 1994, Okazaki et al. 1995) | U05780, NM_001003224, D45070 <br> (Harris et al. 1994, Okazaki and Sugimoto, 1995) | AY573930 (partial) (Blackmore et al. 2004; McLaughlin et al. 2004) |
| Ferret | KX583606* |  | AY702973 (Jackson and Beaton, 2004) |  |
| Fox |  | AY598031 (Beaton and Bradley, 2004) | AY598032 <br> (Reubel et al. 2005) | KF956365* |
| Stoat |  | AY779765 (partial) (Jackson and Beaton, 2004) | AY648050 <br> (Jackson and Beaton, 2004) | AY779766 (Jackson and Beaton, 2004) |
| * This study |  |  |  |  |

Table 2. Accession numbers for the different ZP1 sequences included in the phylogenetic analysis.

| Family | Common name | Scientific name | Accession number |  |
| :--- | :--- | :--- | :--- | :---: |
| Canidae | Dog | Canis lupus | Blast hit chromosom 18 <br> (ENSEMBL 84) |  |
| Canidae | Fox | Vulpes vulpes | This study |  |
| Felidae | Cat | Felis catus | HQ702466 |  |
| Felidae | Cheetah | Acinonyx jubatus | XM_015075436 |  |
| Felidae | Tiger | Panthera tigris | XM_007092010 |  |
| Mustelidae | Ferret | Mustela putorius furo | XM_004770464 |  |
| Odobenidae | Walrus | Odobenus rosmarus | XM_012565789 |  |
| Phocidae | Weddell seal | Leptonychotes weddellii | XM_006743365 |  |
| Otariidae | Antarctic fur seal | Arctocephalus gazella | SRP064853 and Dryad: <br> doi:10.5061/dryad.8kn8c |  |
| Ursidae | Panda | Ailuropoda melanoleuca | XM_002928655 |  |
| Ursidae | Polar bear | Ursus maritimus | XM_008707545 |  |
| OUTGROUPS |  |  |  |  |
| Equidae | Horse | Equus caballus | XM_001493722 |  |
| Pteropodinae | Black flying fox | Pteropus alecto | XM_015588713 |  |
| Rhinoceratidae | White rhinoceros | Cerathotherium simum simum | XM_004437785 |  |
| Vespertilionidae | Natal long-fingered bat | Miniopterus natalensis | XM_016200361 |  |

