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Identification of a Novel *PNMA-MS1* Gene in Marsupials Suggests the LTR Retrotransposon-Derived *PNMA* Genes Evolved Differently in Marsupials and Eutherians

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Abstract

Two major gene families derived from Ty3/Gypsy long terminal repeat (LTR) retrotransposons were recently identified in mammals. The sushi-ichi retrotransposon homologue (*SIRH*) family comprises 12 genes: 11 in eutherians including *Peg10* and *Peg11*/*Rtl1* that have essential roles in the eutherian placenta and 1 that is marsupial specific. Fifteen and 12 genes were reported in the second gene family, para-neoplastic antigen MA (*PNMA*), in humans and mice, respectively, although their biological functions and evolutionary history remain largely unknown. Here, we identified two novel candidate *PNMA* genes, *PNMA-MS1* and *-MS2* in marsupials. Like all eutherian-specific *PNMA* genes, they exhibit the highest homology to a Gypsy12_DR (DR, *Danio rerio*) Gag protein. *PNMA-MS1* is conserved in both Australian and South American marsupial species, the tammar wallaby and grey short-tailed opossum. However, no *PNMA-MS1* orthologue was found in eutherians, monotremes or non-mammalian vertebrates. *PNMA-MS1* was expressed in the ovary, mammary gland and brain during development and growth in the tammar, suggesting that *PNMA-MS1* may have acquired a marsupial-specific function. However, *PNMA-MS2* seems to be a pseudogene. The absence of marsupial orthologues of eutherian *PNMA* genes suggests that the retrotransposition events of the Gypsy12_DR-related retrotransposons that gave rise to the *PNMA* family occurred after the divergence of marsupials and eutherians.

Key words: LTR retrotransposons; *PNMA* family; marsupial-specific genes; mammalian evolution

1. Introduction

Approximately 40–50% of the mammalian genome is derived from transposable elements, such as retrotransposons and DNA transposons.[1–5] The Ty3/Gypsy long terminal repeat (LTR) retrotransposons have been detected in various eukaryotic organisms including fungi, plants, insects, tunicates and echinoderms as well as in several vertebrates, such as fish, amphibians and reptiles, but not in mammals and birds.[6] However, discrete regions within these elements have acquired new functions as novel endogenous genes and are highly conserved in marsupials and eutherians.[7–12] Two major gene families derived from

the Ty3/Gypsy LTR retrotransposons are the sushi-ichi retrotransposon homologue (*SIRH*) family (also called the *MART* or *SUSHI* family) comprising 12 genes encoding a Gag-like protein, each of which has 20–30% similarity to the sushi-ichi retrotransposon Gag in pufferfish (*Takifugu rubripes*),[9–11] and the para-neoplastic antigen MA (*PNMA*) family also encoding the Gag-like protein homologous to the Gypsy12_DR retrotransposon Gag in zebrafish (DR, *Danio rerio*)[13] comprising 15 and 11 genes in humans and mice, respectively. It should be noted that the homology between these two LTR retrotransposons is only 6.5% and 13.6% along with the entire Gag and Pol regions, respectively. *PEG10/SIRH1* is a therian-specific gene, and *PEG11/SIHR2* and the remaining *SIRH3–11* seem eutherian specific, while *SIRH12* was derived from a marsupial-specific retrotransposition event. We previously demonstrated that *Peg10/Sirh1* and *Peg11/Sirh2* are essential for placental formation and function in mice.[7,8] Most *PNMA* genes are expressed in the brains of macaques and mice and their functions remain unknown.[14] *PNMA1–3* were first identified as genes encoding neuronal auto-antigens using sera from patients with para-neoplastic neurological syndromes.[15] Schüller *et al.*[16] and Campillos *et al.*[13] performed genome-wide analyses and identified additional 12 family genes in humans among which *PNMA6* has no mouse orthologue. No Gypsy12_DR Gag-derived sequences were reported in birds,[13] and thus, it is probable that the *PNMA* genes are also mammal specific. However, the search has been limited in several eutherian species and the existence of marsupial orthologues and/or marsupial-specific *PNMA* genes remained unknown.

Here, we conducted comprehensive *in silico* screening for the *PNMA* genes using the whole-genome shotgun (WGS) sequences of the grey short-tailed opossum[4] and the tammar wallaby[5] and identified a novel *PNMAMS1* gene as the first marsupial-specific *PNMA* gene.

2. Materials and methods

2.1. Animals and tissue collection

Tammar wallabies (*Macropus eugenii*) of Kangaroo Island, South Australia origin, were maintained in The University of Melbourne marsupial breeding colony in grassy outdoor enclosures. Lucerne cubes, grass and water were provided *ad libitum* and supplemented with fresh vegetables. The day of birth of pouch young was designated as d0. When the day of birth was unknown, their age was estimated using the head length.[17] Foetal tissues including the head and body were collected from two foetuses at Day 23 and 26 of gestation, and the yolk sac placenta (YSP) from four foetuses sampled between Day 23 and 26 of gestation. Tissues including the brain, liver, lung, kidney, ovary and testis were collected from two pouch young aged Day 60–70 after birth. The liver, lung, pancreas, stomach, bladder, heart, kidney, adrenal, spleen and brain (cerebrum and cerebellum) were collected from Day 152 and 162 pouch young. Adult female tissues, including the brain (thalamus, hypothalamus and pituitary), ovary (ovary with active corpus luteum, corpus luteum, ovary with developing follicle and ovary with primary or secondary follicle), endometrium (gravid endometrium and non-gravid endometrium) and mammary gland (sucked gland and non-sucked gland) were also collected from two adults. Grey short-tailed opossums (*Monodelphis domestica*) were purchased from a breeding colony in the Department of Physiology at the University of Melbourne. The brain, liver, spleen, pituitary and ovary were collected from five adult opossums. Experimental procedures conformed to the Australian National Health and Medical Research Council guidelines[18] and were approved by the Animal Experimentation Ethics Committees of the University of Melbourne.

2.2. Reverse transcriptase polymerase chain reaction

Genomic DNA and total RNA from tissues were prepared by using TRIZOL (Invitrogen), as described in the manufacturer's protocol. cDNA was synthesized from 1 μg of total RNA using Superscript III reverse transcriptase (Invitrogen) with an oligo dT primer. Polymerase chain reaction (PCR) amplification for gene expression profiles were carried out using 10–100 ng of cDNA in a 25-μl reaction mixture containing 1 × *ExTaq* buffer, 2.5 mM deoxynucleotide triphosphasteses, 10 pmol primers and 1.25 U *ExTaq* HS (TaKaRa) and were subjected to 30–35 PCR cycles; 96°C for 15 s, 60–65°C for 30 s and 72°C for 15–120 s depending on the length of PCR products at the ratio of 1 min/kb. PCR products were visualized by agarose gel electrophoresis with ethidium bromide staining. The primers used for the expression profiles were as follows: *PNMAMS1*-F1 (5′-AAC ATG GTG GAG GAG TCT GGA T-3′), *PNMAMS1*-R1 (5′-CAA CGG TAA GGT GAC CTC TTG G-3′), *wGAPDH*-F1 (5′-AGA AAG TGG TGA AGC AGG CAT-3′), *wGAPDH*-R1 (5′-TGG AGG ACA TGT AGA CCA TGA G-3′), *wGAPDH*-F2 (5′-CCT ACT CCA ATG TAT CTG TGT-3′), *wGAPDH*-R2 (5′-GGT GGA ACT CCT TTT TTG ACT G-3′), *LAMA3*-F1 (5′-ACT CTG CAA AGA TCA GCA CAC C-3′), *LAMA3*-R1 (5′-CTC CTG CCT TCA GCA AGA AGA T-3′); *PNMAMS2*-F1 (5′-GGC TAA TGG AAA GTC ATA AGA AAG C-3′), *PNMAMS2*-R1 (5′-GAT TCC TTG ATA CAA ATG GTT GTC C-3′), *PNMAMS2*-F2 (5′-TTG ATG CAT TGT CTG AAA CCA G-3′), *PNMAMS2*-R2 (5′-ATC TAT CAA CCA AGC GCC AAC T-3′); *oOAZ1*-F1 (5′-ATA AAC CCA GCA CCA CCG TCC ACG-3′), *oOAZ1*-R1 (5′-GGT CTC ACA ATC TCA AAG CCC AAA AAG-3′).

2.3. 5′- and 3′-RACE

Rapid amplification of cDNA ends (RACE) reactions were performed with the tammar liver using the RNA SMARTER RACE cDNA Amplification kit (Clontech) according to the manufacturer's recommendations. The 5′- and 3′-RACE fragments were generated with the following gene-specific primers: *PNMAMS1*-5′RACE-GSP1 (5′-TGC GTA TGG AGG GGA GAG TGA GCA AG-3′) and *PNMAMS1*-3′RACE-GSP1 (5′-GAC TGT GCC ATC GGG AGA AGG TGA AC-3′), and nested PCR was performed with following primers: *PNMAMS1*-5′RACE-GSP2 (5′-CAG ACA AGG TGG GGT CTG TCT CTT C-3′) and *PNMAMS1*-3′-RACE-GSP2 (5′-TTC CTG TGA AGG TCT CCC TCT C-3′), respectively.

2.4. Detection and prediction of the Gypsy12_DR Gag-derived genes

For the detection of *PNMA* family genes, we performed TBLASTN searches (*e*-value $<1.0E-9$) using the NCBI server (http://blast.ncbi.nlm.nih.gov/Blast.cgi) against eutherian reference genomic sequences and marsupial WGS sequences using the Gypsy12-I_DR Gag protein sequence from Repbase (http://www.girinst.org/) as a query . After TBLASTN searches, sequences that encoded open reading frames (ORFs) with >100 aa (amino acids) were selected for the next analysis. Secondary screening was performed with all the sequences that were selected by first screening as a query. In addition, only sequences encoding proteins with >100 aa were considered to be candidate *PNMA* family genes and those with <100 aa were considered as *PNMA* pseudogenes. Genome resources used were: *Homo sapiens* (GRCh37.p5), *Mus musculus* (MGSCv37), *M. eugenii* (Meug_1.1) and *M. domestica* (MonDom5). ORF prediction was performed using an ORF finder (http://www.ncbi.nlm.nih.gov/gorf/gorf.html).

2.5. Multiple alignment and phylogenetic tree

PNMA family genes and retrotransposons from Repbase were aligned using the MEGA 5.0 (Molecular Evolutionary Genetics Analysis). Phylogenetic tree analysis was also performed using the MEGA 5.0. The tree was inferred using the neighbour-joining method with the bootstrap test (1000 replicates). The evolutionary distances were computed using the *p*-distance method and are in the units of the number of amino acid differences per site. All ambiguous positions were removed for each sequence pair.

2.6. Comparative genomic analysis

For comparison of the marsupial *PNMA-MS1* and *-MS2* genomic regions with the corresponding regions in eutherian species, we extracted the following sequences from Ensembl (http://www.ensembl.org); *PNMA-MS1*; *M. eugenii* (GeneScaffold: Meug_1.0: 503: 24 720–39 177), *M. domestica* (Chromosome: MonDom5: 3: 260 858 116–260 881 268), *H. sapiens* (Chromosome: GRCh37: 18: 21 343 369–21 355 887), *M. musculus* (Chromosome: GRCm37: 18: 12 572 248–12 578 437), *Ornithorhynchus anatinus* (Chromosome: OANA5: 7: 17 676 195–17 684 806), *Gallus gallus* (Chromosome: WASHUC2: 2: 106 303 674–106 308 473), *Xenopus tropicalis* (Scaffold: JGI4.1: 84: 2 861 161–2 864 246), *T. rubripes* (Scaffold: FUGU4: 285: 98 142–99 106) and for *PNMA-MS2*; *M. domestica* (Chromosome: MonDom5: 1: 416 106 001–416 736 671), Tasmanian devil *Sarcophilus harrisii* (Scaffold: DEVIL_7.0: GL834637.1: 1–311 016), *H. sapiens* (Chromosome: GRCh37: 9: 125 122 856–125 594 315), *M. musculus* (Chromosome: GRCm37: 2: 36 078 175–37 218 455), *O. anatinus* (Chromosome: OANA5 : Ultra70 : 222 463–282 938), *G. gallus* (Chromosome: WASHUC2: 17: 9 467 383–9 508 331), *X. tropicalis* (Scaffold: JGI_4.2: GL173356.1: 228 227–292 347) and *T. rubripes* (Scaffold: FUGU4: scaffold_49: 144 872–154 417).

Alignments were obtained using the VISTA Web server (http://genome.lbl.gov/vista/). *PNMA-MS1* syntenic regions of several species identified above were aligned using the default setting ($>70\%$ identity and >100 bp in length) of mVISTA using the LAGAN global multiple alignment option.

3. Results

3.1. Novel candidate PNMA genes in humans and mice

We validated our approach to search for candidate *PNMA* genes in marsupials by performing TBLASTN analysis against human and mouse reference genomic sequences using the Gypsy12_DR Gag protein as a query. With a cut-off *e*-value of $<1.0E-9$, this screening resulted in 19 and 15 candidates in the human and mouse genomes, respectively. In humans, 15 of the 19 were known *PNMA* genes and the remaining 4 were novel putative *PNMA* genes, *PNMA7/LOC649201*, *PNMA8/LOC649238*, *PNMA9/LOC100128960* and *PNMA16* (Table 1, Humans). In mice, 12 of the 15 were known, with two novel putative *PNMA* genes, *Pnma7/Gm7028* and *Pnma9/Gm6858*, and one pseudogene, *Gm 1832215* identified (Table 1, Mouse).

The putative human *PNMA7–9* genes were located near *PNMA6A–D* cluster on Chromosome Xq28. There is a sequence gap between *PNMA6A–B* and *6C–D*, so additional *PNMA* genes may exist in this region (Supplementary Fig. S1). The high homology (47–57%) between the putative amino acid sequences of the *PNMA7–9* and *PNMA6A–D* genes suggested that they share a common ancestor and evolved by gene duplication (see Fig. 3). The putative murine *Pnma7*, *8* and

Table 1. Candidate list for PNMA family genes in two eutherian and two marsupial species

	PNMA number	Gene name	Accession number	Location
Human	hsPNMA1	PNMA1	NM_006029.4	chr.14:74178486-74181128
	hsPNMA2	PNMA2	NM_007257.5	chr.8:26362196-26371483
	hsPNMA3	PNMA3	NM_013364.4	chr.X:152224766-152228827
	hsPNMA4	PNMA4	NM_022151.4	chr.14:93648541-93651249
	hsPNMA5	PNMA5	NM_052926.2	chr.X:152157368-152162671
	hsPNMA6A	PNMA6A	NM_032882.4	chr.X:152338301-152340107
	hsPNMA6B	PNMA6B	XM_002343859.2	chr.X:152341614-152342813
	hsPNMA6D	PNMA6D	XM_002343858.2	chr.X:152244152-152246070
	hsPNMA6C	PNMA6C	NM_001170944.1	chr.X:152240819-152243402
	hsPNMA7	LOC649201	XP_001127211	chr.X:152584221-152587591
	hsPNMA8	LOC649238	XM_938309.4	chr.X:152662364-152663269
	hsPNMA9	LOC100128960	—	chr.X:152197130-152200901
	hsPNMA10	ZCCHC12	NM_173798.2	chr.X:117957787-117960931
	hsPNMA11	ZCCHC18	NM_001143978.1	chr.X:103357107-103360533
	hsPNMA12	PNMAL1	NM_001103149.1	chr.19:46969748-46974820
	hsPNMA13	PNMAL2	NM_020709.1	chr.19:46994448-46999169
	hsPNMA14	CCDC8	NM_032040.3	chr.19:46913586-46916919
	hsPNMA15	—	—	chr.19:46931182-46931595
	hsPNMA16	—	—	chr.19:47036933-47037357
Mouse	mmPNMA1	Pnma1	NM_027438.3	chr.12:85487081-85489439
	mmPNMA2	Pnma2	NM_175498.4	chr.14:67530045-67538898
	mmPNMA3	Pnma3	NM_153169.2	chr.X:70310126-70313530
	mmPNMA4	Pnma4	NM_001142937.1	chr.12:103978040-103981870
	mmPNMA5	Pnma5	NM_001100461.3	chr.X:70279327-70282442
	mmPNMA7	Gm7028	NG_005480.3	chr.X;70580917-70581762
	mmPNMA8	LOC100416956	NG_017874	chr.X:70642228-70644051
	mmPNMA9	Gm6858	NG_005479.2	chr.X:70295221-70295900
	mmPNMA10	Zcchc12	NM_028325.3	chr.X:33735899-33739153
	mmPNMA11	Zcchc18	NM_001035509.1	chr.X:133527694-133531462
	mmPNMA12	PNMAL1	NM_001007569.1	chr.7:17545144-17547669
	mmPNMA13	PNMAL2	NM_001099636.2	chr.7:17530031-17532427
	mmPNMA14	CCDC8	NM_001101535.1	chr.7:17579937-17581994
	mmPNMA15	—	—	chr.7:17568964-17569311
	mmPNMA pseudo1	Gm18322	NC_000084.5	chr.18:57308641-57309445
Tammar	mePNMA-MS1	mePNMA-MS1	—	GeneScaffold_503:27168-31803
	mePNMA pseudo1	—	—	Scaffold94060:2914-6134
	mePNMA pseudo2	—	—	Scaffold1032:54408-58815
	mePNMA pseudo3	—	—	Scaffold385831:1-1432
	mePNMA pseudo4	—	—	Scaffold57604:6970-11278
	mePNMA pseudo5	—	—	Scaffold428007:1-986
	mePNMA pseudo6	—	—	Scaffold1439:20136-24450
	mePNMA pseudo7	—	—	Scaffold391804:1-1797
	mePNMA pseudo8	—	—	Scaffold46963:6594-10851
	mePNMA pseudo9	—	—	Scaffold3242:41001-45246
	mePNMA pseudo10	—	—	Scaffold407990:1-2479
	mePNMA pseudo11	—	—	Scaffold799:60812-65099
	mePNMA pseudo12	—	—	Scaffold492911:1-878
	mePNMA pseudo13	—	—	Scaffold111753:1-2597
	mePNMA pseudo14	—	—	Scaffold92201:2820-7152
	mePNMA pseudo15	—	—	Scaffold9921:21555-26131
	mePNMA pseudo16	—	—	Scaffold1103:4422-8826
	mePNMA pseudo17	—	—	Scaffold27816:17763-21999
	mePNMA pseudo18	—	—	Scaffold134268:3226-6573
	mePNMA pseudo19	—	—	GeneScaffold_10085:47646-51858
Opossum	mdPNMA-MS1	mdPNMA-MS1	—	chr.3:260874625-260879998
	mdPNMA-MS2	mdPNMA-MS2	—	chr.1:416409687-416414127
	mdPNMA pseudo1	—	—	chr.3:15383915-15388463
	mdPNMA pseudo2	—	—	chr.3:239729898-239734143
	mdPNMA pseudo3	—	—	chr.1:692451545-692456282
	mdPNMA pseudo4	—	—	chr.1:451204818-451209222
	mdPNMA pseudo5	—	—	chr.1:331217342-331221920
	mdPNMA pseudo6	—	—	chr.1:342376567-342381307
	mdPNMA pseudo7	—	—	chr.X:6503247-6507903
	mdPNMA pseudo8	—	—	chr.2:529194963-529199310

Continued

Table 1. Continued

PNMA number	Gene name	Accession number	Location
mdPNMA pseudo9	—	—	chr.2:271702858-271707121
mdPNMA pseudo10	—	—	chr.5:205686598-205690882
mdPNMA pseudo11	—	—	chr.5:229359947-229364330
mdPNMA pseudo12	—	—	chr.6:103527713-103532099

Candidates in humans, mouse, tammar wallaby and opossum. Newly identified *PNMA* family genes in this study are coloured in grey. 'Pseudo' denotes putative ORFs from sequences detected by TBLASTN, which encode <100 aa.

9 are all located in the orthologous region on the X chromosome. However, the *PNMA6* cluster is absent from the mouse genome (Supplementary Fig. S1). This region is occupied by the X-linked leucocyte-regulated complex (*Xlr*) gene cluster.

3.2. *Identification of novel PNMA genes in marsupials*

A comprehensive search of the tammar wallaby (Meug_1.1) and opossum WGS (MonDom5) for *PNMA* genes was then undertaken using the same method as the human and mouse above. Twenty and 14 hits were returned for TBLASTN searches of the tammar and opossum genomes, respectively (Table 1, Tammar wallaby and Opossum). However, most of the sequences were predicted to be pseudogenes or remnants of the original retrotransposons (<100 aa). Only ORFs predicted to encode >100 aa were considered to be marsupial *PNMA* candidate genes. One candidate exhibited the highest homology to the Gypsy12_DR Gag protein along with matrix (MA), N- and C-terminal parts of capsid like (N- and C-CA) and cys-cys-his-cys (CCHC) zinc finger domains and had a putative ORF consisting of 456 and 458 aa in the tammar and opossum, respectively (Fig. 1). Therefore, we named it *PNMA-MS1* as a novel marsupial-specific *PNMA* gene. The marsupial *PNMA-MS1* gene was located on a syntenic segment in the tammar (Gene scaffold_503:27168-31803) and the opossum (Chr.3: 260 874 625–260 879 998). A second *PNMA* candidate was identified in the opossum, *PNMA-MS2*, that had a putative ORF encoding 112 aa with high homology only to a central part of the capsid-like domain of the Gypsy12_DR Gag. It was located on Chromosome 1: 416 409 687–416 414 127, where an olfactory receptor (OR) gene cluster exists (see below). The presence of *PNMA-MS2* in the tammar was inconclusive due to the incomplete assembly of the corresponding region of the genome.

3.3. *Genomic structure of PNMA-MS1 in the tammar wallaby*

The full-length sequence of tammar *PNMA-MS1* consisting of 4290 bp was determined by 5′- and 3′-RACE. It has two exons and encodes a putative ORF encoding a

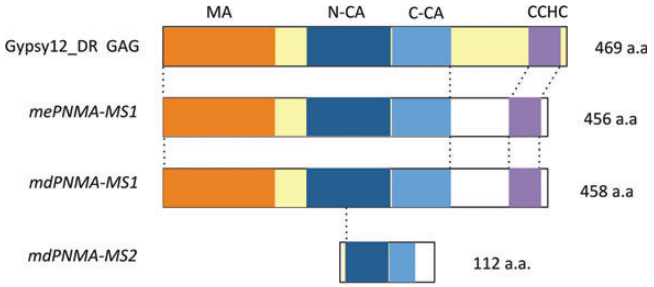

Figure 1. *PNMA-MS1* and *-MS2* have high homology to the Gypsy12_DR retrotransposon Gag protein. Boxes represent ORFs. Regions with significant similarity to a Gag protein of a Gypsy12_DR retrotransposon are shown in colours. *PNMA-MS1* encodes a Gag-like protein including several typical domains and motifs, but lacks a Pol-like protein and LTR sequences attached to either end of the retrotransposons. Although *PNMA-MS2* has a possible protein-coding frame corresponding to a central part of the capsid-like domain of the Gypsy12_DR Gag, it seems to be a pseudogene because no expression was confirmed. MA: matrix domain; N-CA: an N-terminal part of capsid-like domain; C-CA: a C-terminal part of capsid-like domain; CCHC: a CCHC zinc finger motif for RNA-binding site; RT: reverse transcriptase domain; RNaseH: RNase H domain; INT: integrase domain, *me*: *M. eugenii* (tammar wallaby); *md*: *M. domestica* (grey short-tailed opossum).

Figure 2. Genomic structure of full-length tammar wallaby *PNMA-MS1*. An arrow represents the direction of *PNMA-MS1* transcription. UTR and ORF are indicated by light blue and dark blue boxes, respectively. There are no supporting data that the promoter of tammar PNMA-MS1 was derived from an LTR sequence of the original retrotransposon. UTR: untranslated region; ORF: open reading frame.

456 aa sequence (Fig. 2). The PNMA-MS1 putative ORF shared 28% similarity at the amino acid level with the Gag protein of Gypsy12_DR retrotransposon (Fig. 3A). Multiple alignment and phylogenetic tree analyses of the putative PNMA-MS1 and -MS2 amino acid sequences are shown in Fig. 3A and B. The Pol protein and LTR regions are absent from PNMA-MS1 and -MS2, suggesting that they no longer have retrotranspositional activity (Fig. 3A). The marsupial PNMA-MS1 and -MS2 protein sequences were grouped together and

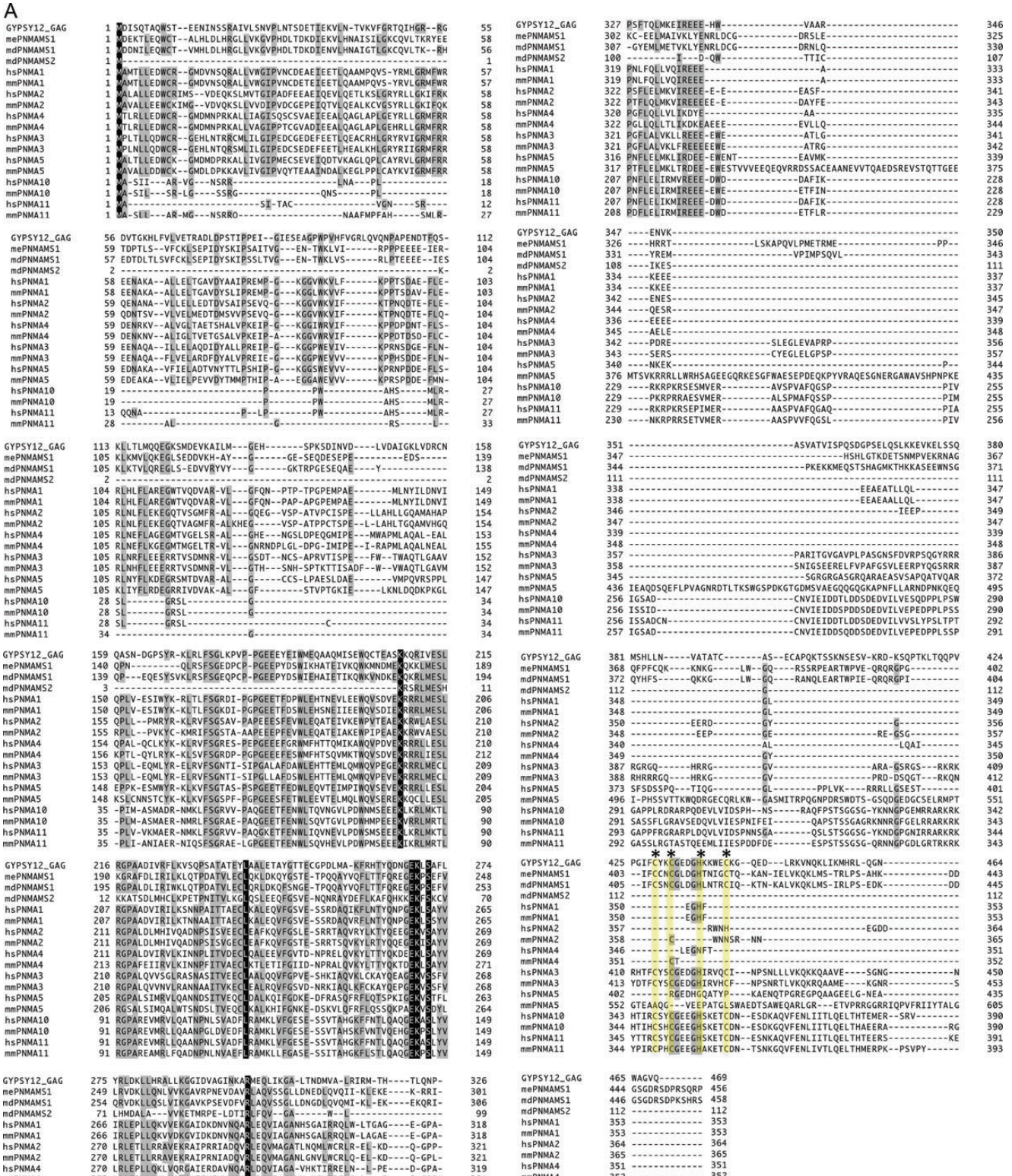

Figure 3. Multiple sequence alignment and phylogenetic tree of the *PNMA* family. (A) Multiple sequence alignment of the amino acid sequence of the Gag-like regions of marsupial *PNMA-MS1*, the human and mouse *PNMA* genes and Gypsy1 2_I_DR Gag. An evolutionarily conserved Gag-derived CX2CX4HX4C zinc finger motif is indicated by yellow shading. Residues conserved in all sequences are shaded black and highly conserved ones in grey. (B) A phylogenetic tree of *PNMA* family genes was constructed by the neighbour-joining method using the multiple alignment shown in Fig. 2. Bootstrap support (%) is shown for branches. *hs*: human:; *mm*: mouse; *md*: opossum; *me*: wallaby.

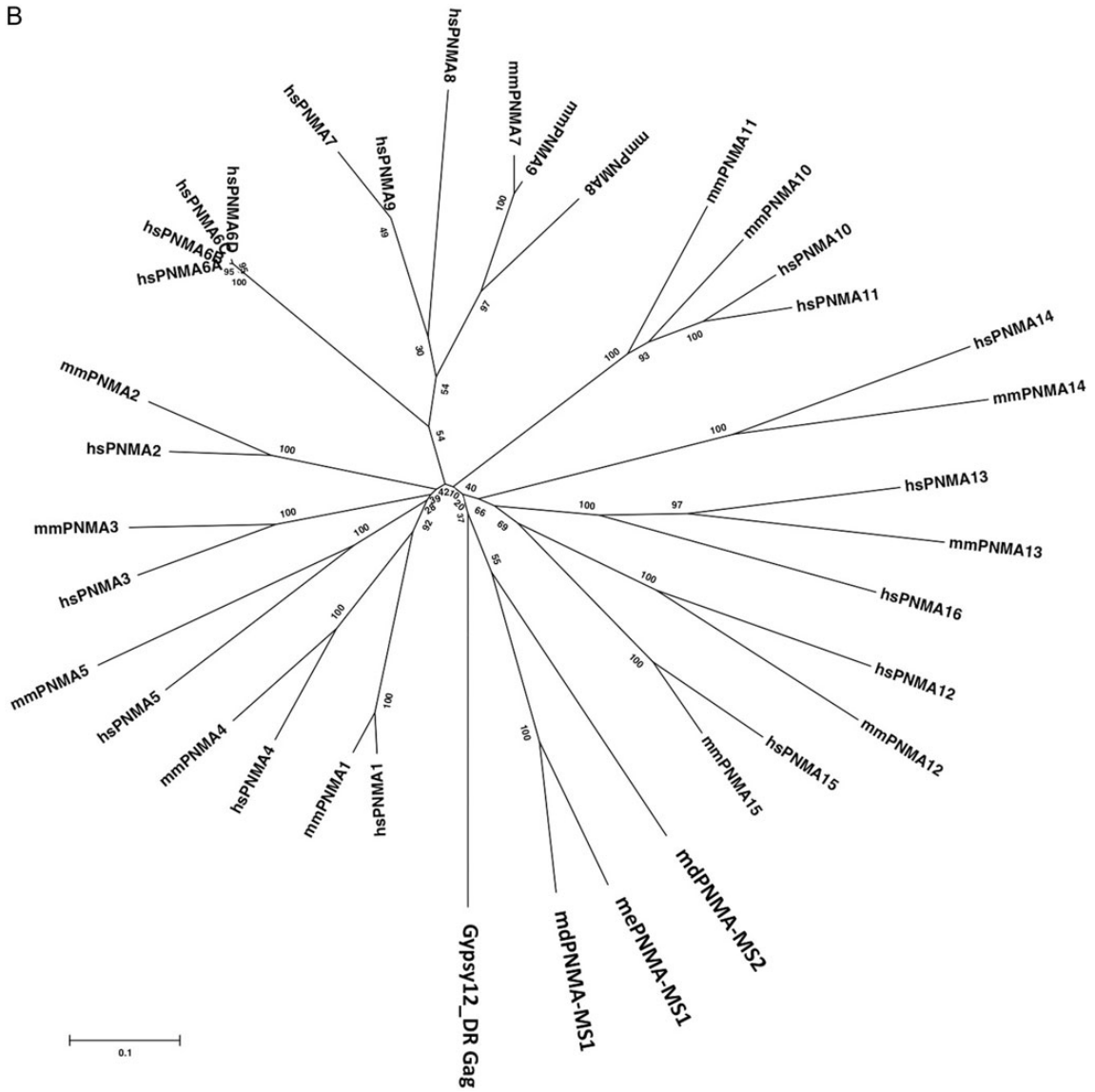

Figure 3. *Continued*

more closely related to the zebrafish Gypsy12_DR Gag than to the mouse and human proteins (Fig. 3B).

3.4. *Comparative genomic analysis of PNMA-MS1 and -MS2*

To elucidate whether *PNMA-MS1* is a marsupial-specific *PNMA* gene, comparative genomic analysis was performed using the VISTA tool with several vertebrate genomic sequences. *PNMA-MS1* was located in the intron 8 of the laminin alpha 3 (*LAMA3*) gene that is highly conserved in vertebrates. No *PNMA-MS1* orthologue was found in the syntenic region of any eutherian species, platypus (monotreme mammals), chicken (birds), frog (amphibian) and fugu (fish), demonstrating that *PNMA-MS1* is marsupial specific (Fig. 4A). It indicates that *PNMA-MS1* retrotransposition occurred only in the marsupial lineage after their divergence from eutherians (Fig. 5).

PNMA-MS2 was located between an *OR1Q1* gene and an *OR1J2*-like pseudogene (*ENSMODG00000019710*) that lies 12-kb upstream of the former, in an OR gene cluster located between prostaglandin-endoperoxide synthase 1 (*PTGS1*) and phosducin-like (*PDCL*) genes[19,20] on opossum Chromosome 1. At present, we cannot confirm the presence or absence of *PNMA-MS2* in the tammar because the corresponding regions encompassing the *PTGS1* and *PDCL* genes are yet to be completely assembled. Recently, another Australian marsupial genome of the Tasmanian devil has been sequenced, and the region syntenic to that between opossum *OR1N2* and *PDCL* became available.

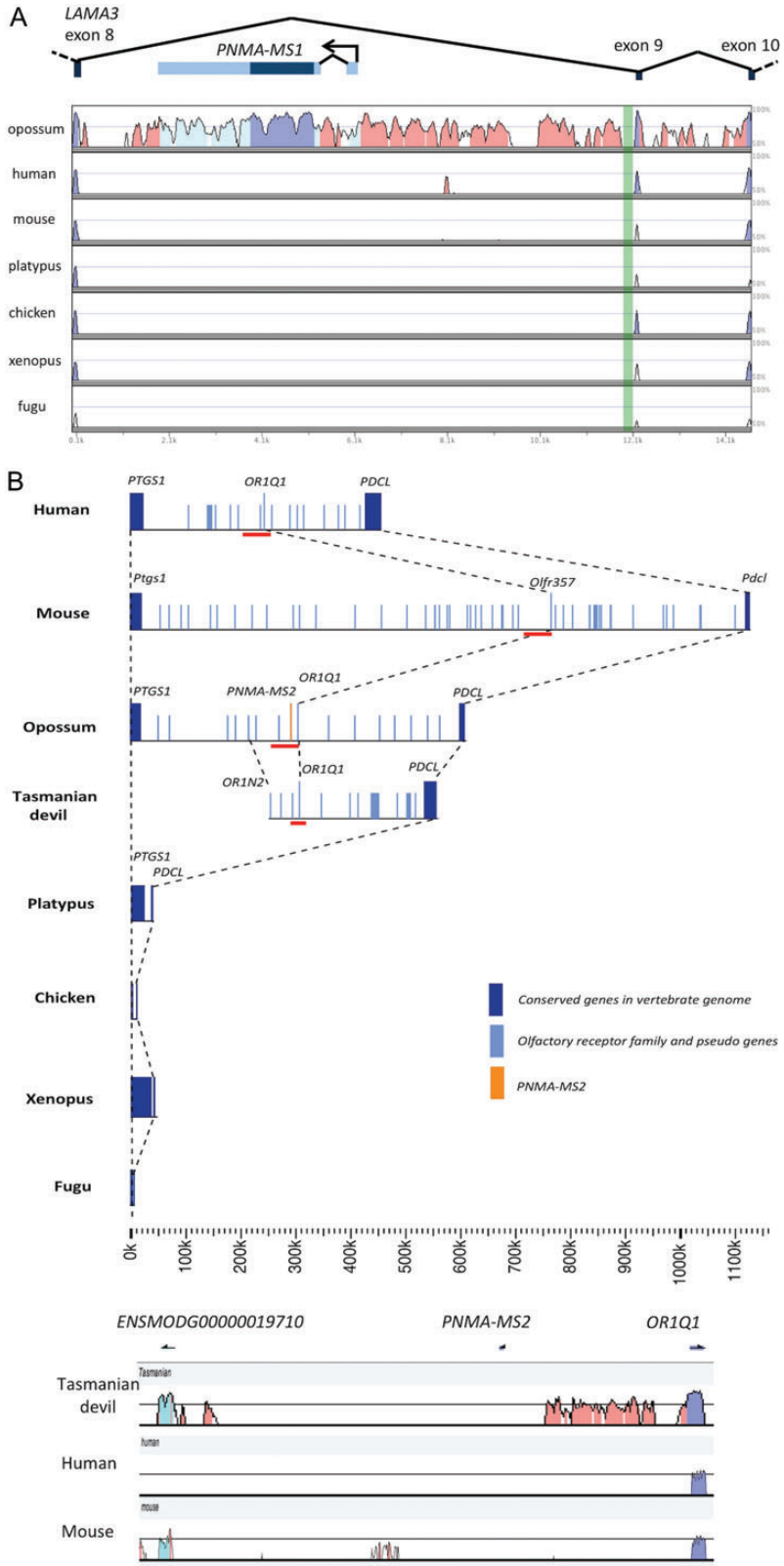

Figure 4. Comparative genomic analysis of the *PNMA-MS1* and *-MS2* regions in vertebrates. (A) *PNMA-MS1*. mLAGAN alignment of the tammar wallaby, opossum, human, mouse, platypus, chicken, frog and fugu *LAMA3* exons 8–10 region produced by mVISTA using the tammar sequence as the basis for comparison. Default parameters for mVISTA were used (conservation level, 70%, 100 bp window). Conserved regions appear as peaks highlighted in pink (>70% identity). Where these regions coincide with ORF sequences of *PNMA-MS1* or *LAMA3*, the peaks are shaded in purple. Where these regions coincide with the UTR region of *PNMA-MS1*, the peaks are shaded in light blue. The

It contains some gaps but none between opossum *OR1Q1* and *ENSMODG00000019710* (*OR1J2*-like pseudogene). A search of this region clearly demonstrated that the *PNMA-MS2* orthologue is absent from the Tasmanian devil genome.

The syntenic OR cluster lies between *PTGS1* and *PDCL* in the human Chromosome 9 and mouse Chromosome 2, respectively, but neither the number nor the order of OR genes and pseudogenes are conserved. As the human and mouse genome sequences in this region are complete and contain no gaps, the absence of the *PNMA-MS2* orthologue was confirmed (Fig. 4B). For the platypus, the *PTGS1* and *PDCL* genes are located next to each other, with no OR gene cluster and no *PNMA-MS2* orthologue, like in the chicken and fugu (Fig. 4B).

These results suggest that the integration of selected OR genes occurred between the *PTGS1* and *PDCL* genes in a common therian ancestor, and that the opossum-specific insertion of *PNMA-MS2* occurred after the divergence of eutherians and marsupials and the geographic separation of Australian and South American marsupials (Fig. 5). However, the possibility that the *PNMA-MS2* orthologue exists in some of Australian marsupial species cannot be excluded. It is possible that *PNMA-MS2* was deleted from Australian marsupial species after integration in a common marsupial ancestor (Fig. 5).

3.5. *Expressions of PNMA-MS1 in the tammar wallaby and PNMA-MS2 in the opossum*

PNMA-MS1 expression was investigated in several tissues in four different stages of the tammar wallaby, including foetal and pouch young stages. Human *LAMA3* is expressed ubiquitously (EST profile Hs.436367). To exclude the possibility that heterogenous nuclear RNA (hnRNA) was detected between exons 8 and 9 of the *LAMA3* gene rather than *PNMA-MS1*, we amplified *PNMA-MS1* using PCR primers designed within exons 1 and 2, respectively. Thus, the PCR product was shorter than its genomic sequence corresponding to hnRNAs of *LAMA3* and *PNMA-MS1*. *LAMA3* expression was analysed using primers designed to exons 79 and 81, near the 3′-UTR, due to the poor genome sequence quality in introns 84–90 of tammar *LAMA3*. Tammar *LAMA3* expression was almost ubiquitous, with the exception of several pouch young tissues.

From Day 23 to 26 pregnancy, *PNMA-MS1* expression was detected in the foetal head and body, but there was no expression in the YSP (Fig. 6A). In pouch young aged Day 60–70, *PNMA-MS1* was detected only in the brain, kidney and ovary, but not in the liver, lung or testis (Fig. 6B). In Day 152 and 162 pouch young, changes in *PNMA-MS1* expression were minimal, with expression detected in the kidney, liver, pancreas, heart, spleen and stomach, but not in the lung, bladder, adrenal, cerebrum or cerebellum (Fig. 6C). In the adult female, the brain (thalamus, hypothalamus and pituitary), ovary (ovary with active corpus luteum, corpus luteum alone, ovary with enlarged developing follicle and ovary with primary or secondary follicles), endometrium (gravid endometrium and non-gravid endometrium) and mammary gland (sucked gland and non-sucked gland) were examined. *PNMA-MS1* expression was detected in the ovary (all four stages), mammary gland (sucked and non-sucked) and thalamus, but not in the hypothalamus or pituitary (Fig. 6D). There was no expression in either the gravid, or non-gravid, endometrium.

PNMA-MS2 expression was analysed in five tissues, the brain, liver, spleen, pituitary and ovary, using three primer sets designed in the putative coding frame. However, there was no expression in these tissues, suggesting that *PNMA-MS2* is not active in the opossum (data not shown). Although we cannot exclude the possibility that it may be expressed in a stage or tissue-specific manner, we conclude that *PNMA-MS2* is a pseudogene.

4. Discussion

4.1. PNMA-MS1 *is a marsupial-specific* PNMA *gene*

In this study, we have identified *PNMA-MS1* as a novel Ty3/Gypsy LTR retrotransposon-derived gene. Comparative genomic analysis showed that *PNMA-MS1* was present only in the marsupial lineage and was absent in the eutherian and monotreme mammals and in the non-mammalian vertebrates. *PEG10/SIRH1* and *SIRH12* are the only Ty3/Gypsy LTR retrotransposon-derived genes (derived from sushi-ichi-related retrotranposons) reported in marsupials so far.[11,21] Therefore, the *PNMA-MS1*, which is also a Ty3/gypsy LTR retrotransposon-derived gene, is the first and only member of the *PNMA* gene family in the marsupials.

The sushi-ichi-related retrotranposon that gave rise to the *SIRH* family was probably active around the

tammar genome sequence has a gap of about 200 bp that located at the 5′-side of exon 9 (shown by a green bar). (B) The region from *PTGS1* to *PDCL* in the opossum, human, mouse, platypus, chicken, frog and fugu genomes is shown (upper). *PNMA-MS2* is located between the *OR1Q1* gene and an *OR1J2*-like pseudgene (*ENSMODG00000019710*) in the opossum (red bar), but is absent in the Tasmanian devil, human and mouse genomes (red bars indicate the equivalent region in these species. An mVISTA alignment of the *OR1Q1-ENSMODG00000019710* region in the opossum (lower) confirms that *PNMA-MS2* is not present in the Tasmanian devil, human or mouse.

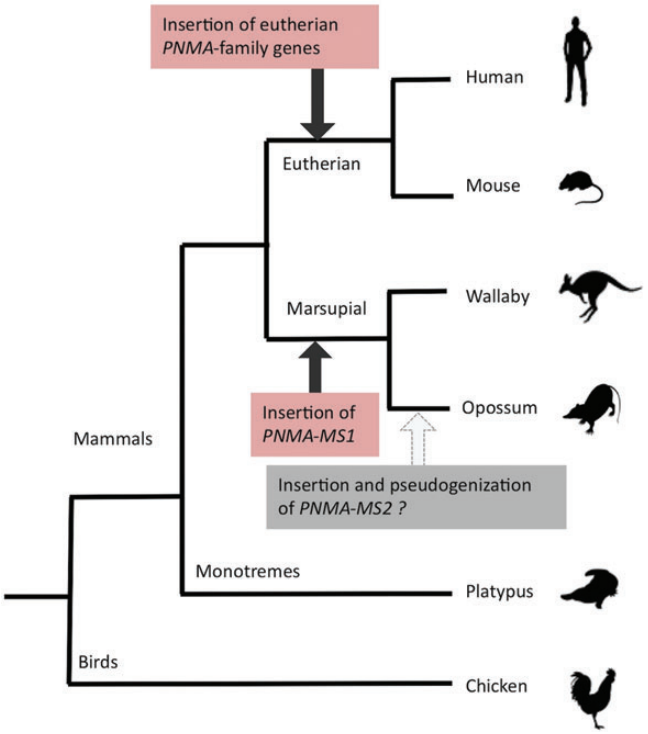

Figure 5. Evolutionary pathway of the *PNMA* family in mammals. *PNMA-MS1* insertion occurred in a marsupial ancestor prior to the radiation of marsupial species. *PNMA-MS2* was only found in the opossum and not in the Tasmanian devil, human and mouse, which suggests that *PNMA-MS2* was acquired only in the opossum lineage after the divergence of the Australian and South American marsupials, but it does not show active transcription. The insertion of eutherian *PNMA* family genes occurred in a eutherian ancestor prior to the radiation of eutherian species. There are no *PNMA* family genes (or pseudogenes) in the platypus (monotremes) and chicken (birds).

time of the divergence between marsupials and eutherians, because *PEG10/SIRH1* is conserved between the eutherians and marsupials,[21] while *SIRH3–11* seems to be eutherian-specific and *SIRH12* evolved from a marsupial-specific retrotransposition event.[11] We did not detect any orthologues of *PNMA-MS1* or *-MS2* in the eutherian genome, nor any orthologues of eutherian *PNMA1–16* genes in the marsupial genomes (data not shown). Due to many sequence gaps in the tammar wallaby, Tasmanian devil and opossum genomes, we cannot exclude the possibility that some marsupial orthologues of eutherian *PNMA* genes exist in such gap regions. Thus, it is possible that some retrotransposition events of Gypsy12_DR-related retrotransposon occurred in the common ancestor of the marsupials and eutherians. However, the higher similarity of *PNMA-MS1* and *-MS2* to Gypsy12_DR Gag than any other eutherian *PNMAs* suggests that their insertions in the marsupial genome were recent events. Taken together, these results suggest that the retrotransposition of Gypsy12_DR-related retrotransposon occurred after the divergence of the marsupials and eutherians. The *PNMA* genes then evolved independently in these two lineages (Fig. 5).

In our analysis, only *PNMA-MS1* was detected in the tammar and opossum in contrast to 19 and 14 *PNMA* genes in humans and mice, respectively. We also observed the same trend in the *SIRH* genes: 11 genes in both humans and mice, while there are only 2 genes (*PEG10* and *SIRH12*) in the tammar genome.[11] This implies that the eutherian genome has a greater ability of exaptation as more Ty3/Gypsy types of LTR retrotransposons were incorporated into the genomes as endogenous genes than in the marsupial genomes.

4.2. *The possible role of* PNMA-MS1 *genes in marsupial development*

In rare cases, some retrotransposons have been incorporated as novel acquired genes into the host genomes and have contributed to the innovation of some eutherian-specific characteristics. Two such advantageous genes, *PEG10/SIRH1* and *PEG11/SIRH2*, play essential roles in the placental development in mice.[7,8]

The role of *PNMA-MS1* in marsupial development and growth is less clear. *PNMA-MS1* expression was detected in the tammar brain, consistent with the expression of eutherian *PNMA* genes in brain. Interestingly, *PNMA-MS1* expression was confirmed only in the thalamus, but not in the hypothalamus, and pituitary in the adult brain. The thalamus has multiple functions including relaying sensation, spatial sense and motor signals to the cerebral cortex,[22] so it is possible that *PNMA-MS1* is involved in the transmission of marsupial-specific sensations and signals. *PNMA-MS1* expression in the Day 60–70 pouch young ovary and adult female ovary suggests the gene may have a role in ovarian function. These issues will be addressed in a future study.

PNMA-MS1 protein has a conserved CCHC zinc finger domain. In retroviruses, this domain forms a part of the nucleocapsid protein that functions in virus genome packaging and the early infection process.[23] Proteins containing the CCHC zinc finger domain are commonly known to interact with single-stranded DNAs (ssDNAs) and RNAs.[24] The *Drosophila* Nanos protein is required for *hunchback* mRNA translational regulation in the early embryo to the establishment of the anterior–posterior body axis.[25] The mammalian cellular nucleic acid-binding protein (CNBP) containing seven CCHC domains is involved in neural crest development, affecting forebrain and craniofacial development.[26] CNBP has a single-stranded nucleic acid-binding ability and is also implicated in both transcriptional and translational regulations.[27,28] Therefore, *PNMA-MS1* may also be involved in a specific-transcriptional or translational regulation by binding ssDNAs or RNAs.

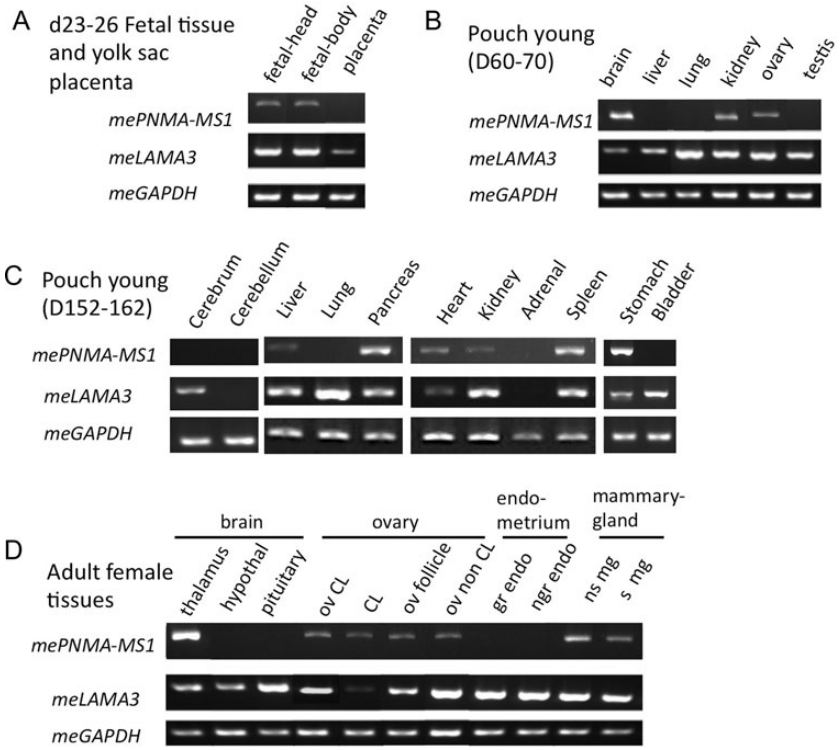

Figure 6. Expression profiles of *PNMA-MS1* in the tammar wallaby. Expression analysis of tammar wallaby *PNMA-MS1* in (A) foetal tissues and YSP at Day 23–26 of pregnancy, in several tissues, from (B) Day 60–70 and (C) Day 152–162 pouch young and (D) the adult female brain, ovary, endometrium and mammary gland. Expression of *GAPDH* and *LAMA3* for each sample is shown as a control. hypothal: hypothalamus; ov CL: ovary with active corpus luteum; CL: corpus luteum; ov follicle: ovary with developing follicle; ov non CL: ovary with primary or secondary follicle; gr endo: gravid endometrium; ngr endo: non-gravid endometrium; ns mg: non-sucked mammary gland; s mg: sucked (lactating) mammary gland.

5. Conclusions

We have identified one novel Ty3/Gypsy LTR retrotransposon-derived gene, *PNMA-MS1* in marsupials as the first marsupial-specific *PNMA* gene reported. The high *PNMA-MS1* expression levels in the thalamus, ovary and mammary gland provide intriguing questions as to its functions in marsupial development and growth as well as its role in marsupial evolution. Our data suggest that, in most of the cases, Ty3/Gypsy LTR retrotransposons have been independently incorporated into the marsupial and eutherian lineages. Consequently, the marsupials and eutherians have completely different sets of *PNMA* and *SIRH* genes, with the exception of *PEG10*. Thus, it is highly likely that these genes have evolved lineage-specific functions in the reproduction and development and contributed in establishing marsupial- or eutherian-specific traits, leading to the diversification of these two viviparous mammalian groups.

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Supplementary Data: Supplementary Data are available at www.dnaresearch.oxfordjournals.org.

Accession Numbers

The National Center for Biotechnology Information GenBank (http://www.ncbi.nlm.nih.gov/Genbank) sequence accession number for tammar PNMA-MS1 is AB646689.

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