Porcine endogenous retroviruses PERV A and A/C recombinant are insensitive to a range of divergent mammalian TRIM5α proteins including human TRIM5α

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The potential risk of cross-species transmission of porcine endogenous retroviruses (PERV) to humans has slowed the development of xenotransplantation, using pigs as organ donors. Here, we show that PERVs are insensitive to restriction by divergent TRIM5α molecules despite the fact that they strongly restrict a variety of divergent lentiviruses. We also show that the human PERV A/C recombinant clone 14/220 reverse transcribes with increased efficiency in human cells, leading to significantly higher infectivity. We conclude that xenotransplantation studies should consider the danger of highly infectious TRIM5α-insensitive human-tropic PERV recombinants.

INTRODUCTION

Pig to human xenotransplantation has been proposed as a way to alleviate the shortage of human donor organs used to treat a wide range of important medical conditions. However, it has been suggested that this process might lead to zoonosis of pathogens from the porcine organ to the human host, particularly after immunosuppression (Stoye & Coffin, 1995; Stoye et al., 1998). Indeed, expression of porcine endogenous retroviruses (PERV) has been demonstrated in pigs and their presence in the germ line will make them difficult, if not impossible, to eliminate (Le Tissier et al., 1997; Patience et al., 2001). The notion that gammaretroviruses can be zoonotic is supported by the presence of highly related gammaretroviruses in unrelated species such as gibbons (gibbon ape leukemia virus) and koalas (koala retrovirus) (Hanger et al., 2000; Tarlinton et al., 2006). Their high degree of relatedness is interpreted as demonstrating zoonosis to gibbons and koalas, possibly from mice (Lieber et al., 1975). Importantly, these viruses are pathogenic, causing leukaemia in both gibbons and koalas. As PERV sequences are closely related to these viruses, it is reasonable to suppose that in the right circumstances they too would be zoonotic, and potentially pathogenic if transmitted to humans.

TRIM5α has recently emerged as an important mediator of antiretroviral innate immunity in mammals. TRIM5α blocks retroviral infection in a species-specific way, for example human immunodeficiency virus type 1 (HIV-1) is restricted by TRIM5α from Old World monkeys, but not by human TRIM5α (Hatziioannou et al., 2004; Stremlau et al., 2004; Yap et al., 2004). Human TRIM5α restricts infection by equine infectious anemia virus (EIAV) and the murine leukemia virus (MLV-N) (Hatziioannou et al., 2004; Keckesova et al., 2004; Yap et al., 2004). TRIM5α encodes RING, B-box and coiled-coil domains, comprising a tripartite motif, as well as a C-terminal B30.2 domain, which determines antiviral specificity, and appears to interact directly with the incoming viral capsid (Stremlau et al., 2006a). TRIM5α is thought to mediate an important barrier to zoonotic transmission of retroviruses by preventing replication early in the viral life cycle, usually before significant reverse transcription. The antiviral mechanism of TRIM5α remains incompletely characterized but appears to involve viral uncoating as well as recruitment to the proteasome (Anderson et al., 2006; Stremlau et al., 2006a; Wu et al., 2006; reviewed by Towers, 2007). As PERVs have been suggested as a possible source of zoonotic infection after pig to human xenotransplantation we sought to examine the sensitivity of PERV isolates to restriction by mammalian TRIM5α molecules. Here, we show that two PERV isolates, prototypic PERV A PK (Bartosch et al., 2002) and a high-titre PERV A/C recombinant PERV-A 14/220 (Bartosch et al., 2004), are insensitive to restriction by divergent mammalian TRIM5α proteins. Furthermore, we show that the higher infectivity of the PERV A/C recombinant gag–pol is due to increased efficiency of reverse transcription.

METHODS

Cell lines and viral titrations. Feline cells expressing TRIM5α proteins from human, African green monkey (Keckesova *et al.*, 2004), rhesus macaque, squirrel monkey (Ylinen *et al.*, 2005), cattle (Ylinen *et al.*, 2006) and rabbit (Schaller *et al.*, 2007) have been described previously.

PERV A and A/C recombinant gag–pol expression vectors were generated by replacing the G ORF with PERV gag–pol derived from PERV A (GenBank accession no. AY099323) and/or PERV A/C 14/220 (GenBank accession no. AY570980) at the *Bam*HI site in phCMV-G, by PCR (Bartosch *et al.*, 2003). Vesicular stomatitis virus glycoprotein (VSV-G) pseudotyped viral vectors derived from HIV-1 (Bainbridge *et al.*, 2001; Zufferey *et al.*, 1997), MLV (Bock *et al.*, 2000) and simian immunodeficiency virus mac (SIVmac) (Negre *et al.*, 2000) encoding green fluorescent protein (GFP) have been described elsewhere and were prepared by transfection of 293T cells as described previously (Besnier *et al.*, 2002). PERV GFP-encoding vectors were prepared similarly using a GFP-encoding genome derived from MLV (Naviaux *et al.*, 1996). PERV A/C gag–pol expression plasmids encoding PERV A protease, reverse transcriptase or integrase were constructed using the unique *Bcl*I site at the protease–reverse transcriptase junction or the unique *Hpa*I site at the reverse transcriptase–integrase junction.

Western blot analysis. A 1 ml sample of each viral supernatant, or supernatant from untransfected cells, was pelleted (123 000 *g*, 90 min) and resuspended in 30 μl Laemmli buffer. A volume of 10 μl was subjected to PAGE, blotted and detected using a rabbit anti-PERV polyclonal antibody (Bartosch *et al.*, 2002) (1 : 1000) and an anti-rabbit horseradish peroxidase linked antibody (1 : 3000; GE Healthcare).

Quantitative PCR (QPCR) to measure products of reverse transcription. TaqMan QPCR to measure viral DNA synthesis was performed using primer/probe sequences specific to GFP as described previously (Passerini *et al.*, 2006). Cells (4×10^5) were infected in six-well plates in triplicate with equivalent doses of virus treated with DNase (70 U ml^{-1} for 2 h; Promega). Six hours after infection, total DNA was extracted from two samples using a QiaAmp DNA extraction kit (Qiagen). The third sample was subjected to FACS analysis 48 h after infection to enumerate infected cells. DNA (100 ng) was subjected to TaqMan QPCR as described previously (Towers *et al.*, 1999). Absolute numbers of GFP DNA per PCR were determined by reference to a standard curve. The number of GFP molecules per 100 ng total DNA were plotted. As a negative control for plasmid contamination of the viral inoculum, cells were infected with virus that had been boiled for 5 min. QPCR was then performed as described above.

RESULTS

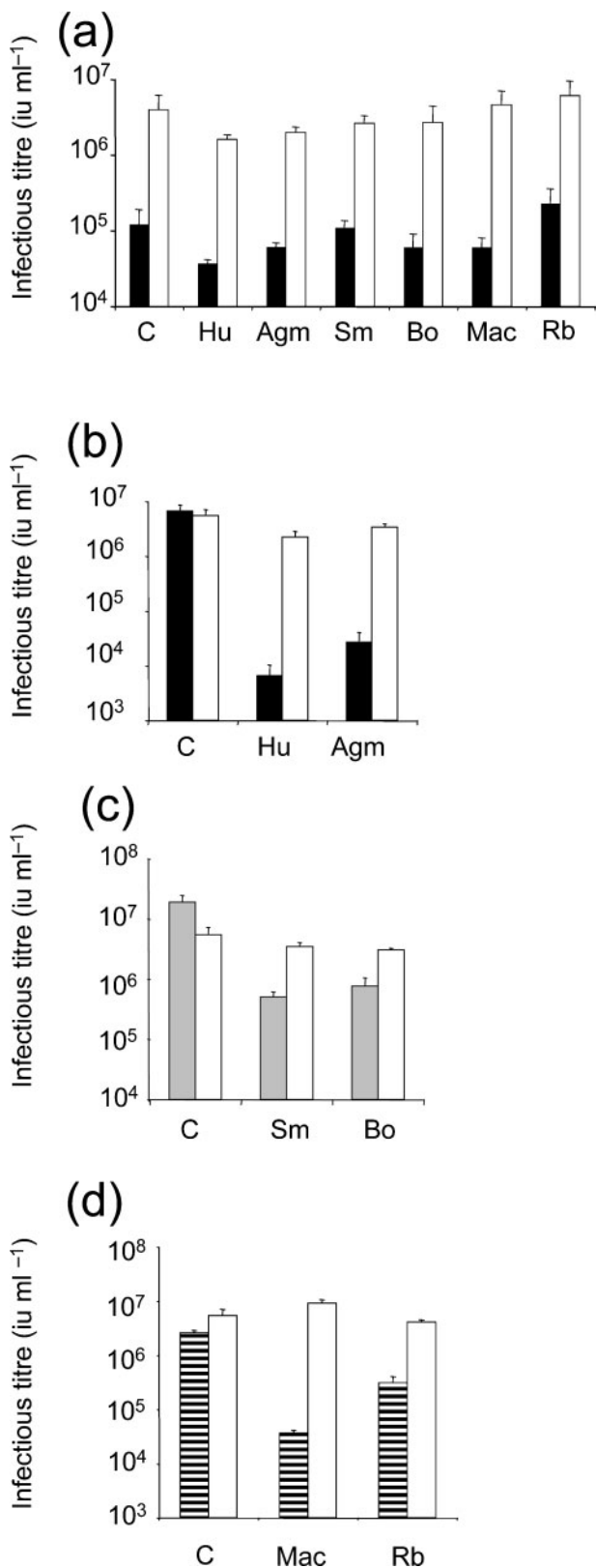### PERVs are insensitive to divergent TRIM5α proteins

Replication-competent PERV sequences have been divided into three classes, PERV A, B and C, according to their envelope sequences (Patience *et al.*, 1997; Takeuchi *et al.*, 1998). PERVs A and B have been shown to be able to infect human cells, and, importantly, naturally occurring high-titre PERV A/C recombinants have been described with the ability to replicate to high titres *in vitro* (Le Tissier *et al.*, 1997; Oldmixon *et al.*, 2002; Patience *et al.*, 1997; Takeuchi

et al., 1998; Wilson *et al.*, 2000). In order to test PERV sensitivity to TRIM5α we made gag–pol expression vectors for the prototypic PERV A PK and the PERV A/C 14/220 recombinant and used these plasmids to make VSV-G pseudotyped vectors packaging GFP-encoding MLV genomes as described previously (Besnier *et al.*, 2002). These viruses were then titrated onto permissive feline Crandall-Reese feline kidney (CRFK) cells expressing TRIM5α proteins from human, African green monkey, rhesus macaque, squirrel monkey, rabbit or cattle or unmodified CRFK cells as a negative control, as described previously (Keckesova *et al.*, 2004; Schaller *et al.*, 2007; Ylinen *et al.*, 2005, 2006) (Fig. 1a). Forty-eight hours after exposure to PERV, infected cells were enumerated by counting fluorescent, GFP-expressing cells, by FACS. Infectious titres of each virus were then calculated and plotted (Fig. 1). Remarkably, the two PERVs were largely insensitive to all TRIM5αs tested. The strongest restriction was by human TRIM5α, but this led to only around a threefold reduction in infectivity.

As a positive control for the expression of each TRIM5α, titres of restriction-sensitive VSV-G pseudotyped GFP-encoding vectors were measured as above. In each case the viruses were selected for sensitivity to the TRIM5α in question. MLV-N infectivity was reduced by two to three orders of magnitude by expression of either human or African green monkey TRIM5α as described elsewhere (Hatziioannou *et al.*, 2004; Keckesova *et al.*, 2004; Perron *et al.*, 2004; Yap *et al.*, 2004) (Fig. 1b). SIVmac infectivity was reduced by one to two orders of magnitude by expression of squirrel monkey or bovine TRIM5α (Fig. 1c) and HIV-1 infectivity was reduced by expression of rabbit or rhesus TRIM5α, as described previously (Si *et al.*, 2006; Song *et al.*, 2005; Stremlau *et al.*, 2004; Ylinen *et al.*, 2005, 2006) (Fig. 1d). MLV-B infectivity acted as a TRIM5α-insensitive control and was not affected by expression of any of the TRIM5α genes, as has been described previously (Hatziioannou *et al.*, 2004; Keckesova *et al.*, 2004; Perron *et al.*, 2004; Schaller *et al.*, 2007; Yap *et al.*, 2004; Ylinen *et al.*, 2005, 2006) (Fig. 1b–d).

PERV A and PERV A/C VSV-G pseudotypes contain similar amounts of p30 capsid protein

Fig. 1 demonstrates that the titre of the VSV-G pseudotyped PERV A/C recombinant is significantly higher than that of the VSV-G pseudotyped PERV A. This is consistent with previous observations made comparing PERV A and PERV A/C viral replication *in vitro* (Bartosch *et al.*, 2004). In order to control for the dose of the two viruses we compared the amounts of PERV capsid in the virus stocks by Western blot analysis using a rabbit anti-PERV polyclonal antibody to detect PERV gag (Fig. 2) (Bartosch *et al.*, 2002). The blot shows that the PERV A stocks (lanes 1 and 2) and PERV A/C stocks (lanes 3 and 4) have similar amounts of p30 capsid, demonstrating that each contained a similar concentration of virions.

Fig. 1. PERV are insensitive to divergent TRIM5α proteins. (a) GFP-encoding VSV-G pseudotypes of PERV A (black bars) or PERV A/C recombinant (white bars) were titrated on CRFK cells expressing TRIM5α from human (Hu), African green monkey (Agm), squirrel monkey (Sm), cattle (Bo), rhesus macaque (Mac) or rabbit (Rb) or unmodified CRFK cells as a control (C). GFP-encoding VSV-G pseudotypes of MLV-N (black bars) or MLV-B (white bars) SIVmac (grey bars) or HIV-1 (striped bars) were titrated onto CRFK cells expressing TRIM5α from human (Hu) or African green monkey (Agm) (b), squirrel monkey (Sm) or cattle (Bo) (c) or rhesus macaque (Mac) or rabbit (Rb) (d) or unmodified CRFK cells (C) as a control. Titres are expressed as infectious units ml^{-1} (iu ml^{-1}). Errors bars indicate SD derived from two experiments performed with independent virus stocks.

PERV A/C has more efficient reverse transcription than PERV A

Next, we sought to map the PERV A protein responsible for the defect in infectivity. We made VSV-G pseudotypes using chimeric PERV A/C gag–pol, encoding individual PERV A proteins. Pseudotypes encoding PERV A protease or PERV A integrase were as infectious as PERV A/C (Fig. 3a). However, PERV A/C encoding PERV A reverse transcriptase was one to two orders of magnitude less infectious, suggesting that PERV-A reverse transcriptase is less efficient, and that reduced DNA synthesis leads to reduced infectivity. To confirm the role for reverse transcriptase we tested whether the PERV A/C recombinant was better able to reverse transcribe than PERV A in target cells. We infected cells with equal doses of PERV A and PERV A/C recombinant for 6 h, purified total DNA and assayed for products of reverse transcription by Taqman QPCR, as described previously (Besnier *et al.*, 2002; Towers *et al.*, 1999). Data are presented as copies of reverse transcriptase (GFP) product per 100 ng total DNA (Fig. 3b). This experiment shows that, indeed, the efficiency of PERV A/C reverse transcription is one to two orders of magnitude greater than PERV A. The increase in reverse transcriptase efficiency leads to an increase in VSV-G pseudotype infectivity by around the
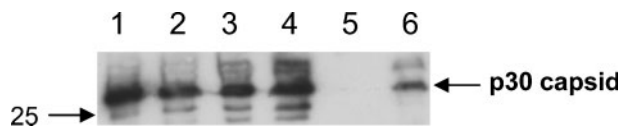
Fig. 2. PERV A and PERV A/C VSV-G pseudotypes contain similar amounts of p30 capsid protein. Two stocks of PERV A (lanes 1 and 2) and two stocks of PERV A/C (lanes 3 and 4) were Western blotted to detect capsid protein. Supernatant from untransfected 293T cells was blotted as a negative control (lane 5) and a total extract of PERV A/C 14/220-infected 293T cells was blotted as a positive control (lane 6). The band representing p30 capsid is marked with an arrow on the right and the position of the 25 kDa size marker (Precision Plus Protein Standards; Bio-Rad) is shown on the left.

Supernatant from untransfected 293T cells and PERV A/C 14/220-infected cell lysate were blotted as controls (lanes 5 and 6, respectively).
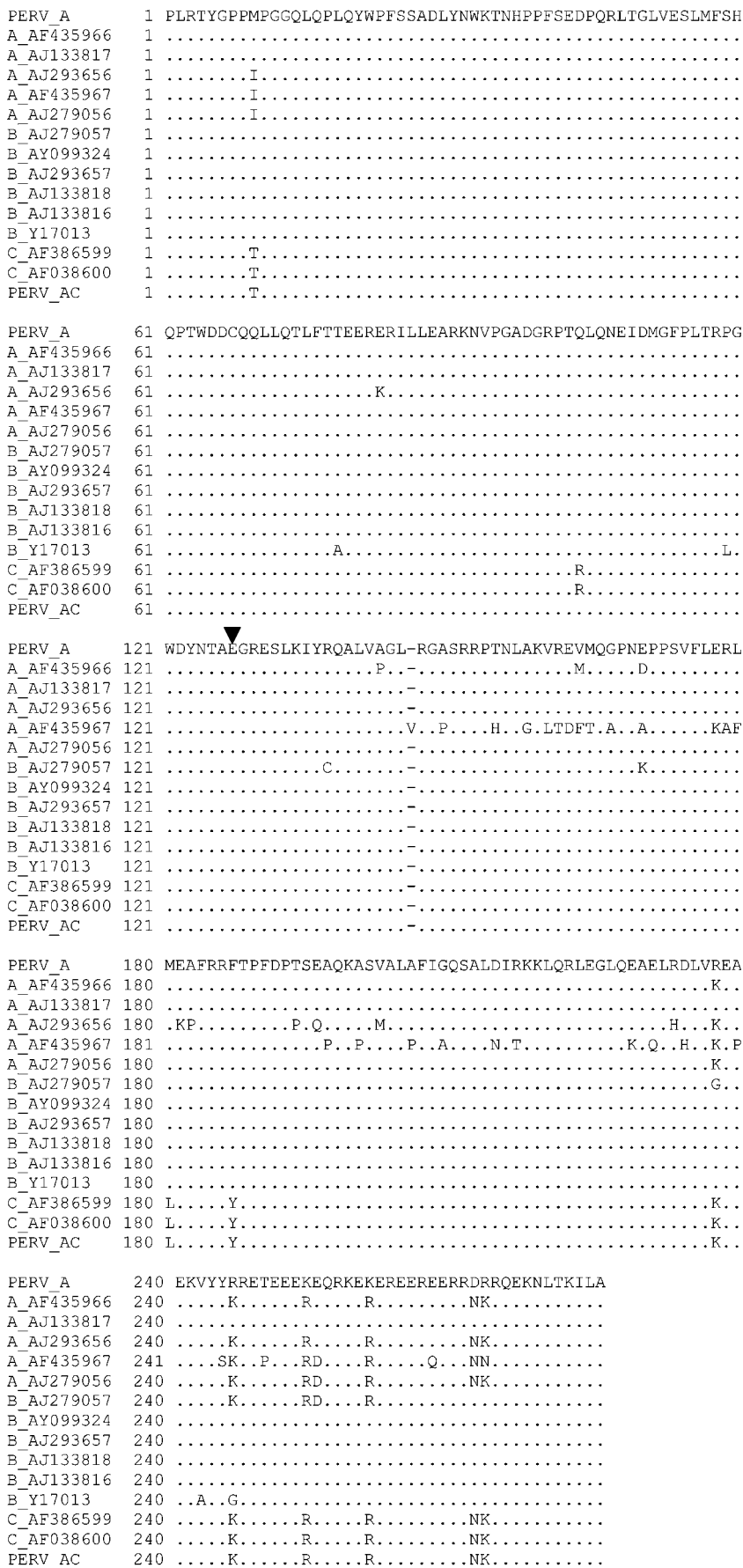
(a)

(b)
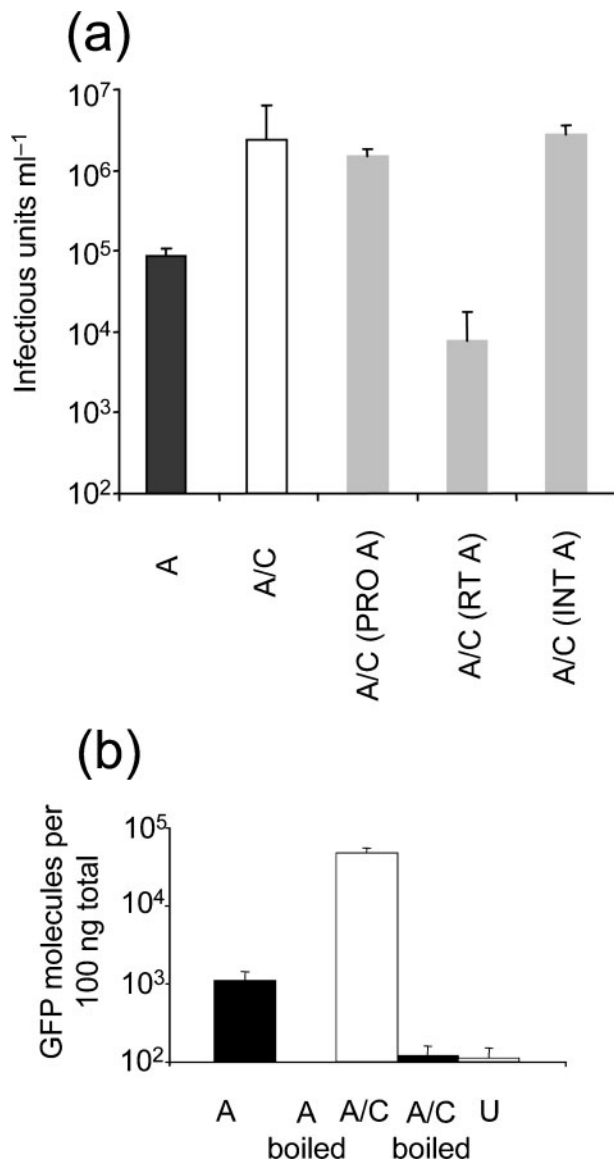
Fig. 3. PERV A/C has more efficient reverse transcription than PERV A. (a) VSV-G pseudotypes of PERV A/C recombinant, PERV A or chimeric PERV A/C recombinants containing the protease, reverse transcriptase or integrase sequences of PERV A [PERV A/C (PRO A); PERV A/C (RT A); PERV A/C (INT A), respectively], were titrated and titres expressed as infectious units ml^{-1}. Errors bars indicate SD derived from two experiments performed with independent virus stocks. (b) Equal doses of PERV A (black bars) and A/C recombinant (white bars) VSV-G pseudotypes were used to infect CRFK cells with a PERV A/C recombinant at an m.o.i. of 0.3 and the cells were incubated for 6 h. Values are expressed as the number of GFP-encoding DNA molecules per 100 ng total DNA. As a negative control, parallel virus samples were boiled for 5 min to inactivate the virus and then used to infect cells as shown. These samples gave background GFP levels, demonstrating that the GFP signal is due to viral reverse transcription. DNA prepared from uninfected cells was also subject to QPCR as a further negative control (grey bar) (U). Error bars indicate SD of duplicate samples and the data are representative of three replicates.

same magnitude (Figs 1a and 3a). The reverse transcriptase region of PERV A/C is derived from PERV C, and its amino acid sequence is identical to that of PERV C MSL (GenBank accession no. AF038600). PERV C reverse transcriptase is therefore more active than that of PERV A, possibly due to PERV C being around five million years younger than PERV A (Bartosch et al., 2004; Niebert & Tonjes, 2005).

DISCUSSION

It appears that PERVs, and perhaps gammaretroviruses in general, are insensitive to restriction by TRIM5α. This is surprising given the broad antiviral activity of some TRIMs against distantly related lentiviruses. For example, bovine TRIM5α restricts all the lentiviruses tested against it, including HIV-1, HIV-2, SIVmac, feline immunodeficiency virus and EIAV (Si et al., 2006; Ylinen et al., 2006). Moreover, rabbit TRIM5α restricts all but SIVmac (Schaller et al., 2007) with the only viruses appearing to be insensitive to these two non-primate TRIM5αs being MLV-B and the two PERVs described herein. Indeed, MLV-B and the two PERVs are not sensitive to any of the TRIM5αs tested. Whilst it is clear that these studies are limited by the relatively small number of viruses they employ, we believe that their diversity is broad enough to demonstrate that gammaretroviruses are significantly less sensitive to restriction by TRIM5α molecules. A recent study has suggested that human TRIM5α protected humans from a gammaretrovirus found endogenized in the chimpanzee genome referred to as ptERV (Kaiser et al., 2007). Whilst this theory seems reasonable, it is somewhat undermined by the observation that neither human nor chimpanzee TRIM5αs restrict MLVs bearing ptERV capsids (Perez-Caballero et al., 2008). This more recent observation suggests that the constructs used by Kaiser et al., which were derived from calculated consensus sequence, do not represent the behaviour of the ptERV virus.

The reason for poor sensitivity of gammaretroviruses to TRIM5α may lie in the capsid structure. Intriguingly, the region of the capsid shown to influence primate lentiviral sensitivity to TRIM5α, referred to as the cyclophilin A-binding loop, is missing in the MLV capsid, although the rest of the N-terminal capsid structure is highly conserved (Mortuza et al., 2004). As changes in the cyclophilin-binding loop affect primate lentiviral sensitivity to restriction by TRIM5α (Berthoux et al., 2005; Keckesova et al., 2006; Lin & Emerman, 2008; Stremlau et al., 2006b; Ylinen et al., 2005), we speculate that this structure in gammaretroviruses has contributed to their general insensitivity to TRIM5α. It is striking that MLV-N is the only MLV shown to be restricted by TRIM5α (Hatziioannou et al., 2004; Keckesova et al., 2004; Perron et al., 2004; Si et al., 2006; Song et al., 2005; Yap et al., 2004; Ylinen et al., 2005, 2006). MLV-N is essentially a point mutant of MLV-B and we suspect that the E110 to R MLV-B capsid change was selected by evolutionary pressure from

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PERV_A       1 PLRTYGPPMPGGQLQPLQYWPFSSADLYNWKTNHPPFSEDPQRLTGLVESLMFSH
A_AF435966   1 ......................................................
A_AJ133817   1 ......................................................
A_AJ293656   1 .......I..............................................
A_AF435967   1 .......I..............................................
A_AJ279056   1 .......I..............................................
B_AJ279057   1 ......................................................
B_AY099324   1 ......................................................
B_AJ293657   1 ......................................................
B_AJ133818   1 ......................................................
B_AJ133816   1 ......................................................
B_Y17013     1 ......................................................
C_AF386599   1 .......T..............................................
C_AF038600   1 .......T..............................................
PERV_AC      1 .......T..............................................


PERV_A      61 QPTWDDCQQLLQTLFTTEERERILLEARKNVPGADGRPTQLQNEIDMGFPLTRPG
A_AF435966  61 ......................................................
A_AJ133817  61 ......................................................
A_AJ293656  61 ..........................K...........................
A_AF435967  61 ......................................................
A_AJ279056  61 ......................................................
B_AJ279057  61 ......................................................
B_AY099324  61 ......................................................
B_AJ293657  61 ......................................................
B_AJ133818  61 ......................................................
B_AJ133816  61 ......................................................
B_Y17013    61 .............A.....................................L.
C_AF386599  61 ....................................R.................
C_AF038600  61 ....................................R.................
PERV_AC     61 ......................................................

                                 ▼
PERV_A     121 WDYNTAEGRESLKIYRQALVAGL-RGASRRPTNLAKVREVMQGPNEPPSVFLERL
A_AF435966 121 ....................P..-..............M.....D.........
A_AJ133817 121 .......................-.............................
A_AJ293656 121 .......................-.............................
A_AF435967 121 ...................V..P....H..G.LTDFT.A..A......KAF
A_AJ279056 121 .......................-.............................
B_AJ279057 121 ..............C........-...............K.............
B_AY099324 121 .......................-.............................
B_AJ293657 121 .......................-.............................
B_AJ133818 121 .......................-.............................
B_AJ133816 121 .......................-.............................
B_Y17013   121 .......................-.............................
C_AF386599 121 .......................-.............................
C_AF038600 121 .......................-.............................
PERV_AC    121 .......................-.............................


PERV_A     180 MEAFRRFTPFDPTSEAQKASVALAFIGQSALDIRKKLQRLEGLQEAELRDLVREA
A_AF435966 180 ...................................................K..
A_AJ133817 180 ......................................................
A_AJ293656 180 .KP.........P.Q.....M.........................H...K..
A_AF435967 181 .............P..P....P..A....N.T.........K.Q..H..K.P
A_AJ279056 180 ...................................................K..
B_AJ279057 180 ...................................................G..
B_AY099324 180 ......................................................
B_AJ293657 180 ......................................................
B_AJ133818 180 ......................................................
B_AJ133816 180 ......................................................
B_Y17013   180 ......................................................
C_AF386599 180 L.....Y............................................K..
C_AF038600 180 L.....Y............................................K..
PERV_AC    180 L.....Y............................................K..


PERV_A     240 EKVYYRRETEEEKEQRKEKEREEREERRDRRQEKNLTKILA
A_AF435966 240 .....K......R.....R.........NK...........
A_AJ133817 240 .........................................
A_AJ293656 240 .....K......R.....R.........NK...........
A_AF435967 241 ....SK..P...RD....R......Q...NN...........
A_AJ279056 240 .....K......RD....R.........NK...........
B_AJ279057 240 .....K......RD....R......................
B_AY099324 240 .........................................
B_AJ293657 240 .........................................
B_AJ133818 240 .........................................
B_AJ133816 240 .........................................
B_Y17013   240 ..A...G..................................
C_AF386599 240 .....K......R.....R.........NK...........
C_AF038600 240 .....K......R.....R.........NK...........
PERV_AC    240 .....K......R.....R........NK...........
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Fig. 4. Alignment of capsid sequences from 15 PERVs indicates a high level of conservation. Sequences were retrieved and aligned using DNADynamo (Bluetractor Software) and Se-Al (Rambaut, 1996). GenBank accession numbers are shown, as is the classification into groups A, B or C according to Takeuchi *et al.* (1998). The PERV A and PERV A/C recombinants used in this study are included. The arrowhead indicates the PERV CA residue homologous to position CA 110 in MLV that influences sensitivity to restriction by TRIM5α. Dots indicate conserved residues.

the murine antiviral Fv1 N, giving an advantage in Fv1 B-encoding mice but rendering it rather sensitive to restriction by TRIM5α.

The experiments performed here have made use of VSV-G pseudotyped retroviral vectors produced in human 293T cells and overexpression of TRIM5α proteins in CRFK cells. It is therefore possible that this experimental system might have influenced the results. However, this system has been very helpful in determining TRIM5α sensitivities in the past. Furthermore, it has been consistent with what we know of tropism of retroviruses *in vivo*, for example the lack of HIV-1 replication in monkeys, which can be bypassed, at least *in vitro*, by obviating TRIM5α and APOBEC3G restriction (Hatziioannou *et al.*, 2006). In our view, overexpression of TRIM5α *in vitro* is unlikely to lead to specificity artefacts, on the basis that TRIM5α is strongly induced by interferon and therefore protein levels are likely to be high during viral infection *in vivo* (Asaoka *et al.*, 2005; Sakuma *et al.*, 2007). Overexpression experiments are therefore a sensitive and relevant test of restriction sensitivity, although reduction of TRIM5α expression in relevant cell types and demonstration that PERV titres are not significantly affected would also augment the experiments described here.

We conclude that the two PERVs are not significantly restricted by any of the TRIM5α molecules tested (Fig. 1a). The strongest restriction is threefold, by human TRIM5α, which is about the same magnitude that HIV-1 is restricted by human TRIM5α when overexpressed (Hatziioannou *et al.*, 2003; Newman *et al.*, 2006; Stremlau *et al.*, 2004; Yap *et al.*, 2004), indicating that it is unlikely to act as a barrier to PERV cross-species transmission. The two PERV sequences tested are likely to be representative of PERV classes A, B and C on the basis that the capsid sequences of these viruses are closely related (Fig. 4). Not only are they highly conserved, but the residue corresponding to MLV CA 110 (indicated by an arrowhead in Fig 4) known to influence MLV sensitivity to TRIM5α (Perron *et al.*, 2004; Towers *et al.*, 2000) is a conserved glutamate as it is in unrestricted MLV-B. This class of PERVs in general are therefore unlikely to be restricted by mammalian TRIM5α molecules. It is clear, however, that TRIM5α is not the only barrier to species-specific retroviral infection. Human APOBEC3G strongly restricts PERVs (Jonsson *et al.*, 2007) and human tetherin is likely to restrict PERVs, given that it restricts closely related MLVs (Neil *et al.*, 2008). There are also many other human TRIM proteins that may restrict PERVs (Nisole *et al.*, 2005). Our data therefore merely consider a single aspect of species barriers to zoonosis, which are likely to be complex and mediated by a large arsenal of species-specific antiviral proteins. Having said that, MLVs do appear to be particularly successful in transmitting between species, as illustrated by the diversity of gammaretroviral sequences in mammalian genomes, suggesting that they might be well adapted to avoiding restriction (Martin *et al.*, 1999, 2003).

We assume that the higher reverse transcriptase activity of the recombinant virus is due to its acquiring a PERV C reverse transcriptase sequence that has been inserted into the pig genome around five million years more recently than the PERV A sequence (Niebert & Tonjes, 2005). The more recent endogenization of the PERV C means that its reverse transcriptase sequence has been subject to fewer deleterious mutations, leading to higher activity. The apparent ease with which the relatively less infectious PERV A can acquire PERV C sequences to become highly infectious illustrates the plasticity of retroviruses and underlines the risk posed by introducing them into immunosuppressed individuals during xenotransplantation. This, and their apparent insensitivity to the important species barrier provided by TRIM5α, underscores the need to consider the possibility of zoonotic transmission occurring in the context of pig to human xenotransplantation.

ACKNOWLEDGEMENTS

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