JOURNAL OF VIROLOGY, Nov. 1993, p. 6737–6741
0022-538X/93/116737-05$02.00/0

Vol. 67, No. 11

Mutation of Amino Acids within the Gibbon Ape Leukemia Virus (GALV) Receptor Differentially Affects Feline Leukemia Virus Subgroup B, Simian Sarcoma-Associated Virus, and GALV Infections

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Received 18 May 1993/Accepted 27 July 1993

The three type C retroviruses, gibbon ape leukemia virus (GALV), simian sarcoma-associated virus (SSAV), and feline leukemia virus subgroup B (FeLV-B), infect human cells by interacting with the same cell surface receptor, GLVR1. Using LacZ retroviral pseudotypes and murine cells transfected with mutant GLVR1 expression vectors, we show that the same 9-amino-acid region of human GLVR1 is critical for infection by the three viruses. Rat cells were not susceptible to infection by LacZ (FeLV-B) pseudotypes because of a block at the receptor level. We found multiple amino acid differences from human GLVR1 in the 9-amino-acid critical region of rat GLVR1. Expression of a human-rat chimeric GLVR1 in murine cells demonstrated that rat GLVR1 could function as a receptor for GALV and SSAV but not for FeLV-B. Substitution of human GLVR1 amino acids in the critical region of rat GLVR1 identified three amino acids as responsible for resistance to FeLV-B infection; two of these affect SSAV infection, but none affects GALV infection.

Retroviral infection is dependent on interactions between the viral envelope glycoprotein and specific cell surface receptors (30). Retroviruses capable of infecting human cells have been assigned to eight receptor groups on the basis of cross-interference of infection (24). This implies the existence of at least eight human cell surface molecules with retroviral receptor function. However, only two of the eight molecules have been identified, the CD4 receptor for human and simian immunodeficiency viruses (3, 15, 22) and GLVR1, the receptor for gibbon ape leukemia virus (GALV) (20), simian sarcoma-associated virus (SSAV) (27), feline leukemia virus subgroup B (FeLV-B) (27), and probably at least one endogenous xenotropic murine virus (18).

GLVR1 encodes a protein with 10 potential transmembrane domains, and its homology to the phosphate transporter of *Neurospora crassa* suggests that its normal function may be as a transporter, though its substrate has not been determined (10). In this respect, it is similar to Rec-1, the murine receptor for ecotropic murine leukemia virus, which functions as an amino acid transporter (2, 14, 29). GALV has been isolated from monkeys with lymphosarcoma or granulocytic leukemia and leads to myeloid leukemias upon inoculation of juvenile gibbons (12, 13). SSAV is highly homologous to GALV (4) and probably represents a zoonotic case of infection of a woolly monkey by GALV. FeLV-B arises as a result of recombination between weakly pathogenic FeLV-A and endogenous envelope sequences (5, 25), and FeLV-B isolation has been correlated with leukemia in cats (9, 21). The FeLV-B and GALV envelope proteins lack significant homology in the amino-terminal region (4, 5), which is known to be involved in determining the receptor specificity of FeLV-B (23). In this report, the region of GLVR1 required for infection by SSAV and FeLV-B has been mapped to the same critical 9-amino-acid sequence required for GALV (11). GALV and SSAV, but not FeLV-B, were shown to infect rat cell lines (27); this differential tropism has now been ascribed to the sequence of the rat 9-amino-acid critical region. Mutations which affect FeLV-B or SSAV but not GALV infection have been identified. Therefore, while the three viruses recognize the same receptor region, their sequence requirements within this region can be distinguished.

MATERIALS AND METHODS

Determination of LacZ pseudotype titer. Chimeric human-murine GLVR1 and mutant human GLVR1 expression plasmids (11) were transfected (8) into *Mus dunni* cells. Transfected cells were selected in G418 for the presence of the cotransfected pSV2neo plasmid, and pools of cells from approximately 50 G418-resistant colonies were used for infectivity assays. The use of *M. dunni* rather than NIH 3T3 cells in this assay resulted in approximately 100-fold-higher sensitivity for SSAV and FeLV-B (data not shown). Viral infectivity was determined by using LacZ pseudotypes of SSAV and FeLV-B; these were prepared as previously described (26), by infection of dog S^+L^- cells or human RD cells, containing an integrated murine leukemia virus vector MFGnlsLacZ (7), with SSAV, FeLV-B, or GALV (SF strain). Supernatant from such persistently infected cell cultures was incubated with transfected *M. dunni* cells for 4 h in the presence of Polybrene at a concentration of 20 μg/ml. After 48 h, infected *M. dunni* cultures were stained with X-Gal (5-bromo-4-chloro-3-indolyl-β-D-galactopyranoside) and the titers of the LacZ pseudotypes were determined. Both clusters of stained cells and single stained cells were attributed to single infection events, and titers were expressed as LacZ CFU per milliliter of dog S^+L^- or RD cell supernatant.

Construction of chimeric and mutant GLVR1 expression plasmids. Chimeric human-mouse GLVR1 cDNAs were con-

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TABLE 1. Sensitivity of *M. dunni* cells expressing mutant chimeric GLVR1 cDNAs to SSAV and FeLV-B

Plasmid	GLVR1 cDNA[a]	Titer of LacZ pseudotype (CFU/ml)	
		SSAV	FeLV-B
	—	0	0
pOJ9 (human)		1.2×10^4	1.4×10^4
pOJ19 (mouse)		0	0
pOJ15		0	0
pOJ20		4.0×10^4	2.0×10^4
pOJ14		0	0
pOJ37		3.2×10^4	3.6×10^4
pOJ36		0	0
pOJ34		0	0
pOJ35		9.2×10^3	2.8×10^4

[a] Hatched bar, scrambled sequence.

structed as described elsewhere (11) by using conserved *Kpn*I and *Pst*I restriction sites. The rat GLVR1 cDNA clone was digested with *Hin*dIII, the end was filled in with Klenow fragment, the cDNA clone was digested with *Pst*I, and the resulting 800-bp fragment was ligated to pOJ9 digested with *Pst*I and *Eco*RV. This resulted in a chimeric human-rat GLVR1 expression plasmid with the C-terminal 162 amino acids derived from the rat cDNA clone. To construct site-directed mutants, the 800-bp *Pst*I-*Hin*dIII fragment of the rat GLVR1 cDNA clone was subcloned into M13mp19. Oligonucleotide-directed mutagenesis was performed as previously described (28); mutants with the correct sequence were inserted in *Pst*I-*Eco*RV-digested pOJ9 as described above.

RESULTS

To determine which region(s) of the human GLVR1 molecule was required for infection by SSAV and FeLV-B, chimeric human-murine GLVR1 and mutant human GLVR1 expression plasmids (11) were transfected into *M. dunni* cells. Table 1 shows that *M. dunni* cells transfected with the human GLVR1 expression vector became sensitive to infection by both LacZ (SSAV) and LacZ (FeLV-B), while cells transfected with the empty vector or a murine GLVR1 vector remained resistant. Human-murine chimeric constructs demonstrated that the C-terminal 162 amino acids of human GLVR1, downstream of the conserved *Pst*I site (11), were required for both LacZ (SSAV) and LacZ (FeLV-B) infection (Table 1). This region is also essential for GALV infection (11). Within this region, two areas of divergence between the amino acid sequences of human and murine GLVR1 have been identified (10) (amino acids 550 to 558 [region A] and 670 to 679 [region B] of human GLVR1; see Fig. 1). Replacement of region A in human GLVR1 with random amino acids or murine region A resulted in loss of infectivity by LacZ (SSAV) and LacZ (FeLV-B), whereas substitution of the murine sequence for region B did not affect infectivity. Furthermore, substitution of human region A in murine GLVR1 was sufficient to confer sensitivity to LacZ (SSAV) and LacZ (FeLV-B) (Table 1). Thus, amino acids 550 to 558 of human GLVR1 are critical for infection by SSAV and FeLV-B. This region is also critical for GALV infection (11); the three viruses therefore share a requirement for the integrity of amino acid sequence(s) within this region of GLVR1 at some stage during the infection process.

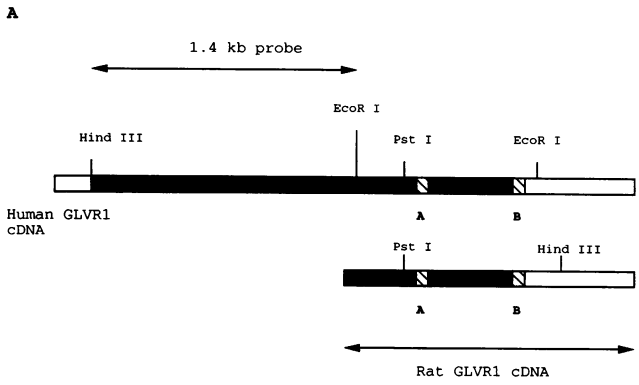
We previously reported that rat cells are sensitive to SSAV but resistant to FeLV-B pseudotype infection (27). Data from experiments using LacZ (SSAV) and LacZ (FeLV-B) pseudotypes confirm these earlier data and demonstrate that three rat cell lines were also sensitive to similar LacZ (GALV) pseudotypes (Table 2). Rat HSN and NRK cells were resistant to LacZ (FeLV-B) infection, and rat XC cells were weakly infectible (Table 2). Such resistance of rat NRK and HSN cells to LacZ (FeLV-B) infection might be ascribed to a block at the level of the receptor, either an amino acid sequence variation or a processing variation (19) in the rat GLVR1, which is widely expressed (10) and therefore likely to be the rat receptor for GALV and SSAV. A postreceptor infection block could also exist, as the LacZ pseudotype carries the *gag* and *pol*

TABLE 2. Host range and titer of LacZ pseudotypes

Cell line	Titer of LacZ pseudotype (CFU/ml)		
	GALV	SSAV	FeLV-B
DOG S^+L^-	2.4×10^5	1.2×10^4	7.2×10^4
Rat HSN	3.1×10^4	1.5×10^4	0
Rat NRK	1.0×10^5	1.1×10^4	0
Rat XC	2.2×10^5	3.4×10^4	2.2×10^3
NRKPOJ9[a]	ND[b]	1.2×10^5	6.8×10^4

[a] NRKPOJ9 cells are rat NRK cells transfected with the human GLVR1 cDNA.

[b] ND, not determined.



B

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                                        Region A
Human   LQILTACFGSFAHGGNDVSNAIGPLVALYLVYDTGDVSSKVATPIWLLLYGGVGI
Mouse   ..............................-KQEA.T.A.............
Rat     ..............................E.R..TT.E.............

Human   CVGLWVWGRRVIQTMGKDLTPITPSSGFSIELASALTVVIASNIGLPISTTHCKV
Mouse   .M..................................................
Rat     .M..............................F...V...............

                                                  Region B
Human   GSVVSVGWLRSKKAVDWRLFRNIFMAWFVTVPISGVISAAIMAIFRYVILRM
Mouse   ..........................................V.K.I..PV
Rat     ..........................................V.KHI..PV
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FIG. 1. (A) Structure of the human and rat GLVR1 cDNA clones. Solid boxes, coding sequence; hatched boxes, regions A and B. (B) Comparison of the deduced sequences of the C-terminal 160 amino acids of the human, mouse, and rat GLVR1 gene products. -, amino acid deletion.

gene products of FeLV-B. To distinguish between these possibilities, human GLVR1 was expressed in NRK cells, which then rendered them sensitive to LacZ (FeLV-B) infection (Table 2). Therefore, a difference between the rat NRK and human GLVR1 molecules must explain the resistance of rat NRK and human GLVR1 molecules must explain the resistance of rat NRK cells to FeLV-B infection.

To determine the sequence of rat GLVR1, a λGT11 clone was obtained by screening a Sprague-Dawley rat liver cDNA library with a 1.4-kb human GLVR1 probe (Fig. 1A). The 1.7-kb partial rat GLVR1 cDNA clone (Fig. 1A) showed greater than 90% homology to human GLVR1 in the last 162 amino acids (Fig. 1B). An identical sequence for the last 162 amino acids of a rat brain GLVR1 cDNA has been reported by Johann et al. (11). Two regions of significant divergence between the human and rat sequences are indicated in Fig. 1; one, at the extreme C terminus (region B), is highly homologous between rat and murine GLVR1s, and the other (region A) corresponds to the region critical in human GLVR1 for GALV, SSAV, and FeLV-B infection and shows many differences between human, mouse, and rat GLVR1s. Such sequence variation in the critical region of rat GLVR1 might therefore account for its differential ability to allow GALV and SSAV infection but not FeLV-B infection. The sequence of region A of GLVR1 in the two rat cell lines resistant to FeLV-B infection, HSN and NRK, and in the weakly infectible XC cells was also determined by polymerase chain reaction from RNA (primers were 20-mers corresponding to codons 517 to 523 and 604 to 610 of the rat GLVR1 sequence). All three sequences were identical to that of the rat liver GLVR1 (Fig. 1B). The differential infectibility of XC cells compared with that of NRK and HSN cells cannot, therefore, be explained by region A sequence variation and may result either from sequence variation elsewhere, from differential receptor expression levels, or from a greater efficiency of infection at a step other than receptor recognition.

To demonstrate that the rat GLVR1 sequence could determine the infectivity of rat HSN and NRK cells by GALV and SSAV but not by FeLV-B, a chimeric human-rat receptor was constructed. When this chimeric human-rat GLVR1 was expressed in *M. dunni* cells, they became sensitive to infection by LacZ (GALV) and LacZ (SSAV) but not by LacZ (FeLV-B) (Fig. 2, rat region A sequence). Thus, sequences within the 162 C-terminal amino acids were responsible for the inability of rat GLVR1 to allow FeLV-B infection. The role of region A was demonstrated by mutating amino acids within this region of the human-rat chimeric GLVR1 molecule. Figure 2 shows that mutation of four amino acids in the rat region A, E-550, R-552, T-556, and E-558 (adopting the amino acid numbering of human GLVR1), to restore the sequence to essentially that of the human GLVR1, restored the ability of the chimeric human-rat GLVR1 to allow LacZ (FeLV-B) infection. T-555 was not mutated, as the human and murine receptors are homologous at this position. Thus, the rat region A sequence was responsible for the lack of LacZ (FeLV-B) infection. A single amino acid change in the rat region A, R-552→Gly, restored full LacZ (FeLV-B) infection; E-550→Asp and E-558→Val, alone or in combination, partially restored infectivity (Fig. 2).

Analysis of the same mutants for their ability to allow LacZ (GALV) and LacZ (SSAV) infection revealed a surprising difference between the two viruses (Fig. 2). While all the mutants conferred fully efficient infection by LacZ (GALV), mutation of E-550 to Asp greatly reduced infection by LacZ (SSAV); the effect of this mutation could be compensated by mutating E-558 to Val (Fig. 2). The mutational analysis of human GLVR1 by Johann et al. (11) showed that changing E-550 or T-551 to Lys abolished GALV infection. The identical mutations were therefore introduced into the rat GLVR1 region A containing G-552, which was permissive for GALV, SSAV, and FeLV-B. Mutation of E-551 to a residue with a positively charged side chain abolished infection by all three viruses; this residue is therefore critical for receptor function. However, mutation of T-551 to Lys inhibited only GALV and SSAV infection. These data demonstrate that, while the same region of GLVR1 was critical for infection by GALV, SSAV, and FeLV-B, subtle differences between the sequences required by the three viruses could be detected.

DISCUSSION

While GALV and SSAV have highly homologous sequences, the FeLV-B envelope shows little homology in the region involved in receptor recognition (4, 5, 23). The recognition of a common receptor by GALV, SSAV, and FeLV-B has therefore probably arisen from convergent evolution of viral envelopes to adopt the use of a receptor which is favorable for viral proliferation. GLVR1 may be a suitable receptor because of its broad distribution of expression in tissue (10). It may also be the case that only certain cell surface proteins can function effectively to allow viral entry (6). A third possibility is that viral envelope interaction with GLVR1

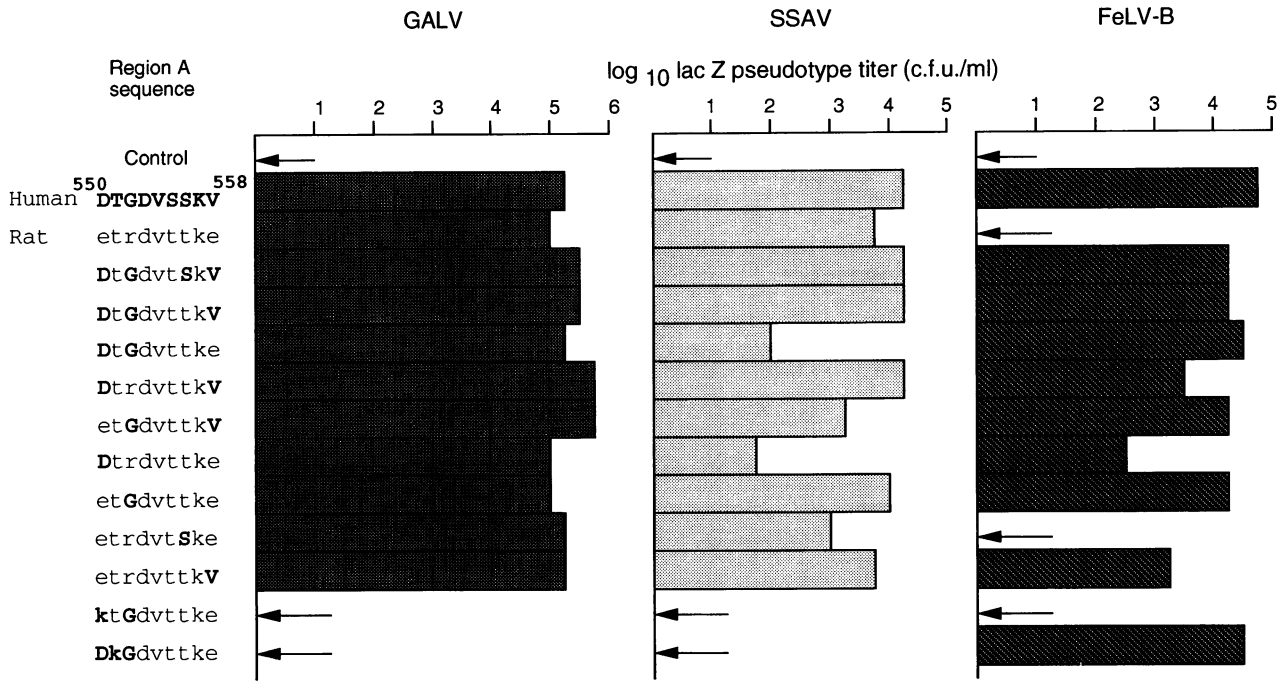

FIG. 2. Region A sequence determines the pattern of viral infectivity. *M. dunni* cells transfected with pSV2neo alone (control), pSV2neo with human GLVR1 pOJ9 cDNA (Human), or human-rat chimeric cDNAs including the rat region A sequence (Rat) and its mutants as shown were assayed for their ability to be infected by GALV, SSAV, and FeLV-B. Mutated amino acids in rat region A are in boldface.

stimulates cell proliferation, by analogy with murine leukemic viruses, which would be favorable for virus production (16, 17).

The three viruses require the same 9-amino-acid sequence of GLVR1, which is predicted from hydrophobicity analysis to form part of an extracellular loop (20), for cell infection. The data presented here do not clarify at which step in the infection process this loop is required. This may involve initial virus-envelope interaction or postbinding steps required for viral internalization. Whether cell surface expression of this loop is sufficient to allow viral infection has also not been determined; other regions of the receptor may also be required. These possibilities could potentially be distinguished by cell surface-targeted expression of truncated GLVR1 molecules. Similar studies of the receptor for ecotropic murine retroviruses have identified three amino acids within an extracellular loop which are critical for viral infection (1, 31). In this case, a mutant of the human ecotropic receptor homolog capable of conferring viral infection failed to bind significant levels of viral envelope protein, suggesting that the affinity of envelope-receptor interaction does not control the efficiency of infection in this system (1).

It is significant that the 9-amino-acid critical loop of GLVR1 is one of the regions of the molecule that is most highly divergent between species (references 10 and 11 and this report). This suggests that conservation of its sequence is not required for the cellular function of GLVR1. Therefore, viral envelope interaction with this region may not affect the maintenance of an essential cellular transport process.

Exploitation of this species divergence allowed us to demonstrate that FeLV-B has additional sequence requirements for infection, within the 9-amino-acid critical region, compared with GALV. GALV has also been shown to require acidic Glu or Asp, not basic Lys, at amino acid 550 and not to tolerate Lys in place of polar Thr at amino acid 551 (11). FeLV-B does not require Thr at amino acid 551 but has an additional requirement for the small, polar Gly in place of the bulky, basic Arg at amino acid 552. FeLV-B also prefers Asp at amino acid 550 and Val, in place of Glu, at amino acid 558. Despite its degree of sequence homology with GALV, SSAV can also be shown to have different sequence preferences for infection within the 9-amino-acid critical region. In particular, SSAV favors Glu at amino acid 550 but will tolerate Asp if Val is present at amino acid 558. These data demonstrate that at least four of the amino acids within the 9-amino-acid critical region are involved in determining viral infectivity. Furthermore, they show that subtle receptor sequence differences can control differential viral tropism.

ACKNOWLEDGMENT

This work was funded by the Wellcome Trust and the Cancer Research Campaign.

REFERENCES

1. **Albritton, L. M., J. W. Kim, L. Tseng, and J. M. Cunningham.** 1993. Envelope-binding domain in the cationic amino acid transporter determines the host range of ecotropic murine retroviruses. J. Virol. **67**:2091–2096.
2. **Albritton, L. M., L. Tseng, D. Scadden, and J. M. Cunningham.** 1989. A putative murine ecotropic retrovirus receptor gene encodes a multiple membrane-spanning protein and confers susceptibility to virus infection. Cell **57**:659–666.
3. **Dalgleish, A. G., P. C. L. Beverley, P. R. Clapham, D. H. Crawford, M. F. Greaves, and R. A. Weiss.** 1984. The CD4 (T4) antigen is an essential component of the receptor for the AIDS retrovirus. Nature (London) **312**:763–766.
4. **Delassus, S., P. Sonigo, and S. Wain-Hobson.** 1989. Genetic organisation of gibbon ape leukemia virus. Virology **173**:205–213.
5. **Elder, J. H., and J. I. Mullins.** 1983. Nucleotide sequence of the envelope gene of Gardner-Arnstein feline leukemia virus B re-

veals unique sequence homologies with a murine mink cell focus-forming virus. J. Virol. **46**:871–880.
6. **Etienne-Julan, M., P. Roux, S. Carillo, P. Jeanteur, and M. Piechaczyk.** 1992. The efficiency of cell targetting by recombinant retroviruses depends on the nature of the receptor and the composition of the artificial cell-virus linker. J. Gen. Virol. **73**: 3251–3255.
7. **Ferry, N., O. Duplessis, D. Houssin, O. Danos, and J. M. Heard.** 1991. Retroviral mediated gene transfer to hepatocytes in vivo. Proc. Natl. Acad. Sci. USA **88**:8377–8381.
8. **Gorman, C.** 1985. High efficiency gene transfer into mammalian cells, p. 143–190. *In* D. Glover (ed.), DNA cloning, vol. 2. Academic Press, New York.
9. **Jarrett, O., W. D. Hardy, M. C. Golder, and D. Hay.** 1978. The frequency of occurrence of feline leukemia virus subgroups in cats. Int. J. Cancer **21**:334–387.
10. **Johann, S. V., J. J. Gibbons, and B. O'Hara.** 1992. GLVR1, a receptor for gibbon ape leukemia virus, is homologous to a phosphate permease of *Neurospora crassa* and is expressed at high levels in the brain and thymus. J. Virol. **66**:1635–1640.
11. **Johann, S. V., M. van Zeijl, J. Cekleniak, and B. O'Hara.** 1993. Definition of a domain of GLVR1 which is necessary for infection by gibbon ape leukemia virus and which is highly polymorphic between species. J. Virol. **67**:6733–6736.
12. **Kawakami, T. G., S. D. Huff, P. M. Buckley, D. L. Dungworth, and S. D. Snyder.** 1972. C-type virus associated with gibbon lymphosarcoma. Nature (London) New Biol. **235**:170–171.
13. **Kawakami, T. G., G. Kollias, and C. Holmberg.** 1980. Oncogenicity of gibbon type C myelogenous leukemia virus. Int. J. Cancer **25**:841–846.
14. **Kim, J. W., E. I. Closs, L. M. Albritton, and J. M. Cunningham.** 1991. Transport of cationic amino acids by the mouse ecotropic retrovirus receptor. Nature (London) **352**:725–728.
15. **Klatzmann, D., E. Champagne, S. Chamaret, J. Gruest, D. Guetard, T. Hercend, J.-C. Gluckman, and L. Montagnier.** 1984. T-lymphocyte T4 molecule behaves as the receptor for human retrovirus LAV. Nature (London) **312**:767–768.
16. **Li, J.-P., and D. Baltimore.** 1991. Mechanism of leukemogenesis induced by mink cell focus-forming murine leukemia viruses. J. Virol. **65**:2408–2414.
17. **Li, J. P., A. D. D'Andrea, H. F. Lodish, and D. Baltimore.** 1990. Activation of cell growth by binding of Friend spleen focus-forming virus gp55 glycoprotein to the erythropoietin receptor. Nature (London) **343**:762–764.
18. **Lieber, M. M., C. J. Scherr, G. J. Todaro, R. E. Beneviste, R. Callahan, and H. G. Coon.** 1975. Isolation from the Asian mouse *Mus caroli* of an endogenous type C virus related to infectious primate type C viruses. Proc. Natl. Acad. Sci. USA **72**:2315–2319.
19. **Miller, D. G., and A. D. Miller.** 1992. Tunicamycin treatment of CHO cells abrogates multiple blocks to retrovirus infection, one of which is due to a secreted inhibitor. J. Virol. **66**:78–84.
20. **O'Hara, B., S. V. Johann, H. P. Klinger, D. G. Blair, H. Rubinson, K. J. Dunn, P. Sass, S. M. Vitek, and T. Robins.** 1990. Characterization of a human gene conferring sensitivity to infection by gibbon ape leukemia virus. Cell Growth Differ. **1**:119–127.
21. **Rojko, J. I., E. A. Hoover, L. E. Mathes, R. G. Olsen, and J. P. Schaller.** 1979. Pathogenesis of experimental feline leukemia virus infection. JNCI **47**:881–889.
22. **Sattentau, Q. J., P. R. Clapham, R. A. Weiss, P. C. L. Beverley, L. Montagnier, M. F. Alhabi, J. C. Gluckman, and D. Klatzmann.** 1988. The human and simian immunodeficiency viruses HIV-1, HIV-2 and SIV interact with similar epitopes on their cellular receptor, the CD4 molecule. AIDS **2**:101–105.
23. **Sheets, R. L., R. Pandey, V. Klement, C. K. Grant, and P. Roy-Burman.** 1992. Biologically selected recombinants between feline leukemia virus subgroup A and an endogenous FeLV element. Virology **190**:849–855.
24. **Sommerfelt, M. A., and R. A. Weiss.** 1990. Receptor interference groups of 20 retroviruses plating on human cells. Virology **176**:58–69.
25. **Stewart, M. A., M. Warnock, A. Wheeler, N. Wilkie, J. I. Mullins, D. E. Onions, and J. C. Neil.** 1986. Nucleotide sequence of a feline leukemia virus subgroup A envelope gene and long terminal repeat and evidence for the recombinational origin of subgroup B viruses. J. Virol. **58**:825–834.
26. **Takeuchi, Y., G. Simpson, R. G. Vile, R. A. Weiss, and M. K. L. Collins.** 1992. Retroviral pseudotypes produced by rescue of a Moloney murine leukemia virus vector by C-type, but not D-type, retroviruses. Virology **186**:792–794.
27. **Takeuchi, Y., R. G. Vile, G. Simpson, B. O'Hara, M. K. L. Collins, and R. A. Weiss.** 1992. Feline leukemia virus subgroup B uses the same cell surface receptor as gibbon ape leukemia virus. J. Virol. **66**:1219–1222.
28. **Taylor, J. W., J. Ott, and F. Eckstein.** 1985. The rapid generation of oligonucleotide-directed mutations at high frequency using phosphorothioate-modified DNA. Nucleic Acids Res. **13**:8765–8785.
29. **Wang, H., M. P. Kavanaugh, R. A. North, and D. Kabat.** 1991. Cell-surface receptor for ecotropic murine retroviruses is a basic amino-acid transporter. Nature (London) **352**:729–731.
30. **Weiss, R. A.** 1993. Viral glycoproteins and cellular receptors involved in retrovirus infection, p. 1–108. *In* J. A. Levy (ed.), The Retroviridae, vol 2. Plenum Press, New York.
31. **Yoshimoto, T., E. Yoshimoto, and D. Meruelo.** 1993. Identification of amino acid residues critical for infection with ecotropic murine leukemia retrovirus. J. Virol. **67**:1310–1314.