JOURNAL OF VIROLOGY, Oct. 1997, p. 8078–8081 Vol. 71, No. 10
0022-538X/97/$04.00+0

Mutational Analysis of the Proposed Gibbon Ape Leukemia Virus Binding Site in Pit1 Suggests that Other Regions Are Important for Infection

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Received 27 February 1997/Accepted 30 June 1997

Region A of Pit1 (residues 550 to 558 in domain IV) and related receptors has remained the only sequence implicated in gibbon ape leukemia virus (GALV) infection, and an acidic residue at the first position appeared indispensable. The region has also been proposed to be the GALV binding site, but this lacks empirical support. Whether an acidic residue at the first position in this sequence is a definitive requirement for GALV infection has also remained unclear; certain receptors retain function even in the absence of this acidic residue. We report here that in Pit1 an acidic residue is dispensable not only at position 550 but also at 553 alone and at both positions. Further, the virus requires no specific residue at either position. Mutations generated a collection of region A sequences, often with fundamentally different physicochemical properties (overall hydrophobicity or hydrophilicity and net charge of −1, or 0, or +1), and yet Pit1 remained an efficient GALV receptor. A comparison of these sequences and a few previously published ones from highly efficient GALV receptors revealed that every position in region A can vary without affecting GALV entry. Even Pit2 is nonfunctional for GALV only because it has lysine at the first position in its region A, which is otherwise highly diverse from region A of Pit1. We propose that region A itself is not the GALV binding motif and that other sequences are required for virus entry. Indeed, certain Pit1/Pit2 chimeras revealed that sequences outside domain IV are specifically important for GALV infection.

The gibbon ape leukemia virus (GALV) and the amphotropic murine leukemia virus (A-MuLV), both type C mammalian retroviruses, use related cell surface proteins for entry into cells. The human receptor for GALV is Pit1 (25), and that for A-MuLV is Pit2 (23, 31). Another type C retrovirus, feline leukemia virus subgroup B, also uses Pit1 for entry (30), while the murine retrovirus 10A1 can use both receptors (24, 32). The genes for Pit1 and Pit2 map to distinct loci (12, 15), and the deduced polypeptides are 60% identical. The Pit1 sequence is also significantly homologous to the sodium-dependent phosphate permease of *Neurospora crassa*, and the predicted membrane topologies of the two proteins are similar. It was suggested, therefore, that Pit1, too, may be a phosphate transporter (13). Subsequent empirical data demonstrated that both Pit1 and Pit2 are indeed sodium-dependent phosphate symporters (16, 26). Although physiologically cognate, as viral receptors the two transporters are distinct; Pit1 allows only GALV entry, and Pit2 allows only A-MuLV entry (23, 27, 30). The predicted topological features of Pit1, Pit2, and rat Pit2 are apparently identical; 10 transmembrane regions, 5 extracellular domains, and a large intracellular region between the sixth and seventh transmembrane domains (13, 23, 31).

Previous studies have shown that a stretch of nine residues (550 to 558) in the fourth extracellular domain of Pit1 is required for GALV infection, and in this region aspartate 550 appeared indispensable. That an acidic residue at this position may be crucial for infection has been supported by a number of observations. (i) Deletion of aspartate 550 renders Pit1 nonpermissive to GALV infection (14). (ii) Murine homologs of Pit1 typically have lysine at 550 and are nonfunctional. When this lysine is replaced with an acidic residue, however, the receptors efficiently allow GALV infection (13, 14, 29, 33). (iii) Pit2 and its murine homologs do not permit GALV infection because they have lysine at the corresponding position (522). But a Pit2 mutant with glutamate at this position is a strong receptor for GALV (8). (iv) The hamster Pit2 homolog, HaPit2, has glutamate at 522 and is permissive for GALV infection (32).

It remains unclear, however, whether an acidic residue at the first position in region A of these receptors is a definitive requirement for GALV infection. Indeed, all efficient GALV receptors, naturally occurring ones and mutant derivatives, have an acidic residue in region A at the first position, the fourth, or both. We thought it likely that each acidic residue might serve as the functional substitute when the other is absent, as in MolPit1, an efficient GALV receptor that has isoleucine at the first position and aspartate at the fourth (28). To assess the role of acidic residues at these positions, we carried out site-directed mutagenesis of Pit1. We chose Pit1 because it has aspartate at both positions (550 and 553) and because it is commonly used as the standard for GALV infection.

An acidic residue at 550 or 553 in Pit1 is dispensable for GALV infection. To assess their importance for GALV infection, aspartates at positions 550 and 553 were replaced with a number of residues by site-directed mutagenesis with the Sculptor kit (Amersham, Arlington Heights, Ill.). The plasmid used for this purpose was IIKS(+)-572, derived by subcloning the 572-bp *Pst*I-*Spe*I fragment of Pit1 cDNA in pBluescript II KS(+) (Stratagene, La Jolla, Calif.). The subcloned fragment encodes a region of Pit1 encompassing extracellular domains IV and V. The *Escherichia coli* strain XL1-Blue (Stratagene) was used as the host for all recombinant work. The full-length mutant receptors were expressed by using the retroviral vector pLNSX (21). The effect of each mutation on GALV infection was assessed by expressing the receptor in *Mus dunni* tail

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TABLE 1. Relative GALV infection permissivity of Pit1 region A mutants

Receptor	Region A sequence[a] (residues 550–558)	Relative permissivity[b]
Pit1	DTGDVSSKV	100
Pit1-D550G	**G**TGDVSSKV	230 ± 24
Pit1-D553G	DTG**G**VSSKV	230 ± 18
Pit1-D553I	DTG**I**VSSKV	192 ± 13
Pit1-D553K	DTG**K**VSSKV	298 ± 28
Pit1-D553Q	DTG**Q**VSSKV	107 ± 5
Pit1-GQ	**G**TG**Q**VSSKV	80 ± 13
Pit1-QG	**Q**TG**G**VSSKV	219 ± 33
Pit1-GG	**G**TG**G**VSSKV	36 ± 4
Pit1-II	**I**TG**I**VSSKV	177 ± 3

[a] Residues present in the mutant receptors are in boldface.

[b] The mean titer with Pit1 in each experiment was considered 100, and all other titers were normalized to this value. The results are from two sets of experiments. For one set (Pit1, Pit1-553Q, Pit1-GG, and Pit1-II), the Pit1 titer was 51,100 ± 2,400 blue-forming units/ml, and for the other it was 62,200 ± 4,380 blue-forming units/ml. The values are means ± standard errors of the means.

fibroblasts (MDTF). Wild-type MDTF are resistant to GALV infection, evidently because their Pit1 homolog has lysine at 550 and is thus nonfunctional (33). These cell lines were derived using the retroviral vector packaging cells PA317 as previously described (7, 20) but were selected in 625 μg of G418 per ml. The GALV infection susceptibility of MDTF expressing various receptors was determined by infection with GALV vector produced from the cell line PG13/G1BgSvN (19, 22). A day before the assay, cells (20,000/well) were seeded in 24-well plates. The next day, 0.5 ml of GALV supernatant was added, undiluted or in 10-fold serial dilutions. Incubation with GALV was carried out for 20 to 24 h, and after a further 65 to 72 h the cells were processed for β-galactosidase activity. All assays were done with the same batch of vector supernatant containing 5 μg of Polybrene per ml. Suitable dilutions were selected for counting of the blue cells to determine the titer that each receptor afforded. We first assessed the importance of each acidic residue by replacing it with a neutral one. The results show that glycine at position 550 or 553 alone had no adverse effect on receptor function (Table 1). Further, replacing aspartate 553 with even the highly hydrophobic isoleucine also failed to impair receptor function. Because lysine at 550 in the Pit1 group of receptors or at the corresponding position in Pit2 group abrogates GALV entry (8, 13, 14, 29), we replaced aspartate 553 with lysine to see whether this substitution, too, would destroy receptor function. Surprisingly, lysine at 553 had no adverse effect on virus entry. Indeed, all these mutations somewhat enhanced infection efficiency. There was also no loss of receptor function when aspartate 553 was replaced with glutamine. These results clearly demonstrate that each acidic residue alone is dispensable for GALV infection. However, whether the receptor would retain function in the absence of both acidic residues remained unclear. We therefore assessed this possibility next.

GALV requires no specific residue at positions 550 and 553 in Pit1. Substitutions at either position 550 or 553 alone resulted in receptor variants that retained one of the two acidic residues. Because of their physical proximity, we thought that these acidic residues might be functionally substitutive and that only one might be required for GALV entry. To assess this possibility, the two acidic residues were simultaneously replaced with neutral ones. The presence of glutamine at 550 and glycine at 553 together or the highly hydrophobic isoleucine at both positions increased infection efficiency, much like the single substitutions (Table 1). Glycine at 550 and glutamine at 553 together and glycine at both positions were the only mutations that slightly decreased efficiency (Table 1). These results demonstrate that the acidic residues at positions 550 and 553 are simultaneously dispensable for GALV infection. The results further show the virus requires no specific residue at either position and no specific combination of residues at these positions. Moreover, region A not only can have an overall negative, positive, or zero charge but also can have substantial hydrophobicity (Pit1-II), and yet the receptor retains full function.

Every position in region A of functional GALV receptors can vary without affecting virus entry. A large collection of region A sequences from the current mutational analysis and many previously reported ones from strong GALV receptors now exists. Comparison of these sequences reveals that the region is highly diverse, and every position is variable (Table 2). And yet, all these variants are efficient GALV receptors. It is unlikely that a short sequence could embody such high degree of variation, often with fundamentally different physicochemical properties, and still retain a constant structure with a definitive role in GALV entry. We propose that region A per se is not the GALV binding site and that it is likely that the region is not directly important for virus entry at all.

It seems that in previous studies region A had appeared crucial for GALV entry because lysine at the first or the second position or deletion of aspartate 550 in Pit1 abrogates infection. Indeed, lysine at the first position is detrimental for GALV infection via any Pit1 or Pit2 group receptor (8, 13, 14, 29, 33). The mechanism by which lysine at this position blocks virus entry is unclear, but the effect appears to be negative dominant. This may explain why all receptors, despite high diversity in region A (Table 2), are functional as long as lysine is absent from the first two positions.

Certain Pit1/Pit2 chimeras suggest that receptor regions outside domain IV are specifically important for GALV infection. Pit2 is the related human phosphate transporter that serves as the receptor for A-MuLV but not for GALV (23, 31, 32). Pit2 region A (residues 522 to 530) is very different from Pit1 region A, but this diversity per se is not the reason Pit2 is nonfunctional for GALV. Rather, the receptor is nonfunctional because it has lysine at 522; replacement of this lysine with glutamate is sufficient to render Pit2 highly efficient for GALV infection (8).

To assess the possibility that regions outside domain IV that are specifically important for GALV infection exist, we made chimeras carrying the extracellular domains I, II, III, and V of Pit2 and IV of Pit1 with various mutations. Previous studies have shown that such differences, if any, could not be revealed

TABLE 2. Region A of a few highly efficient GALV receptors

Receptor[a]	Sequence[b]
MusPit1-DT (13)	**DT**QEASTKA
RatPit1 (29)	ETRDVTTKE
MolPit1 (28, 33)	ITGDVSSKV
Pit1-553K	DTG**K**VSSKV
Pit1-II	**I**TG**I**VSSKV
Pit1 (25)	DTGDVSSKV
Pit2-522E (8)	**E**QGGVTQEA
Pit2-EM	**E**QGGV**M**QEA

[a] Numbers in parentheses are references from which sequence data were obtained. All other data were obtained in this study.

[b] Residues 550-558 in Pit1 and 522-530 in Pit2. The mutant residues are shown in boldface.

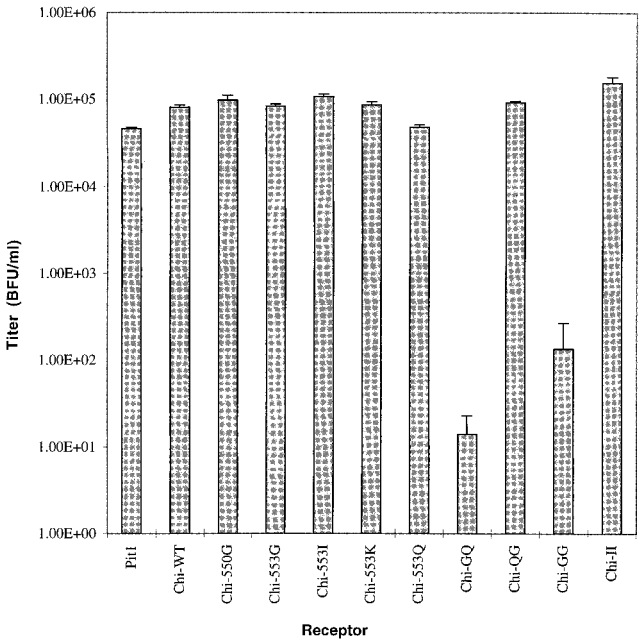

FIG. 1. Efficiency of GALV infection via Pit1/Pit2 chimeras containing domains I, II, III, and V of Pit2 and domain IV of Pit1 with various mutations. Titers were determined as described for data in Table 1 and are from three sets of experiments. In each set, Pit1 and Pit2 were included as controls. The Pit1 titers were 46,000 ± 1,820, 51,100 ± 2,400, and 62,200 ± 4,380 blue-forming units (BFU)/ml. The Pit1 titer plotted here is 51,100 ± 2,400 BFU/ml. The GALV titer afforded by wild-type Pit2 was consistently zero (not shown). The chimeras were constructed by replacing the 603-bp *Bgl*II-*Pfl*MI Pit2-encoding fragment in pLNS-Pit2 with the corresponding fragment encoding Pit1 with various mutations. The wild-type chimera was also made for comparison. The recombinant work required intermediate constructs because the Pit1 gene lacks the *Bgl*II site.

with chimeras of wild-type Pit1 and Pit2 (27). Our rationale for making these chimeras was that the structural features common to the two receptors and important for GALV entry may embody subtle differences and could be revealed by the presence of certain mutations in region A of Pit1. The results show that most mutant chimeras, like the wild-type construct, were somewhat stronger than Pit1 (Fig. 1). This suggests that domain IV of Pit1 with a number of mutations is fully compatible with the Pit2 sequence in the chimeras. But GALV infection via the chimeras containing the double mutations GG and GQ proved dramatically inefficient (Fig. 1). Chi-GQ, for example, was nearly 7,000-fold less efficient than the permuted construct Chi-QG and nearly 4,000-fold less efficient than Pit1-GQ. Thus, the highly detrimental effect of GG and GQ mutations is selective for chimeras, not native Pit1.

The mechanism by which GG and GQ mutations exert their detrimental effect in chimeras is unclear. But the two mutations could cause global malfolding of these receptors, thereby impairing their transport to the cell surface, which would account for dramatic reduction in GALV infection. To assess this possibility, Chi-GG and Chi-GQ were expressed in CHO K1 cells to see whether they remained efficient A-MuLV receptors. CHO K1 cells are normally resistant to A-MuLV but become highly susceptible when expressing the human receptor (Pit2) for this virus (31). Indeed, A-MuLV infection via Pit2 and the two chimeras proved nearly identical (data not shown). Thus, the adverse effect of GG and GQ mutations in chimeras is specific for GALV infection, and the results suggest the presence of a receptor region outside domain IV that is important for GALV entry. Identification of this sequence is under way in our laboratory.

Our findings contradict the previous notion that for GALV infection an acidic residue at position 550 is indispensable. But the issue is readily resolved by reinterpreting the previous data: Pit1 and other functional GALV receptors, naturally occurring ones and mutant derivatives, were permissive because they lacked lysine at the first two positions, not because they had an acidic residue at 550. Thus, infection permissivity of these receptors and the presence of an acidic residue at 550 were merely coincidental. Likewise, all nonfunctional GALV receptors, such as Pit2, were nonfunctional because they had lysine at the corresponding position, not because they lacked an acidic residue.

An important goal of our studies with the Pit1 and Pit2 family of receptors is to identify the structural commonalities—primary and possibly secondary structures—that impart GALV infection permissivity to these proteins. Such studies may help elucidate the molecular events that effect viral entry into cells. A secondary structure analysis, done by Garnier Protein Structure Prediction (GeneWorks, IntelliGenetics, Inc., Mountain View, Calif.), of domain IV and the flanking sequences of a number of receptors revealed no common secondary structure in region A. However, the predicted structure of the domain IV sequence that precedes region A is a β-strand, in both the Pit1 and Pit2 groups. It is possible that this structure is directly important for GALV infection and that lysine at the first or the second position in region A exerts its negative dominant effect by disrupting this β-strand. Alternatively, lysine could exert its negative dominant effect by forming a salt bridge with a strategically placed acidic residue, thereby disrupting the authentic, as-yet-unidentified motif that GALV requires for entry. Indeed, the highly differential effects of the mutations GG and GQ in Pit1 and Pit1/Pit2 chimeras do suggest the presence of yet another region outside domain IV that may prove crucial for GALV infection. Assessment of these possibilities is now under way in our laboratory.

Finally, it is unclear how Pit1 and Pit2 group receptors effect GALV or A-MuLV entry into cells. However, two distinct biochemical events must occur for enveloped-virus entry; viral SU binding to a cell surface receptor and subsequent fusion of viral envelope with plasma membrane (11, 18). For the human immunodeficiency virus, CD4 functions in primary binding (3, 17) and certain multimembrane-spanning chemokine receptors are required for fusion (1, 2, 4–6, 9, 10). So far, however, Pit1 and Pit2 group proteins are the only ones known that are required for GALV entry. If no other protein is required for GALV infection, then these receptors must carry out binding as well as the fusion function. Alternatively, they may be crucial only for fusion, and the primary receptor that affords initial binding with viral SU may be another protein. This protein may be ubiquitous and therefore may have eluded identification as the primary GALV receptor.

We thank Karen B. Farrell for making the mutant receptor Pit2-EM.

REFERENCES

1. **Alkhatib, G., C. Combadiere, C. C. Broder, Y. Feng, P. E. Kennedy, P. M. Murphy, and E. A. Berger.** 1996. CC CKR5: a RANTES, MIP-1α, MIP-1β receptor as a fusion cofactor for macrophage-tropic HIV-1. Science **272:** 1955–1958.
2. **Choe, H., M. Farzan, Y. Sun, N. Sullivan, B. Rollins, P. D. Ponath, L. Wu, C. R. Mackay, G. LaRosa, W. Newman, N. Gerard, C. Gerard, and J. Sodoroski.** 1996. The β-chemokine receptors CCR3 and CCR5 facilitate infection by primary HIV-1 isolates. Cell **85:**1135–1148.
3. **Dalgleish, A. G., P. C. L. Beverely, 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 **312:**763–766.
4. **Deng, H., R. Liu, W. Elmeier, S. Choe, D. Unutmaz, M. Burkhart, P. Di**

Marzio, S. Marmon, R. E. Sutton, C. M. Hill, C. B. Davis, S. C. Peiper, T. J. Schall, D. R. Littman, and N. R. Landau. 1996. Identification of a major coreceptor for primary isolates of HIV-1. Nature **381:**661–666.

5. **Doranz, B. J., J. Rucker, Y. Yi, R. J. Smyth, M. Samson, S. C. Peiper, M. Parmentier, R. G. Collman, and R. W. Doms.** 1996. A dual-tropic primary HIV-1 isolate that uses fusin and the β-chemokine receptors CKR-5, CKR-3, and CKR-2B as fusion cofactors. Cell **85:**1149–1158.
6. **Dragic, T., V. Litwin, G. P. Allaway, S. R. Martin, Y. Huang, K. A. Nagashima, C. Cayanan, P. J. Maddon, R. A. Koup, J. P. Moore, and W. A. Paxton.** 1996. HIV-1 entry into $CD4^+$ cells is mediated by the chemokine receptor CC-CKR-5. Nature **381:**667–673.
7. **Eglitis, M. A., M. V. Eiden, and C. A. Wilson.** 1993. Gibbon ape leukemia virus and the amphotropic murine leukemia virus 4070A exhibit an unusual interference pattern on E36 chinese hamster cells. J. Virol. **67:**5472–5477.
8. **Eiden, M. V., K. B. Farrell, and C. A. Wilson.** 1996. Substitution of a single amino acid residue is sufficient to allow the human amphotropic murine leukemia virus receptor to function as a gibbon ape leukemia virus receptor. J. Virol. **70:**1080–1085.
9. **Endres, M. J., P. R. Clapham, M. Marsh, M. Ahuja, J. Davis-Turner, A. McKnight, J. F. Thomas, B. S. Stoenbenay-Haggarty, S. Choe, P. J. Vance, T. N. C. Wells, C. A. Power, S. S. Sutterwala, R. W. Doms, N. R. Landau, and J. A. Hoxie.** 1996. CD4-independent infection by HIV-2 is mediated by CXCR-4. Cell **87:**745–756.
10. **Feng, Y., C. C. Broder, P. E. Kennedy, and E. A. Berger.** 1996. HIV-1 entry cofactor: functional cDNA cloning of a seven-transmembrane, G-protein coupled receptor. Science **272:**872–877.
11. **Fields, B. N., and D. M. Knipe (ed.).** 1996. Virology, 3rd ed. Raven Press, New York, N.Y.
12. **Garcia, J. V., C. Jones, and A. D. Miller.** 1991. Localization of the amphotropic murine leukemia virus gene to the pericentromeric region of human chromosome 8. J. Virol. **65:**6316–6319.
13. **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.
14. **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.
15. **Kaelbling, M., R. Eddy, T. B. Shows, N. G. Copeland, D. J. Gilbert, N. A. Jenkins, H. P. Klinger, and B. O'Hara.** 1991. Localization of the human gene allowing infection by gibbon ape leukemia virus to human chromosome region 2q11-q14 and to the homologous region on mouse chromosome 2. J. Virol. **65:**1743–1747.
16. **Kavanaugh, M. P., D. G. Miller, W. Zhang, W. Law, S. L. Kozak, D. Kabat, and A. D. Miller.** 1994. Cell surface receptors for gibbon ape leukemia virus and amphotropic murine leukemia virus are inducible sodium-dependent phosphate symporters. Proc. Natl. Acad. Sci. USA **91:**7071–7075.
17. **Maddon, P. J., A. G. Dalgleish, J. S. McDougal, P. R. Clapham, R. A. Weiss, and R. Axel.** 1986. The T4 gene encodes the AIDS virus receptor and is expressed in the immune system and the brain. Cell **47:**333–348.
18. **Marsh, M., and A. Helenius.** 1989. Virus entry into animal cells. Adv. Virus Res. **36:**107–151.
19. **McLachlin, J. R., N. Mittereder, M. B. Daucher, M. Kadan, and M. A. Eglitis.** 1993. Factors affecting retroviral function and structural integrity. Virology **195:**1–5.
20. **Miller, A. D., and C. Buttimore.** 1986. Redesign of retrovirus packaging cell lines to avoid recombination leading to helper virus production. Mol. Cell Biol. **6:**2895–2902.
21. **Miller, A. D., and G. J. Rosman.** 1989. Improved retroviral vectors for gene transfer and expression. BioTechniques **7:**980–990.
22. **Miller, A. D., J. V. Garcia, N. von Suhr, C. M. Lynch, C. Wilson, and M. V. Eiden.** 1991. Construction and properties of retrovirus packaging cells based on gibbon ape leukemia virus. J. Virol. **65:**2220–2224.
23. **Miller, D. G, R. H. Edwards, and A. D. Miller.** 1994. Cloning of the cellular receptor for amphotropic murine leukemia virus reveals homology to that for gibbon ape leukemia virus. Proc. Natl. Acad. Sci. USA **91:**78–82.
24. **Miller, D. G., and A. D. Miller.** 1994. A family of retroviruses that utilize related phosphate transporters for cell entry. J. Virol. **68:**8270–8276.
25. **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.
26. **Olah, Z., C. Lehel, W. B. Anderson, M. V. Eiden, and C. A. Wilson.** 1994. The cellular receptor for gibbon ape leukemia virus is a novel high affinity phosphate transporter. J. Biol. Chem. **269:**25426–25431.
27. **Pedersen, L., S. V. Johann, M. van Zeijl, F. S. Pedersen, and B. O'Hara.** 1995. Chimeras of receptors for gibbon ape leukemia virus/feline leukemia virus B and amphotropic murine leukemia virus reveal different modes of receptor recognition by retrovirus. J. Virol. **69:**2401–2405.
28. **Schneiderman, R. D., K. B. Farrell, C. A. Wilson, and M. V. Eiden.** 1996. The Japanese feral mouse Pit1 and Pit2 homologs lack an acidic residue at position 550 but still function as gibbon ape leukemia virus receptors: implications for virus binding motif. J. Virol. **70:**6982–6986.
29. **Tailor, C. S., Y. Takeuchi, B. O'Hara, S. V. Johann, R. A. Weiss, and M. K. L. Collins.** 1993. 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 infection. J. Virol. **67:**6737–6741.
30. **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:**1219–1223.
31. **van Zeijl, M., S. V. Johann, E. Closs, J. Cunningham, R. Eddy, T. B. Shows, and B. O'Hara.** 1994. A human amphotropic retrovirus receptor is a second member of the gibbon ape leukemia virus receptor family. Proc. Natl. Acad. Sci. USA **91:**1168–1172.
32. **Wilson, C. A., K. B. Farrell, and M. V. Eiden.** 1994. Properties of a unique form of the murine amphotropic leukemia virus receptor expressed on hamster cells. J. Virol. **68:**7697–7703.
33. **Wilson, C. A., K. B. Farrell, and M. V. Eiden.** 1994. Comparison of cDNAs encoding the gibbon ape leukemia virus receptor from susceptible and nonsusceptible murine cells. J. Gen. Virol. **75:**1901–1908.