Blocking of HIV-1 Infection by Targeting CD4 to Nonraft Membrane Domains


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Abstract

Human immunodeficiency virus (HIV)-1 infection depends on multiple lateral interactions between the viral envelope and host cell receptors. Previous studies have suggested that these interactions are possible because HIV-1 receptors CD4, CXCR4, and CCR5 partition in cholesterol-enriched membrane raft domains. We generated CD4 partitioning mutants by substituting or deleting CD4 transmembrane and cytoplasmic domains and the CD4 ectodomain was unaltered. We report that all CD4 mutants that retain raft partitioning mediate HIV-1 entry and CD4-induced Lck activation independently of their transmembrane and cytoplasmic domains. Conversely, CD4 ectodomain targeting to a nonraft membrane fraction results in a CD4 receptor with severely diminished capacity to mediate Lck activation or HIV-1 entry, although this mutant binds gp120 as well as CD4wt. In addition, the nonraft CD4 mutant inhibits HIV-1 X4 and R5 entry in a CD4+ cell line. These results not only indicate that HIV-1 exploits host membrane raft domains as cell entry sites, but also suggest new strategies for preventing HIV-1 infection.

Key words: CD4 • lipid rafts • HIV-1 • Lck • infection inhibition

Introduction

The plasma membrane is a specialized structure that channels and integrates the information that flows continuously between a cell and its environment. The cell plasma membrane also constitutes the initial barrier against infection by intracellular pathogens. Contrary to the view of the plasma membrane as a homogenous phospholipid backbone loaded with proteins, it is now established that it is a highly sophisticated structure assembled of distinct lipid domains that functionally organize the proteins embedded in the bilayer. One of these microdomain types, termed rafts, is formed by glycosphingolipids (GSL),* sphingomyelin, and cholesterol packaged in the external leaflet of the plasma membrane (1). Due to the high melting point of lipids, membrane rafts are in a rigid, ordered state (2). Rafts nonetheless retain substantial lateral and rotational mobility. They are viewed as moving platforms of ordered membrane-bearing proteins with a specific preference for this lipid environment, such as glycosylphosphatidylinositol (GPI)-anchored and double-acylated cytoplasmic proteins.

Rafts may function as devices to control membrane protein–protein interactions and several mechanisms can be envisioned. First, it is reported that interactions occur preferentially between proteins sharing identical lipid environments (3). Accordingly, the interaction of raft-associated proteins with membrane nonraft proteins is very restricted (4). Second, proteins initially segregated in distinct elementary raft units might be brought together by raft coalescence, which could generate supramolecular complexes of raft-associated proteins in a single clustering event. For instance, lateral cross-linking of GPI-anchored raft proteins triggers raft-associated tyrosine kinase activation (2) even though these two types of proteins cannot directly interact. A third possibility is that a protein that initially partitions in a nonraft membrane region might be recruited into a pre-existing raft, enabling raft-dependent protein–protein interactions. Therefore, raft domains may organize protein interactions in time and space by regulating raft coalescence.
and/or controlling the recruitment of nonraft proteins to these domains. Nevertheless, this scenario might be even more complex as membrane protein segregation not only between raft and nonraft domains, but also between distinct raft subtypes, influences lateral organization of the plasma membrane (5).

The temporal and spatial control of protein interactions at the plasma membrane regulates cell signaling integration and pathogen infection of cells (6). CD4 takes part in these two processes, as it participates in the integration of TCR signaling by recruiting p56lck (5, 14, 21–23). A recent report suggests that large CD4–gp120 complexes (20), which may be formed by lateral raft rearrangements, viral entry would thus be enabled if CD4 and chemokine receptor partition into raft domains. According to this latter interpretation, CD4 partitioning in nonraft membranes would not affect HIV-1 entry. Conversely, if HIV-1 uses host raft membranes as entry sites, CD4 partitioning into nonraft membranes would impede viral infection.

Here, we analyzed these possibilities by generating CD4 mutants in the cytoplasmic and transmembrane domains. These mutants shared the extracellular domain of the WT CD4 form. We generated a CD4 mutant that partitions in the nonraft plasma membrane fraction by replacing CD4 transmembrane and cytoplasmic domains with the transmembrane and a very short cytoplasmic tail from the low density lipoprotein (LDL)-R. This CD4 mutant (CD4-LDL) neither activates Lck after CD4 cross-linking nor mediates HIV-1 entry, which are two independent CD4 functions. The failure of the CD4–LDL mutant to mediate these processes is the sole consequence of CD4 extracellular domain localization in a nonraft membrane fraction, because a raft-associated CD4–GPI mutant that lacks transmembrane and cytoplasmic CD4 domains activates Lck and mediates HIV-1 entry. Moreover, the nonraft CD4 mutant prevents X4 and R5 HIV-1 strain infection of CD4+ T cells. These results highlight the fundamental role of membrane rafts in regulating the protein–protein interactions required for HIV-1 entry and suggest new strategies for preventing HIV-1 infection.

Materials and Methods

Generation of CD4 Mutants. Selected transmembrane amino acids of WT CD4 were replaced with alanine by site-directed mutagenesis (Stratagene). The synthetic oligonucleotide primer pairs 5’-GCAGCGCAATTGCGCCGCTGCAGGCGGAGGCGTCCGGC-3’ and 5’-CGCGACAGCCCGCCGGCCCAAGCGCCGCCAATTGCGTCG-3’ (CD4-4A374); 5’-CCCTGTAGTGGGTGCTGTCGCAATGGCCGAGGCGGAGG-3’ (CD4-4A387); 5’-GGGGGCGTCGCCGGCCGGCCGGCCGGCTTCATTGGGCTAGGC-3’ and 5’-GGCTAGCCCAATGGAAGCGGCGCCGCCGAGGCGGACGCCCCC-3’ (CD4-3A383); 5’-CCCGCCGCCCTCCTGATTGGCCGTGGGCAGTCATC-3’ and 5’-GATTGCCTAGCCCCGGCAAGACAGGAGGCGGCGGC-3’ (CD4-2A386); 5’-CATTGGGCTAGCCGGCCGGCCGGCTCGTGTCAGGGCGG-3’ and 5’-GGCCGACCCGTGACACAGGCGGCGGCGGCGGCGGCCGCCGCTGTCAG-3’ (CD4-3A384); 5’-GGCTGAGCCCTGAGCCCTGCCGCGCGGCGGCGGCGGCCGCCGCCCTG-3’ and 5’-CCGGTGCGCCGCTGCGGCGGGGGGCGCTAGCCCAATGGCCGAGGCGGACGCCCCC-3’ and 5’-GGCCGACCCGTGACACAGGCGGCGGCGGCGGCGGCCGCCGCTGTCAG-3’ (CD4-3A391); 5’-GGCTGAGCCCTGAGCCCTGCCGCGCGGCGGCGGCGGCCGCCGCCGCCCTG-3’ and 5’-CCGGTGCGCCGCTGCGGCGGGGGGCGCTAGCCCAATGGCCGAGGCGGACGCCCCC-3’ and 5’-GGCCGACCCGTGACACAGGCGGCGGCGGCGGCGGCCGCCGCTGTCAG-3’ (CD4-3A392); 5’-CTCTGGTCAAGGGCCGCCCGCGCGAGGCGG-3’ and 5’-CCGCTTGGGTGCCGGCCGCCCTACAGA-3’ (CD4-C397A); and 5’-GCTGGCCTTCGGTGCCGGGCCCTGACAGCGGCG-3’ and 5’-GGCCGACCCGTGACACAGGCGGCGGCGGCGGCGGCCGCCGCTGTCAG-3’ (CD4-C397A). These mutants shared the extracellular domain of the WT CD4 form. We generated a CD4 mutant that partitions in the nonraft plasma membrane fraction by replacing CD4 transmembrane and cytoplasmic domains with the transmembrane and a very short cytoplasmic tail from the low density lipoprotein (LDL)-R. This CD4 mutant (CD4-LDL) neither activates Lck after CD4 cross-linking nor mediates HIV-1 entry. Moreover, the nonraft CD4 mutant prevents X4 and R5 HIV-1 strain infection of CD4+ T cells. These results highlight the fundamental role of membrane rafts in regulating the protein–protein interactions required for HIV-1 entry and suggest new strategies for preventing HIV-1 infection.
HEK-293 cells were transfected using a standard calcium phosphate method. Transfection efficiency was 74–85%, as determined with an enhanced green fluorescent protein vector. CD4 levels were maximal 24–96 h after transfection as analyzed by FACS® (EPICS; Coulter) using an FITC-anti-CD4 (Immuno-tech) or an FITC-labeled control antibody. The percentage of CD4+ cells observed after subtracting the control was multiplied by the average fluorescence intensity to calculate surface CD4 expression for each mutant (26).

**Flotation Experiments.** HEK-293 cells expressing the CD4 mutants were lysed at 4°C in TXNE buffer (50 mM Tris-HCl, pH 7.4, 150 mM NaCl, 5 mM EDTA, 0.5% Triton X-100) plus protease inhibitors. Detergent-resistant membranes (DRMs) were isolated by ultracentrifugation (170,000 g for 4 h at 4°C in a 30–35% OptiPrep™ gradient (Nycomed; reference 21)). Normalized protein amounts were analyzed by Western blot with anti-CD4 (Leu3A; Becton Dickinson), anti-transferin receptor (TR; Zymed Laboratories), and anti-VIP–21 (Santa Cruz Biotechnology, Inc.) antibodies.

**Immunofluorescence and gp120-induced Patching.** For colocalization of CD4 with GM1, HEK-293 transfected with CD4 mutants were incubated for 30 min at 12°C with anti-CD4 (Leu3A) followed by a Cy3-anti–mouse antibody (Jackson Immunoresearch Laboratories). Finally, FITC-cholera toxin was added for 5 min at 12°C.

For gp120 copatching, HEK-293 cells expressing CD4 mutants were incubated with recombinant gp120 (T cell line–anti–mouse antibodies (27). Plates were then incubated at 37°C after transfection by flow cytometry. HIV-1emgag was introduced into effector HEK-293 cells by infection for 1 h at 37°C with recombinant vaccinia virus. 12 h after infection, 106 effector cells cultured in 100 μg/ml rifampicin were mixed with HEK-293-C4D–expressing cells for 6 h at 37°C, and cell–cell fusion was analyzed by luciferase activity measurement in cell lysates (25 mM Tris-phosphate, pH 7.8, 1% Triton X-100, 1 mM EDTA, 1 mM DTT, 8 mM MgCl2, 15% glycerol). Luciferase activity was calculated as the quotient between firefly and renilla activity values.

**Generation of Recombinant Replication-defective HIV Pseudotypes.** For single-round infections, pNL4.3-Luc.R-E– (provided by N. Landau, AIDS Research and Reference Reagent Program, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, MD) was pseudotyped with HIV-1NL4.3 env, HIV-1Δd6, and vesicular stomatitis virus (VSV)-G env as previously described (14). HEK-293-CR5 or MT-2CCR5 cells (provided by J. Alcamí, Instituto Salud Carlos III, Madrid, Spain) expressing selected CD4 mutants were transduced with viral supernatants (1 and 0.1 multiplicity of infection) for 2 h at 37°C, and infectivity was determined after 24 h.

**Biotinylation of Cells.** Mock, CD4wt, or CD4–LDL cells were biotinylated using EZ-Link Sulfo-NHS-Biotin (Pierce Chemical Co.) according to the manufacturer’s instructions. Cells were lysed with RIPA (50 mM Tris-HCl, pH 7.5, 150 mM NaCl, 1% NP-40, 0.1% SDS, 0.5% deoxycholate) and equal amounts (100 μg) of lysates were precipitated with aspirase-avidin for 1 h at 4°C. Pellets were washed and resolved in SDS-PAGE. Western blots were probed sequentially with anti-6xHis (Sigma–Aldrich), anti-CD4 (Leu3A), and peroxidase-streptavidin (Sigma–Aldrich).

**HIV-1 Infection of MT-2-CCR5 Cells.** Mock-, CD4wt-, or CD4–LDL-transfected MT-2-CCR5 cells were incubated with NL4-3 or BaL viral stocks (1 or 10 ng p24 antigen/106 cells) for 2 h at 37°C. 0.5 × 105/ml cells were cultured in complete RPMI medium. Cell-free supernatants were collected daily and tested for p24 antigen (Coulter).

**Results**

**Generation of CD4 Mutants with Differential Raft Partitioning.** Double acylation and GPI modification are major signals for protein partitioning in rafts by anchoring proteins to the inner or outer leaflet of the membrane raft, respectively. Nonetheless, integral membrane proteins have no clear consensus signal that indicates preferential raft association. The best studied raft-associated transmembrane protein is the influenza hemagglutinin, whose raft targeting is determined by three acylation acceptor cysteines and specific amino acids in its transmembrane domain (31, 32). CD4 has a 26-amino acid transmembrane region with two
putative palmitoylation acceptor cysteines in the juxtamembrane domain (33). We generated a panel of CD4 chimeras and mutants that affect both transmembrane and cytoplasmic domains (Fig. 1 A). The CD4 extracellular domain was fused to the LDL-R transmembrane and juxtamembrane region (CD4–LDL). As a control for this construct, a CD4 mutant was generated by replacing the CD4 transmembrane domain with that of the LDL-R (CD4–LDL–CD4). This mutant retains the palmitoylated cysteines. The CD4 ectodomain was also fused to a GPI consensus sequence (CD4–GPI) to target CD4 luminal domain to rafts. Finally, we generated CD4 mutants, including three in which palmitoylated Cys394 and/or Cys397 are eliminated by alanine scanning of the transmembrane and juxtamembrane CD4 domains.

We analyzed raft partitioning of the CD4 mutants by isolating a DRM fraction enriched in raft-associated proteins (6). HEK-293 cells expressing the CD4 mutants were extracted with Triton X-100 and the DRM fraction was isolated in density gradients. A large proportion of CD4wt, CD4–GPI, and CD4–LDL–CD4 proteins copurify with caveolin in the DRM fraction, whereas CD4–LDL copurifies with the TRβ in the nonraft compartment (Fig. 1 B). Because CD4–LDL and CD4–LDL–CD4 have identical transmembrane domains, the results suggest that the transmembrane sequence does not contain the main determinants for CD4 partitioning in rafts. Supporting this idea, all CD4 transmembrane mutants showed DRM partitioning comparable to that of CD4wt (unpublished data). Single CD4–3A392, CD4–C397A (unpublished data), or double CD4–C394/397A (Fig. 1 B) palmitoylation mutants also partition in the DRM fraction, suggesting that CD4 acylation is not a major determinant for CD4 association to DRM.

DRM analysis proved useful in identifying parameters affecting raft partitioning of proteins, although weak raft associations might be lost after detergent extraction (6). These misinterpretations can be avoided in copatching experiments, as antibody-induced lateral clustering stabilizes protein–lipid interactions. We analyzed raft partitioning of the CD4 constructs in live HEK-293 cells by copatching CD4 and the cholera toxin β subunit, which binds to the raft-associated ganglioside GM1. Confocal analysis indicated that CD4wt (Fig. 1 C), CD4–GPI (Fig. 1 D), CD4–LDL–CD4 (Fig. 1 F), the palmitoylation CD4–C394/397A mutant (Fig. 1 G), as well as the transmembrane CD4 mutants (unpublished data), colocalize extensively with GM1. Conversely, CD4–LDL and GM1 show segregated staining patterns (Fig. 1 E), confirming that this chimera does not partition in rafts.

Partitioning of the CD4 Ectodomain in Rafts Is Sufficient to Activate LCK. We studied CD4 chimera and mutant association to, and activation of, raft-p56lck. Lck association with the palmitoylation-deficient CD4 mutants was reported (33), which suggests that neither the CD4 transmembrane nor juxtamembrane domain plays a role in Lck activation. Accordingly, chimeras with the CD4 cytoplasmic domain bind to Lck in cotransfected HEK-293 cells independently of the transmembrane domain (Fig. 2 A). Because CD4–GPI and CD4–LDL do not associate with Lck directly (Fig. 2 A), they were used to analyze CD4 partitioning effects on Lck activation. HEK-293 cells were cotransfected with the CD4 constructs, p56lck, and a chimeric protein composed of the CD8 extramembrane and transmembrane domains fused to the CD3ζ chain (CD8ζ; reference 28), an Lck substrate (34). Cross-linking of CD4–GPI induces Lck association with CD8ζ in a time-dependent manner and also induces an increase in CD8ζ tyrosine phosphorylation (Fig. 2 B). This is not observed in cells expressing the nonraft CD4–LDL chimera. Furthermore, CD4–GPI cross-linking increases Lck activity in anti-Lck immunoprecipitates, as measured by IVK assays (Fig. 2 C).

Again, CD4–LDL cross-linking produces no detectable increase in Lck activity (Fig. 2 C). These results suggest that if the CD4 extracellular domain is located in rafts, the cytoplasmic CD4 domain is not necessary to activate Lck. Both Lck recruitment to CD8ζ and Lck activation are more robust in CD4wt– (Fig. 2, B and C) or CD4–LDL–CD4–cross-linked cells (unpublished data) than in CD4–GPI cells, which suggests that prior Lck interaction with the CD4 cytoplasmic tail enhances subsequent binding to targets and kinase activation.

Figure 1. Partitioning of CD4 mutants into distinct membrane domains. (A) The scheme shows the amino acid sequence of the CD4 mutants generated. Mutations or foreign sequences added to the CD4 extracellular domain are indicated in bold. (B) HEK-293 cells expressing CD4 mutants were isolated in density gradients. A large proportion of CD4wt, CD4–GPI, and CD4–LDL–CD4 proteins copurify with caveolin in the DRM fraction, whereas CD4–LDL copurifies with the TRβ in the nonraft compartment (Fig. 1 B). Because CD4–LDL and CD4–LDL–CD4 have identical transmembrane domains, the results suggest that the transmembrane sequence does not contain the main determinants for CD4 partitioning in rafts. Supporting this idea, all CD4 transmembrane mutants showed DRM partitioning comparable to that of CD4wt (unpublished data). Single CD4–3A392, CD4–C397A (unpublished data), or double CD4–C394/397A (Fig. 1 B) palmitoylation mutants also partition in the DRM fraction, suggesting that CD4 acylation is not a major determinant for CD4 association to DRM.

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Exclusion of CD4 Extracellular Domain from Raft Domains Impedes HIV-1 Entry. We analyzed whether raft partitioning of CD4 affects its HIV-1 receptor function. We confirmed that gp120 binding was comparable among the distinct CD4 mutants (Fig. 3 A), indicating that chimeric domains do not affect correct CD4 ectodomain folding. No significant gp120 binding was detected in nontransfected cells (unpublished data). The CD4 constructs were tested in a luciferase-based, HIV-1
\textit{env} IIIB–mediated cell–cell fusion assay. Because HIV-1–induced fusion is receptor density dependent (35), a DNA concentration range was used to confirm similar mutant CD4 cell surface expression (Fig. 3 B). HEK-293Env–HEK-293CD4 fusion increases luciferase activity at comparable levels in raft-associated CD4wt, CD4–GPI, CD4–LDL–CD4 (Fig. 3 C), and the transmembrane and juxtamembrane mutant-expressing cells (unpublished data). Nonetheless, fusion is completely abrogated in cells expressing nonraft CD4–LDL (Fig. 3 C). CD4–LDL and CD4–LDL–CD4 share an identical transmembrane domain, indicating that the inserted LDL fragment does not influence Env–mediated fusion. As efficient HIV–1–mediated fusion occurs in cells expressing CD4–GPI, the lack of HIV–1 fusion in CD4–LDL cells is probably due to partitioning of this mutant in a nonraft membrane fraction.

To analyze the effect of CD4 partitioning on viral entry, we performed single-round infections with a replication-defective HIV–1 NL4–3 variant pseudotyped with HIV–X4 (NL4–3), HIV–R5 (Ada), or VSV–G envelopes. HEK-293–CCR5 cells, an established cell line expressing CCR5 at high levels, were used as targets. Efficient viral entry was observed in all raft–associated CD4 mutants, whereas cells expressing the nonraft CD4–LDL mutant were refractory to infection by either X4– or R5–pseudotyped HIV–1 variants (Fig. 3 D). CD4–LDL cells are nonetheless infected by VSV envelope–pseudotyped NL4–3 variants (Fig. 3 D), which indicates that raft partitioning of CD4 is a specific requisite for HIV–1 entry. Although CD4–LDL drastically affects X4 and R5 virus entry, we found that the inhibitory effect of the nonraft CD4–LDL mutant is more dramatic for X4 enveloped viruses than for the R5 pseudotypes. This difference may be the consequence of the high, nonphysiological CCR5 levels expressed by this cell line. Indeed, coreceptor density has been shown to influence both HIV–1 infectivity and entry inhibitor sensitivity (36, 37).

CD4 Partitioning in Rafts Is Required for gp120-induced Receptor Clustering. According to the raft hypothesis, CD4–LDL may not support HIV–1 entry, as the CD4–gp120 coreceptor fusion complex cannot be formed. Using confocal microscopy, we analyzed the ability of selected CD4 mutants to form high order molecular complexes of gp120, CD4, and CXCR4. We observed gp120–induced patches in cells expressing raft–associated CD4wt (Fig. 4 A), CD4–GPI (Fig. 4 B), and CD4–LDL–CD4 (Fig. 4 C), in which gp120 (red), CXCR4 (blue), and CD4 (green) colocalize (white staining). Conversely, in CD4–LDL–expressing cells, anti–gp120–induced patching promotes small aggregates of gp120 and CD4 (yellow) that do not colocalize with CXCR4 (Fig. 4 D). Thus, when gp120–CD4 complexes are formed in rafts, anti–gp120–induced clustering may trigger lateral coalescence of CD4–gp120– and CXCR4–bearing rafts, resulting in the assembly of gp120,
CD4, and CXCR4 complexes. However, CD4–LDL–gp120 complexes formed in nonraft membranes will not trigger coalescence of CXCR4-containing rafts, resulting in the inability of this mutant to form CD4–gp120–CXCR4 complexes. These results suggest that CD4 partitioning in membrane rafts is necessary for the CD4–gp120–CXCR4 complex formation.

**Nonraft CD4–LDL Prevents HIV-1 Infection in CD4⁺ T Cells.** The immunofluorescence results provide a molecular basis to explain why the nonraft CD4–LDL mutant does not support HIV-1 entry. As this mutant binds to HIV-1Env, we examined whether CD4–LDL prevents HIV-1 infection of CD4⁺ cells. The MT-2-CCR5 cell line expresses CD4 as well as CXCR4 and CCR5 coreceptors, rendering it susceptible to infection by X4 and R5 viral strains (14). Therefore, we transfected MT-2-CCR5 cells with the nonraft CD4–LDL mutant. A transfection efficiency of 44% was estimated using a green fluorescent protein reporter plasmid. We analyzed ectopic cell surface CD4 expression by the biotinylation of mock-, CD4wt- and CD4–LDL-transfected MT-2-CCR5 cells. CD4–LDL has a 6xHis tag. Anti-6xHis antibody detects a specific band in avidin-precipitated cell lysates (Fig. 5 A), indicating that CD4–LDL is biotinylated and therefore expressed on the surface of these cells. The total CD4 levels in these blots confirm ectopic CD4wt expression (Fig. 5 A).

Productive HIV-1 infection was examined daily by recording p24 levels in mock-, CD4wt-, or CD4–LDL-expressing MT-2-CCR5 cells infected with NL4-3 (X4) or BaL (R5) strains. CD4–LDL expression delays p24 kinetics compared with mock- or CD4wt-expressing cells (Fig. 5 B) independently of the viral strain tested. This suggests
cells were infected with a HIVNL4–3/LDL. (C) Mock-, CD4wt-, and CD4–LDL-expressing MT-2-CCR5 cells were exposed to cholesterol or inhibit GSL synthesis provided indirect evidence that these entry steps are unlikely to occur at random on the cell surface, but are confined to specific membrane regions termed rafts (14–18). The primary finding in this study is that CD4 partitioning into raft domains is critical for its function as an HIV receptor, as well as for CD4-mediated signaling, two independent CD4 processes. By engineering the transmembrane and cytoplasmic CD4 domains, we generated the nonraft CD4–LDL mutant that retains HIV-1-binding capacity, but does not allow viral infection by blocking viral entry. These results provide direct evidence that HIV-1 exploits raft domains on the host plasma membrane as entry sites into the cell. Earlier studies indicated that the cytoplasmic, transmembrane, or juxtamembrane regions are not needed for CD4 function as an effective HIV-1 receptor (38, 39). Concurring with this, we found that the CD4–GPI mutant mediates HIV-1 entry as efficiently as CD4wt. Even though this mutant cannot directly interact with Lck, CD4–GPI cross-linking induces Lck activation, further suggesting that CD4 cytoplasmic and transmembrane domains are unnecessary for CD4-mediated signal transduction. It is not known how GPI-anchored proteins communicate with the intracellular milieu, although GPI-induced signaling is thought to depend on the raft structure in membranes (2). Because rafts normally contain few molecules, the clustering of GPI-anchored proteins would cause small rafts to coalesce, bringing raft-associated transmembrane proteins into proximity. Alternatively, the clustering of GPI-anchored proteins may induce transmembrane protein recruitment to rafts, which may function as adaptors between GPI proteins and intracellular kinases (2). In contrast to CD4–GPI, the nonraft CD4–LDL mutant, which also lacks CD4 transmembrane and cytoplasmic domains, does not activate Lck and cannot mediate HIV-1 infection. These results suggest that CD4 extracellular domain location in rafts is the major determinant of CD4 function in mediating signaling and viral infection.

Nevertheless, the potential role of cytoplasmic and/or transmembrane domains in determining CD4 association to rafts remains an open question. The affinity of a membrane protein for rafts can be increased by oligomerization, acylation, coupling to a raft-associated molecule, or conformational changes in a transmembrane region (6). The mutation of specific amino acids in the transmembrane domain, replacement of the membrane-spanning region with that of the LDL-R, or the elimination of the acylation acceptor cysteines is insufficient to force CD4 partitioning to rafts, for instance, by enabling interaction with p56lck. This is nonetheless unlikely, as CD4–GPI–CD4 is also raft associated, even in the absence of Lck expression. Oligomerization is an important determinant of transmembrane protein partitioning in rafts. Proteins such as LDL-R, which does not partition in rafts by DRM criteria, are partially raft associated. Cross-linking with anti-CD4 does not increase raft partitioning of the CD4–LDL mutant, however, which lacks the cytoplasmic LDL-
R region. This differential raft partitioning by LDL-R and CD4–LDL may explain the HIV-1 infection described in cells expressing a CD4–LDL–R chimera (38), whereas our CD4–LDL mutant fails to support viral infection. A final, intriguing possibility is that multiple determinants in the cytoplasmic, transmembrane, or even in the extracellular domain of CD4 are responsible for drawing CD4 into membrane rafts. Decoding the molecular signals that trigger CD4 association to rafts warrants additional research.

The most striking finding in this study is that the nonraft CD4–LDL mutant hinders infection by X4 and R5 viruses in a CD4+ MT–2 cell line. This inhibition probably occurs at initial phases of infection, as CD4–LDL also prevents MT–2 infection by a replication-deficient virus variant. The true inhibitory ability of the CD4–LDL mutant on HIV-1 infection is nonetheless difficult to assess based on the experiments presented here. First, only 40% of the MT–2-CCR5 cells are transfected by the nonraft mutant. Second, CD4–LDL expression would decrease throughout the spreading infection, as cell expression of this mutant is not selected during the experimental period. These two features may cause underestimation of the inhibitory capacity of CD4–LDL on spreading and single-round HIV-1 infection of CD4+ cells. We are currently generating stable cell lines expressing distinct CD4wt/CD4–LDL ratios.

A mechanism by which CD4–LDL inhibits HIV-1 infection may be postulated from the observation that the formation of high order complexes between gp120 and cell receptors is impaired in cells expressing the nonraft CD4–LDL mutant. The plasma membrane is probably in dynamic equilibrium between domains in raft and nonraft phases, which may preclude or predispose to protein–protein interactions. CD4–LDL may therefore be unable to mediate HIV-1 entry, as the CD4–Env complexes formed in a nonraft membrane fraction cannot further interact with coreceptors. This mechanism may also operate in CD4+ MT–2 cells, suggesting that CD4–LDL acts as a competitive inhibitor by preventing HIVEnv interaction with “fusion-competent” CD4 molecules on the cell surface. Alternatively, gp120 binding to CD4–LDL in a nonraft environment may prevent viral interaction with other host cofactors involved in HIV-1 entry. The GSL may act as alternative HIV-1 entry cofactors, due to their direct, CD4-dependent association with the viral envelope (17, 18, 40). Because rafts are GSL-enriched, such an interaction would not occur in cells expressing nonraft CD4–LDL. Finally, it is also possible that CD4–LDL binding to gp120 outside rafts cannot promote the conformational changes in the viral Env protein necessary for coreceptor binding. If this is the case, CD4–LDL partitioning in nonraft membranes would again be the major cause of this failure, as the raft-associated CD4–LDL–CD4 mutant, which also has the LDL-R transmembrane domain, efficiently mediates the formation of ternary CD4–gp120 coreceptor complexes.

In light of this study and reports showing the importance of lipid components in HIV budding (41, 42), it is tempting to speculate that the manipulation of specific host membrane raft components would be useful in designing new strategies to prevent and/or block HIV-1 infection. These therapeutic approaches would be suitable for both X4 and R5 viral strains and would obviate the problem of resistance mutants observed using current treatments.

We thank C. Hernández for technical assistance, M. Muñoz and K. Harshman for DNA sequencing, and C. Mark for editorial assistance.

S. Jiménez-Baranda is supported by a predoctoral fellowship from the Pharmacia Corporation. The Department of Immunology and Oncology was founded and is supported by the CSIC and the Pharmacia Corporation.

Submitted: 25 February 2002
Revised: 20 May 2002
Accepted: 10 June 2002

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