A Role for Lipid Rafts in B Cell Antigen Receptor Signaling and Antigen Targeting

By Paul C. Cheng,* Michelle L. Dykstra,* Richard N. Mitchell,‡ and Susan K. Pierce*

From the *Department of Biochemistry, Molecular Biology, and Cell Biology, Northwestern University, Evanston, Illinois 60208; and the ‡Immunology Research Division, Department of Pathology, Brigham and Women's Hospital and Harvard Medical School, Boston, Massachusetts 02115

Summary

The B cell antigen receptor (BCR) serves both to initiate signal transduction cascades and to target antigen for processing and presentation by MHC class II molecules. How these two BCR functions are coordinated is not known. Recently, sphingolipid- and cholesterol-rich plasma membrane lipid microdomains, termed lipid rafts, have been identified and proposed to function as platforms for both receptor signaling and membrane trafficking. Here we show that upon cross-linking, the BCR rapidly translocates into ganglioside GM1-enriched lipid rafts that contain the Src family kinase Lyn and exclude the phosphatase CD45R. Both Igα and Lyn in the lipid rafts become phosphorylated, and subsequently the BCR and a portion of GM1 are targeted to the class II peptide loading compartment. Entry into lipid rafts, however, is not sufficient for targeting to the antigen processing compartments, as a mutant surface Ig containing a deletion of the cytoplasmic domain is constitutively present in rafts but when cross-linked does not internalize to the antigen processing compartment. Taken together, these results provide evidence for a role for lipid rafts in the initial steps of BCR signaling and antigen targeting.

Key words: membrane microdomain • B lymphocyte • immunoglobulin • Igα/Igβ • endocytosis

The B cell antigen receptor (BCR) is a multicomponent complex on the cell surface that is composed of a cell surface (s)Ig that mediates antigen binding and a noncovalently associated heterodimer, Igα/Igβ, that functions as a signal transduction complex (for review see reference 1). After antigen binding and cross-linking, the BCR transmits signals through several signaling pathways that result in the expression of a variety of genes associated with B cell activation. Early key events in the BCR signal transduction cascade include the activation of protein tyrosine kinases of the Src and Syk/Zap70 families and the phosphorylation of tyrosine residues in the immune receptor tyrosine-based activation motifs (ITAMs) in the cytoplasmic domains of Igα and Igβ (1–3).

Although necessary for the activation of B cells, the signals transmitted through the BCR alone are not sufficient to induce the proliferation and differentiation of B cells. The B cell antibody response to the vast majority of protein antigens requires B cell interaction with antigen-specific T cells (for review see reference 4). The interactions of B cells and helper T cells are dependent on the processing and presentation of antigen by B cells to the helper T cells (5). The BCR plays an important role in antigen processing by targeting bound antigen to the class II peptide loading compartment (IIPLC; for review see reference 6). Indeed, BCR-mediated antigen processing is thousandsfold more efficient in B cells compared with the processing of antigen taken up nonspecifically by fluid phase pinocytosis.

Recent evidence indicates that the two functions of the BCR, signaling and antigen targeting, are interrelated (7). Monovalent antigens bound to the BCR are processed and presented, but less efficiently than multivalent antigens (8). Cross-linking the BCR results in internalization of a larger number of receptors and a significant acceleration of the targeting of the BCR to the IIPLC and of the degradation of BCR and bound antigen (9). The accelerated delivery of antigen to the IIPLC may play an important role in vivo during periods of rapid antigen-driven B cell expansion and T cell–dependent selection. The effects of BCR cross-linking appear to be the result of BCR signaling rather than ag-
aggregation of the BCR because kinases inhibitors that block BCR signaling block accelerated targeting and degradation (10). In addition, Aluvihare et al. (11) recently showed that accelerated antigen targeting by the BCR is dependent on Igα and Igβ. Further evidence for an important role of Igα/Igβ in BCR antigen targeting was demonstrated by the behavior of two mutant Ig's that do not associate with Igα/Igβ (12). An s Ig in which the short, three-amino acid cytoplasmic domain was deleted (mut μCytoΔ) was expressed on the cell surface without Igα/Igβ. The μCytoΔ was glycosylphosphatidylinositol (GPI) linked (13) and, after antigen binding, failed to internalize and target antigen to the IiPLC (12). Another s Ig in which Y597 and S588 in the transmembrane domain was changed to VV (μYS/VV) was also expressed on the cell surface in the absence of Igα/Igβ (14). μYS/VV was competent to internalize bound antigen and, although the antigen was degraded, it was not presented by the class II molecules, suggesting that correct targeting of the BCR to the IiPLC was dependent on Igα/Igβ (15). Another s Ig containing a single Y597→F transmembrane mutation that associated with Igα/Igβ was signaling competent but like μYS/VV did not target antigen for processing. Thus, both the signaling function and the nature of the s Ig transmembrane region appear to dictate the behavior of the BCR, that is, to specify the correct targeting of the BCR to the IiPLC and to accelerate the rate at which the antigen is targeted to the IiPLC. At the time of this writing, the molecular mechanisms by which the targeting and signaling functions of the BCR are coordinated after antigen binding and receptor cross-linking on the cell surface are not known.

Recent advances in membrane biology have led to the identification of glycosphingolipid- and cholesterol-rich plasma membrane microdomains, or lipid rafts, that have been proposed to function as platforms for both signal transduction and membrane trafficking (for review see reference 16). Lipid rafts can be isolated based on their insolubility in Triton X-100 detergent and buoyant density on sucrose gradients (17–20). Several proteins have been identified as residents of these lipid microdomains, including caveolin (21), GPI-linked membrane proteins (17, 22), influenza hemagglutinin (23), the high-affinity IgE receptor (24, 25), the mouse IgG2b,2 conjugated rabbit anti-mouse IgG plus IgM (H and L chain); horseradish peroxidase (HRP)-conjugated goat anti-mouse IgG plus IgM (H and L chain); HRP-conjugated rabbit F(ab')2 anti-mouse γ chain and anti-human μ chain; and FITC-conjugated goat anti-mouse γ chain, anti-human γ chain, and anti-human μ chain, which were purchased from Jackson ImmunoResearch. Cholera toxin B subunit (CTB) conjugated to HRP and methyl-β-cyclodextrin were obtained from Sigma Chemical Co. Antibodies specific for mouse CD45R and Lyn were obtained from Pharmingen. The goat polyclonal antibody specific for actin was obtained from Santa Cruz Biotechnology, and the rat mAb YL1/2 specific for tubulin (42) was a gift from Dr. Douglas T. Fearon (University of Cambridge, U.K.). RC20H phosphotyrosine-specific recombinant antibody conjugated to HRP was purchased from Transduction Labs. Polyclonal antibodies specific for H2-M were generated in rabbits using a peptide representing the cytoplasmic tail domain of H2-M (residues 224–245) containing a T cell epitope derived from tetanus toxoid (residues 582–599). The mouse IgG2a hybridoma 17.3.3s producing an mAb specific for I-Ek, the mouse IgG2a hybridoma HB3 (MK-D6) producing an mAb specific for I-Ak, and the rat IgG2a hybridoma R17 217.1.3 producing an mAb specific for the transferrin receptor (TIR) were obtained from the American Tissue Type Culture Collection. The rat hybridoma 903a, producing an IgG1 mAb specific for the cytosolic domain of mouse Igα, was generated and characterized in the Pierce laboratory at Northwestern University. All hybridomas were maintained in the Pierce laboratory, and mAbs were purified from culture supernatant by affinity chromatography.

Goat Fab anti-mouse μ chain; rabbit anti-human IgG plus IgM (H and L chain); horseradish peroxidase (HRP)-conjugated goat anti-mouse IgG plus IgM (H and L chain); HRP-conjugated rabbit F(ab')2 anti-mouse γ chain and anti-human μ chain; and FITC-conjugated goat anti-mouse γ chain, anti-human γ chain, and anti-human μ chain, which were purchased from Jackson ImmunoResearch. Cholera toxin B subunit (CTB) conjugated to HRP and methyl-β-cyclodextrin were obtained from Sigma Chemical Co. Antibodies specific for mouse CD45R and Lyn were obtained from Pharmingen. The goat polyclonal antibody specific for actin was obtained from Santa Cruz Biotechnology, and the rat mAb YL1/2 specific for tubulin (42) was a gift from Dr. Douglas T. Fearon (University of Cambridge, U.K.). RC20H phosphotyrosine-specific recombinant antibody conjugated to HRP was purchased from Transduction Labs. Polyclonal antibodies specific for H2-M were generated in rabbits using a peptide representing the cytoplasmic tail domain of H2-M (residues 224–245) containing a T cell epitope derived from tetanus toxoid (residues 582–599). The mouse IgG2a hybridoma 17.3.3s producing an mAb specific for I-Ek, the mouse IgG2a hybridoma HB3 (MK-D6) producing an mAb specific for I-Ak, and the rat IgG2a hybridoma R17 217.1.3 producing an mAb specific for the transferrin receptor (TIR) were obtained from the American Tissue Type Culture Collection. The rat hybridoma 903a, producing an IgG1 mAb specific for the cytosolic domain of mouse Igα, was generated and characterized in the Pierce laboratory at Northwestern University. All hybridomas were maintained in the Pierce laboratory, and mAbs were purified from culture supernatant by affinity chromatography.

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Immunoprecipitation.

The diluted lysate was overlaid with 6 ml 35% sucrose in TNEV and finally 3.5 ml 5% sucrose in TNEV. The samples were centrifuged in an SW 41 rotor at 200,000 g for 16–20 h at 4°C. 1 ml fractions were collected from the top of the gradient.

Measurement of HRP Activity.

The samples were subjected to 10% SDS-PAGE. Gels with metabolic labeled samples were dried and exposed to film, and gels were quantified by densitometry.

Results

C cross-linking the BCR results in its rapid translocation into lipid rafts. The present evidence indicates that the plasma membrane contains sphingolipid- and cholesterol-enriched microdomains, or lipid rafts, proposed to play a role in membrane trafficking and signal transduction. These microdomains are resistant to Triton X-100 detergent solubilization, allowing for their isolation in discontinuous sucrose density gradients. The location of the BCR in unactivated B cells and after BCR cross-linking with regard to lipid rafts was determined. The CH27 B lymphoma cells that were surface biotinylated were either untreated or treated with anti-Ig at 4°C for 15 min, washed, and warmed to 37°C for 0 or 30 min. The cells were lysed in 1% Triton X-100 lysis buffer on ice, and the lysates were subjected to discontinuous sucrose density gradient centrifugation. Individual fractions from the gradient were subjected to SDS-PAGE and immunoblotting. The position of the lipid rafts in the sucrose gradient was determined by the presence of the ganglioside GM1, detected using GM1-specific ligand CTB (Fig. 1). As shown in Fig. 1, GM1 is enriched in the fractions at the top of the sucrose gradient, fractions 3–6. There was no detectable GM1 in fractions 7–9 and only a small amount of GM1 in the solubilized material located at the bottom of the gradient, fractions 10–12, indicating a clear separation of the lipid rafts from the Triton X-100-soluble membranes and components. To determine where in the gradients the BCR resided, immunoblots were probed with antibodies specific for mouse IgM and an mAb specific for Igα. In untreated cells, Ig and Igα were found in the soluble fractions of the sucrose gradient and not in the detergent-insoluble lipid raft region, indicating that in resting cells the BCR is excluded from the lipid rafts (Fig. 1). After BCR cross-linking, a significant portion of both the Ig and Igα are translocated into the lipid raft regions of the sucrose gradient. Both Ig and Igα are present in the lipid rafts immediately after cross-linking and warming to 37°C. Somewhat less Ig and Igα are detected in the lipid raft region 30 min after cross-linking.

To determine where in the gradient the fractions the surface BCR resided, the position of biotinylated sIg and sIgα was examined. The biotinylated CH27 lymphoma cells were either untreated or treated with anti-Ig and analyzed as described above. Biotinylated proteins were immunoprecipitated from the Triton X-100 detergent lysates using strepta-
and 1-ml fractions were collected. To determine the location of lipid rafts or 30 min and lysed in 1% Triton X-100 in TNEV buffer. The lysates were subjected to discontinuous sucrose density gradient centrifugation, and 1-ml fractions were collected. To determine the location of lipid rafts in the gradient, 100 µl of the individual fractions were subjected to 10% SDS-PAGE. After transfer onto PVDF, the membranes were probed for the presence of µ heavy chain and Igα using specific antibodies. The ganglioside GM1 was detected using CTB–HRP. To determine the location of surface BCR in the gradient, biotinylated proteins were immunoprecipitated from the gradient fractions using streptavidin–agarose. The immunoprecipitates were subjected to 10% SDS-PAGE and immunoblot probing with antibodies specific for Ig and Igα detected with HRP-conjugated secondary antibodies and ECL. Representative blots of three separate experiments are shown.

Figure 1. BCR cross-linking results in translocation of the BCR into GM1-containing lipid rafts. CH27 cells were surface biotinylated at 4°C and incubated with anti-Ig on ice for 15 min. The cells were warmed for 0 or 30 min and lysed in 1% Triton X-100 lysis buffer and subjected to discontinuous sucrose density gradient centrifugation, and the gradient fractions were analyzed by SDS-PAGE and immunoblotting for the presence of Lyn and CD45R. The kinase Lyn is concentrated in the lipid raft region of the gradient in resting cells and remains in rafts after BCR cross-linking, at least for the 30-min time course of this experiment (Fig. 2). In contrast, the phosphatase CD45R is excluded from the lipid rafts in resting cells and remains excluded after BCR cross-linking (Fig. 2). The location of H2-M, a class II–like protein that at steady state has been shown to reside primarily in the IiPLC in CH27 cells, was also determined. As anticipated, H2-M was found in the Triton X-100–soluble membrane fractions in resting cells, and its presence in soluble membranes did not change upon BCR cross-linking. A portion of the cytoskeleton protein actin was found to be constitutively associated with lipid rafts (Fig. 2). In contrast, tubulin was found to be completely excluded from the lipid rafts in both anti-Ig–treated and untreated cells.

Phosphorylated Igα and Lyn Are Present in Lipid Rafts after BCR Cross-linking. The presence of Lyn in the lipid raft suggests that the Igα present in the lipid rafts after BCR cross-linking may be phosphorylated. To determine the plasma membrane location of phosphorylated proteins, B cells were untreated or treated with anti-Ig at 4°C and warmed to 37°C for 0, 10, or 30 min. At the end of each time point, the cells were lysed in 1% Triton X-100 lysis buffer and subjected to discontinuous sucrose density gradient centrifugation. The gradient fractions were analyzed by SDS-PAGE and immunoblot probing for phosphorytropic-containing proteins using the phosphorytropic-specific recombinant antibody R C 20H. In the absence of cross-linking, phosphorylated proteins are present in the Triton X-100–soluble membrane fractions, and only faint bands of phosphorytropic-containing proteins were observed in the Triton X-100–soluble membrane fractions of anti-Ig–treated cells. In contrast, upon BCR cross-linking, phosphorylated proteins were present in the Triton X-100–soluble membrane fractions, and only faint bands of phosphorytropic-containing proteins were observed in the Triton X-100–soluble membrane fractions of anti-Ig–treated cells.

Lyn and Igα Are Present in Lipid Rafts after BCR Cross-linking. The results of experiments described above indicate that upon cross-linking, the BCR is rapidly translocated into lipid rafts. As stated above, BCR cross-linking results in the initiation of a signal transduction cascade involving the phosphorylation of Igα/Igβ ITAM tyrosines. The Src family kinase Lyn is an essential protein tyrosine kinase involved in the initial phosphorylation events. The BCR response is ultimately terminated by dephosphorylation of BCR signaling components involving plasma membrane phosphatases such as CD45R. Thus, the location of Lyn and CD45R in membrane fractions was determined in unactivated and activated B cells. B cells were untreated or incubated with anti-Ig at 4°C for 30 min, washed, and warmed to 37°C for 0 or 30 min. The cells were lysed in 1% Triton X-100 lysis buffer and subjected to discontinuous sucrose gradient centrifugation, and the gradient fractions were analyzed by SDS-PAGE and immunoblotting for the presence of Lyn and CD45R. The kinase Lyn is concentrated in the lipid raft region of the gradient in resting cells and remains in rafts after BCR cross-linking, at least for the 30-min time course of this experiment (Fig. 2). In contrast, the phosphatase CD45R is excluded from the lipid rafts in resting cells and remains excluded after BCR cross-linking (Fig. 2). The location of H2-M, a class II–like protein that at steady state has been shown to reside primarily in the IiPLC in CH27 cells, was also determined. As anticipated, H2-M was found in the Triton X-100–soluble membrane fractions in resting cells, and its presence in soluble membranes did not change upon BCR cross-linking. A portion of the cytoskeleton protein actin was found to be constitutively associated with lipid rafts (Fig. 2). In contrast, tubulin was found to be completely excluded from the lipid rafts in both anti-Ig–treated and untreated cells.

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phorylated proteins can be detected in the lipid raft region of the gradient (Fig. 3), reflecting the constitutive level of protein tyrosine phosphorylation in CH27 cells. Upon BCR cross-linking, the intensity and number of phosphorylated proteins increase immediately in the fractions that contain detergent-soluble and -insoluble membranes and then return to the levels present in unactivated cells by 30 min. To determine if the phosphorylated proteins in the lipid rafts include either Igα or Lyn, immunoblots were probed with antibodies specific for Igα and Lyn. As shown, the Igα band at 34 kD and the Lyn bands at 53 and 56 kD align with phosphotyrosine-containing proteins (Fig. 3). By immunoblotting, Lyn appears to be present in the lipid rafts in approximately the same amount in untreated and anti-Ig-treated cells throughout the 30-min chase; however, the phosphorylation state of Lyn appears to change with BCR cross-linking. Igα enters the raft after BCR cross-linking, with maximal translocation occurring 10 min after BCR cross-linking; by 30 min, the amount of Igα in lipid rafts decreases. At each time point, the Igα present in the raft region appears to be phosphorylated. It is difficult to determine if Lyn and Igα phosphorylation is restricted to the lipid rafts because of the complexity of the pattern of phosphorylated proteins in the Triton X-100-soluble fractions, although there are no obvious phosphoproteins aligning with Igα and Lyn. Taken together, these results suggest that after cross-linking, the BCR enters the lipid rafts, where the Lyn kinase is concentrated to facilitate initiation of signal cascades, including Igα and Lyn phosphorylation. The exclusion of CD45R from the lipid rafts indicates that only BCRs outside the lipid rafts would be targets of CD45R phosphatase activity.

Antigen Bound to the BCR Is Rapidly Translocated to Lipid Rafts after BCR Cross-linking. The results described above provide evidence that upon cross-linking, the BCR rapidly translocates into lipid rafts. To verify that the BCR that moved into lipid rafts was the BCR bound to anti-Ig as a surrogate antigen, B cells were untreated or treated with HRP-anti-Ig at 4°C for 15 min, washed, and warmed at 37°C for 0, 15, or 30 min. The cells were lysed in 1% Triton X-100 lysis buffer and subjected to discontinuous sucrose density gradient centrifugation, and the HRP activity in the gradient fractions was measured (Fig. 4 A). In untreated cells, there was little endogenous peroxidase activity detected in the lipid raft region of the gradient, and a small amount of endogenous peroxidase activity was detected in the soluble membrane fractions at the bottom of the gradient. In HRP-anti-Ig-treated cells, HRP activity was found to be highly concentrated in the lipid raft regions immediately after warming to 37°C. There appears to be a slight increase in the HRP activity in the lipid raft regions 15 min after warming to 37°C and a small decrease in HRP activity after 30 min. However, the enzyme activity was not measured in a quantitative fashion, so the small differences may not be significant.

To gain a more quantitative measure of the translocation of the antigen bound to the BCR into lipid rafts, B cells were incubated for 1 h with monovalent 125I-Fab-anti-Ig and subsequently left untreated or treated with rabbit anti-mouse Ig and warmed to 37°C for 0–30 min (Fig. 4 B). In the absence of cross-linking, ~12% of the 125I-Fab-anti-Ig is located in lipid rafts. After cross-linking, this percentage increases to ~26% and then decreases to 18% by 30 min after cross-linking. The presence of the 12% of 125I-Fab in

![Figure 3](https://example.com/figure3.png)
percentage of 125I–Fab–anti-Ig in rafts after anti-Ig treat- 
cross-linking the BCR. Nevertheless, the increase in the 
HRP was used to label GM1 at the B cell surface at 4 
untreated B cells and in B cells treated with anti-Ig. CTB– 
9 
some aggregated Fab–anti-Ig or F(ab) 
dependent experiments is shown. 

Figure 4. BCR -bound antigens translocate into rafts after BCR cross- 
linking. (A) B cells were untreated (0–) or treated with HRP-anti-Ig at 4C for 1 h, washed, and warmed to 37C for 0, 15, or 30 min (0+, 15+, and 30+, respectively). The cells were lysed in 1% Triton X-100 in TNEV buffer, the lysates subjected to discontinuous sucrose density gra- 
dient centrifugation, and the fractions assayed for HRP activity. (B) CH27 cells were incubated at 4C for 1 h with 125I–Fab-anti-Ig. During the last 30 min of incubation, the cells were untreated (0–) or treated 
with anti-Ig to cross-link the BCR and then warmed to 37C for 0-30 
min (0+ to 30+). The cells were lysed in 1% Triton X-100 in TNEV 
buffer, the lysates subjected to discontinuous sucrose gradient cen- 
trifugation, and the cpm of each fraction was measured and expressed as a 
percent of the total cell-associated 125I. The average and SEM of three in- 
dependent experiments is shown. 

the lipid rafts in unactivated cells, even though sIg and Igα 
were not detected in lipid rafts by immunoblotting (Fig. 1), 
suggests that the 125I–Fab-anti-Ig preparation likely contained 
some aggregated Fab-anti-Ig or F(ab’)2-anti-Ig capable of 
cross-linking the BCR. Nevertheless, the increase in the 
percentage of 125I–Fab-anti-Ig in rafts after anti-Ig treatment 
correlated with the translocation of biotinylated sIg and Igα and HRP-anti-Ig into lipid rafts. 

BCR Cross-linking Triggers the Targeting of GM1 to the IIPLC. Using a nondisruptive chemical cross-linking technique, we previously showed that upon cross-linking the BCR is rapidly targeted from the plasma membrane through TfR-containing early endosomes to the IIPLC (45). To determine if the BCR remains associated with components of the lipid raft during intracellular targeting, the same chemical cross-linking technique was used to follow the intra- 
cellular movement of the lipid raft ganglioside GM1 in untreated B cells and in B cells treated with anti-Ig. CTB- 
HRP was used to label GM1 at the B cell surface at 4C and to follow the movement of GM1 into the cell. Any protein 

present in the same compartment as CTB-HRP will be polymerized into insoluble aggregates in the presence of 
membrane-soluble DAB and H2O2 but not in the absence of H2O2. The insoluble polymers can be removed by cen- 
trifugation, and thus the absence of a protein in the lysate indicates its presence in CTB-HRP-containing compart- 
ments. As detailed elsewhere, the HRP-mediated polymerization of proteins depends on the presence of the protein, 
HRP, DAB, and H2O2 in the same subcellular compartment, and nonspecific, promiscuous polymerization of pro- 
teins outside HRP-containing compartments is not observed (9, 45). The movement of GM1 from the plasma membrane into early endosomes and to the IIPLC was followed. To detect 
the movement of CTB-HRP into early endosomes, the CTB after BCR cross-linking are sim- 
ilar to those previously observed for BCR contact with the 
TfR upon warming to 37C or the presence of anti-Ig. The cells were washed and 
warmed to 37C for varying lengths of time up to 120 min. 

At the end of each time point, the cells were exposed to 
the chemical cross-linking reagent DAB in the presence or 
absence of H2O2 and lysed, and the lysates were centrifuged to remove insoluble polymers. TfR was immunoprecip- 
itated from the cleared lysate and subjected to SDS-PAGE 
and immunoblot probing for biotinylated proteins using 
streptavidin-HRP. In cells in which the BCR was not cross- 
linked, CTB-HRP briefly contacts ~50% of TfR at 4C, and by 30 min is in contact with a steady 
state level of ~20% of the biotinylated TfR (Fig. 5). 
Because it is difficult to rule out the presence of aggregated or 
multimerized CTB in the CTB-HRP conjugate prepara- 
tion, it is not possible to be certain that the observed con- 
tact of the CTB-HRP with TfR reflects the constitutive be- 
vavior of GM1 or whether the contact with TfR is induced 
by aggregated CTB–HRP. In B cells in which the BCR is 
cross-linked, CTB-HRP appears to contact more of the 
TfR upon warming to 37C (>90%) and to stay in contact with 
the TfR longer (>60 min) before returning to steady 
state levels of 20% by 120 min. The kinetics of contact of 
CTB-HRP with the TfR after BCR cross-linking are sim- 
ilar to those previously observed for BCR contact with the 
TfR after BCR cross-linking (45). 

To determine if any GM1 is targeted to the IIPLC, B cells 
were pulsed for 15 min with [35S]methionine in the pre- 
ence of CTB-HRP and in the presence or absence of anti- 
Ig. The cells were washed, warmed to 37C, and chased for 
60–180 min. Times were selected that allowed for the de- 
tection of newly assembled class II molecules that first bind 
peptide and adopt SDS-stable conformation in the IIPLC, 
~60–90 min after synthesis (9, 46). At the end of each chase 
time, the cells were treated with DAB in the presence or 
absence of H2O2 to cross-link proteins present in the same 
compartment as the CTB-HRP. The lysates were centrifuged to remove insoluble cross-link proteins, and class 
II molecules were immunoprecipitated from the cleared lys- 
sate. In untreated B cells, SDS-stable class II heterodimers 
first appear faintly at 60 min of chase and continue to in- 
crease over 150 min and then decrease by 180 min as the
class II molecules exit the IIPLC and traffic to the plasma membrane (Fig. 6). The intense band above the class II α/β dimers present at 60 min and decreasing thereafter has been previously determined to contain Ii dimers. Significantly, the amount of SDS-stable class II molecules formed was equivalent at each time point in the presence or absence of \( \text{H}_2\text{O}_2 \) (Fig. 6), indicating that CTB–HRP was not present in the peptide loading compartment. In contrast, in B cells in which the BCR was cross-linked, the number of SDS-stable class II molecules was decreased in the presence of \( \text{H}_2\text{O}_2 \) beginning after 90 min of chase time. The reduction of SDS-stable class II molecules was maximal (~30%) at 120–150 min and less by 180 min as class II molecules exited the peptide loading compartment.

Taken together, these results indicate that in unactivated B cells, the CTB–HRP bound to GM1 briefly enters early endocytic TfR-containing compartments but is not targeted to the late IIPLC. Cross-linking the BCR, which, as shown previously, results in BCR targeting to the IIPLC (9, 45), results in a concomitant targeting of GM1-bound CTB–HRP to the IIPLC. GM1 appears to stay in contact with the BCR en route to the IIPLC, as shown by the ability of CTB–HRP to cause Ig\( \alpha \) polymerization throughout the chase period (data not shown). Thus, the BCR appears to remain associated with a portion of the lipid raft GM1 as the BCR is targeted to the IIPLC.

The GPI-linked Ig Mutant \( \mu \text{Cyto}_D \) Is Constitutively Concentrated in Lipid Rafts but Is Not Targeted to the IIPLC. The results presented above showed that the BCR is excluded from lipid rafts in unactivated cells and upon cross-linking is translocated into lipid rafts and targeted to the IIPLC. The targeting of the BCR to the IIPLC was accompanied by the movement of a portion of the lipid raft GM1 to the IIPLC. To determine the relationship between residency of a receptor in lipid rafts and targeting to the IIPLC, we analyzed a human Ig, \( \mu \text{Cyto}_D \), in which the cytoplasmic domain was deleted. Previous characterization showed that \( \mu \text{Cyto}_D \) stably transfected into mouse A20 cells (A20\( \mu \text{Cyto}_D \)) is expressed as a GPI-linked protein that does not associate with the Ig\( \alpha \)/Ig\( \beta \) complex (13, 14). As a GPI-linked protein, \( \mu \text{Cyto}_D \) is predicted to reside in lipid rafts. The behavior of \( \mu \text{Cyto}_D \) was compared with that of the endogenous mouse Ig in A20\( \mu \text{Cyto}_D \) cells and to that of a WT human Ig (\( \mu \text{WT} \)) in A20\( \mu \text{WT} \) cells. By flow cytometry, both \( \mu \text{Cyto}_D \) and \( \mu \text{WT} \) are expressed at levels similar to that of the endogenous mouse IgG in both cell lines (Fig. 6 A). The staining is specific, and the cells do not stain using FITC-labeled antibodies specific for the human \( \text{g} \) chain.

The lipid raft localization of \( \mu \text{Cyto}_D \), \( \mu \text{WT} \), and endogenous mouse IgG was determined using HRP-conjugated antibodies as described above. In brief, A20\( \mu \text{Cyto}_D \)
or A20 μWT cells were untreated or incubated with HRP-conjugated antibodies specific for either mouse IgG or human IgM in CH27 cells. Also shown as controls are the stainings of human 114 cells with FITC-labeled anti-mouse IgG and nontransfected A20 cells with FITC-labeled anti-human IgG and anti-human IgM (black shaded areas). Cells were surface biotinylated and untreated or treated with PI-PLC at 37°C for 1 h. Solubilized proteins in the supernatant and lysates from the cell pellets were immunoprecipitated for human Ig, and the immunoprecipitates were subjected to 10% SDS-PAGE and immunoblot probing for biotinylated proteins using streptavidin–HRP and ECL.

![Figure 6](image_url)  
**Figure 6.** BCR cross-linking results in CTB–HRP targeting to the class II peptide loading compartment. (A) CH27 cells were labeled with [35S]methionine for 15 min in the presence of CTB–HRP and in the presence or absence of anti-Ig and chased for 60–180 min. At the end of each time point, the cells were treated with DAB in the presence or absence of H2O2, and lysed in 1% Triton X-100 lysis buffer, and insoluble polymers were removed by centrifugation. The I-Ek class II molecules were immunoprecipitated from the lysate and subjected to SDS-PAGE without boiling or reducing the samples, conditions under which peptide-bound class II α/β dimers are stable. (B) The α/β dimer bands of at least three independent experiments were quantified by densitometry, and the average amounts for each chase time are shown as the percent of the total amount of SDS-stable class II immunoprecipitated from all time points. (C) The percent of SDS-stable class II immunoprecipitated in B is shown as the percent reduction in DAB-reacted cells at each time point.

![Figure 7](image_url)  
**Figure 7.** Cytoplasmic tail deletion Ig mutation is expressed on the cell surface as a GPI-linked protein. (A) A20μCytoΔ and A20μWT cells were analyzed by flow cytometry using FITC-labeled antibodies specific for mouse IgG, human IgG, and human IgM (gray shaded areas). Also shown as controls are the stainings of human 114 cells with FITC-labeled anti-mouse IgG and nontransfected A20 cells with FITC-labeled anti-human IgG and anti-human IgM (black shaded areas). (B) Cells were surface biotinylated and untreated or treated with PI-PLC at 37°C for 1 h. Solubilized proteins in the supernatant and lysates from the cell pellets were immunoprecipitated for human Ig, and the immunoprecipitates were subjected to 10% SDS-PAGE and immunoblot probing for biotinylated proteins using streptavidin–HRP and ECL.
To determine if the inclusion of μCytoΔ in the buoyant fractions was dependent upon the integrity of the lipid rafts and to determine if aggregation of the receptor alone dictates its behavior on sucrose gradients, A20μCytoΔ cells were treated with anti-Ig and the cholesterol-sequestering drug methyl-β-cyclodextrin that disrupts cholesterol-dependent rafts. In cyclodextrin-treated cells, μCytoΔ is no longer present in the buoyant region of the sucrose gradient but rather in the Triton X-100-soluble dense region of the gradient, even in the presence of cross-linking antibody (Fig. 9). The effect of cyclodextrin was partially reversible after 3 h with the addition of cholesterol (Fig. 9). Taken together, these results indicate that the localization in buoyant regions of the sucrose gradient is dependent on the integrity of the lipid rafts, and aggregation of sIg with anti-Ig alone does not result in appearance of the sIg in the buoyant gradient functions.

To determine if the μCytoΔ is targeted to the IIPLC after cross-linking, A20μCytoΔ cells were pulsed with [35S]methionine for 15 min in the presence of HRP-conjugated antibodies specific for either mouse IgG or human IgM. The cells were washed and incubated for 60–180 min at 37°C. At the end of each time point, the cells were treated with DAB in the presence or absence of H2O2 and lysed, and the I-Aβ class II molecules were immunoprecipitated. The immunoprecipitates were subjected to SDS-PAGE without reducing or boiling the samples, conditions under which peptide-bound class II αβ dimers are stable. In cells treated with HRP–anti–mouse IgG, the number of class II αβ dimers is decreased after treatment with DAB plus H2O2, as compared with DAB alone (Fig. 10). The reduction in class II molecules is observed at 60 min, reaches a maximum of 40% at 120 min, and decreases thereafter as the class II molecules exit the IIPLC. Similar results were obtained by analysis of treated or incubated with antibodies specific for mouse IgG or human IgM at 4°C for 1 h, washed, and incubated at 37°C for 30 min. The cells were lysed in 1% Triton X-100 in TNEV buffer and fractionated on a discontinuous sucrose density gradient centrifugation. Fractions were collected and HRP activity measured. Shown are untreated A20μCytoΔ (●), A20μCytoΔ treated with HRP–anti–human Ig (▲), and A20μCytoΔ treated with HRP–anti–human Ig (▲). Shown is a representative experiment of three independent experiments.

Figure 8. Cytoplasmic tail deletion mutants of sIg are localized in lipid rafts in resting cells. (A) A20μCytoΔ and A20μWT cells were incubated with HRP-conjugated rabbit anti–human IgM or goat anti–mouse IgG for 1 h at 4°C, washed, and chased for 30 min. The cells were then lysed in 1% Triton X-100 in TNEV buffer, and the lysates were subjected to discontinuous sucrose density gradient centrifugation. Fractions were collected and HRP activity measured. Shown are untreated A20μCytoΔ (●), A20μCytoΔ treated with HRP–anti–human Ig (▲) or HRP–anti–mouse Ig (▲), and A20μWT treated with HRP–anti–human Ig (▲). Shown is a representative experiment of three independent experiments. (B) A20μCytoΔ cells were treated with either anti–human IgM or anti–mouse IgG at 4°C for 1 h, washed, and warmed to 37°C for 30 min. The cells were lysed in 1% Triton X-100 in TNEV buffer and subjected to discontinuous sucrose gradient centrifugation. The gradient fractions were analyzed by 10% SDS-PAGE and immunoblot probing with either mouse IgG- or human IgM-specific antibodies and ECL.
lyzing μWT in A20μWT cells using HRP-anti-human IgM, in which case 25% of newly synthesized SDS-stable class II molecules were cross-linked after 120 min of chase time. These results are in agreement with those previously shown for the contact of WT IgM BCR with newly synthesized I-Ek in CH27 cells (9, 45). In contrast, in A20μCytoΔ cells treated with HRP-anti-human IgM, there was no reduction in the number of class II molecules in cells treated with DAB plus H2O2 as compared with DAB alone (Fig. 10). Moreover, in A20μCytoΔ cells treated with antibodies specific for mouse IgG and HRP-conjugated antibodies specific for human IgM, μCytoΔ was not targeted to the IPILC (data not shown). Thus, μCytoΔ resident in the lipid raft did not accompany the WT mouse BCR to the IPILC. These findings indicate that the human IgM that constitutively resides in the lipid rafts is not targeted to the IPILC after cross-linking, in agreement with previous results showing that the μCytoΔ did not target antigen for class II processing (15). Moreover, these results indicate that residency in the lipid rafts region alone is not sufficient for targeting to the IPILC.

Discussion

The BCR plays two key roles in the B cell response to antigen. The first is to transmit signals through several intracellular pathways that ultimately dictate the fate of the B cell’s encounter with antigen (1–3). BCR signaling itself has been recently appreciated to be a complex phenomenon that is directly influenced both positively and negatively by B cell coreceptors, including CD19/CD21, CD22, CD40, and FcγRIIB (1). How the components of the BCR signaling cascade and the coreceptors are organized on the plasma membrane to affect the final outcome is not known. In addition to signaling, the BCR physically transports antigen from the cell surface to the IPILC (6). The current evidence indicates that the signaling function of the BCR is required to specify both the targeting of the BCR to the IPILC and the rate at which the targeting is achieved.

How the signaling and targeting functions of the BCR are coordinated is not known. In this report, we show that after cross-linking, the BCR is rapidly translocated into lipid rafts that contain the Src family kinase Lyn, a key kinase in the initiation of the BCR signal transduction cascade, and exclude the phosphatase CD45R. Moreover, we show that phosphorylated Igα and Lyn are present in the lipid rafts after BCR cross-linking. Taken together, these results suggest that the recruitment of the BCR to the lipid rafts may represent an important, previously unappreciated event in BCR signaling, allowing the concentration of the BCR and the enzymes and adaptors of the signaling pathway.

Upon BCR cross-linking, it has been observed that sg becomes associated with the actin cytoskeleton and that cytoskeletal attachment is not dependent on Igα/β signaling (47). Furthermore, sg with cytoplasmic tail sequence KVK replaced with the Igα tail was shown to have reduced ability to associate with cytoskeletal actin (48). Although the significance of cytoskeletal attachment remains unknown, we provide evidence that the WT BCR translocated into the lipid raft, along with the raft component GM1, is subsequently targeted to the IPILC in an accelerated fashion. Thus, the lipid raft may provide components necessary for the correct and accelerated targeting of the BCR to the IPILC. Our result showing that μCytoΔ is constitutively localized in lipid rafts but is not targeted to the IPILC suggests that raft localization alone is not sufficient for efficient internalization and proper intracellular targeting. Targeting may require initiation of signaling, a function for which μCytoΔ is deficient. However, rafts may provide a means for efficient
cytoskeletal association of sIg either directly or through associated factors. Taken together, the results presented here are consistent with the hypothesis that lipid rafts serve as platforms for both signaling and trafficking of membrane receptors (16).

The molecular mechanisms by which the BCR is translocated to lipid rafts remain to be elucidated. The translocation of the BCR to lipid rafts was nearly instantaneous after cross-linking. The rapidity of the translocation was similar to that reported by Montixi et al. (36), who showed that the engagement of the TCR triggers an immediate accumulation of the TCR and protein tyrosine kinases to lipid rafts, readily detectable within 10 s. Cross-linking the BCR may result in a conformational change of some sort in the BCR, that allows its rapid translocation into lipid rafts by destabilizing its interaction with Igα/Igβ or the replacement of Igα/Igβ by some other membrane component. Indeed, Vilen et al. (49) recently provided evidence that after antigen binding, the sIg–Igα/Igβ complex is destabilized such that Igα/Igβ no longer coimmunoprecipitates with sIg. However, the results presented here show that both sIg and Igα enter the rafts, indicating that the BCR remains intact after cross-linking. A conformational change could also be the result of a specific phosphorylation event on one of the tyrosines within the Igα/Igβ ITAMs. Presumably, such a phosphorylation event is insufficient to initiate significant downstream signaling before translocation to the lipid rafts. The current evidence concerning the mechanism of the translocation of the TCR into lipid rafts upon TCR engagement suggests that phosphorylation of the TCR outside the lipid rafts promotes translocation. Alternatively, a conformational change could be induced by the clustering or aggregation of the BCR by cross-linking. Analysis of additional BCR constructs in which both the association of sIg with Igα and Igβ and the signaling potential of the Igα/Igβ complex are altered should be informative with regard to the molecular basis of the trigger that leads to BCR translocation.

The BCR is similar to two other immune receptors in its behavior on the plasma membrane after cross-linking, namely the TCR and the IgE receptor, both of which become concentrated in lipid rafts after engagement. Given that these receptors share many common features in terms of the processes by which signal transduction cascades are initiated and regulated, the observation that similar strategies are used to allow concentration of the components of the signaling cascade is perhaps not surprising. As the composition of the lipid rafts is further characterized and the molecular mechanism underlying the triggering of these receptors to translocate to lipid rafts is defined, there are likely to be more commonalities discovered as well as interesting differences revealed.
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