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The Gαq/11 Proteins Contribute to T Lymphocyte Migration by Promoting Turnover of Integrin LFA-1 through Recycling

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Abstract

The role of Gαi proteins coupled to chemokine receptors in directed migration of immune cells is well understood. In this study we show that the separate class of Gαq/11 proteins is required for the underlying ability of T cells to migrate both randomly and in a directed chemokine-dependent manner. Interfering with Gαq or Gα11 using dominant negative cDNA constructs or siRNA for Gαq causes accumulation of LFA-1 adhesions and stalled migration. Gαq/11 has an impact on LFA-1 expression at plasma membrane level and also on its internalization. Additionally Gαq co-localizes with LFA-1- and EEA1-expressing intracellular vesicles and partially with Rap1- but not Rab11-expressing vesicles. However the influence of Gαq is not confined to the vesicles that express it, as its reduction alters intracellular trafficking of other vesicles involved in recycling. In summary vesicle-associated Gαq/11 is required for the turnover of LFA-1 adhesion that is necessary for migration. These Gα proteins participate directly in the initial phase of recycling and this has an impact on later stages of the endo-ecyclic pathway.

Introduction

Small chemoattractant peptides called chemokines direct T lymphocytes (T cells) to arrest on post-capillary venules at sites of infection or injury [1,2]. Chemokines bind to G protein-coupled receptors (GPCRs), initiating signalling that activates integrins such as lymphocyte function-associated antigen-1 (LFA-1, CD11a/CD18, αβ2) [3,4]. The chemokine GPCRs are coupled to heterotrimeric G proteins composed of α, β and γ subunits and signal through active Gαi-GTP and Gβγ dimers leading to generation of intracellular effectors such as Ca2+ and diacylglycerol [5,6]. One of the key downstream effectors of chemokine triggered signalling is the GTPase Rap1. It has several critical roles in immune cell functions such as migration but less is known about how they mediate their effects compared with Gαi proteins [6,8]. Gαq and Gα11 are widely expressed and are the most homologous members of this family with many of their activities considered to be over-lapping. There are conflicting reports about the involvement of these Gαq/11 proteins in migration. A positive role was demonstrated by the failure both of Gα11-inhibited myeloid leukaemia cells to migrate to lymphoid tissues and of the LFA-1-mediated tissue invasion of a Gα11-inhibited T cell hybridoma [9,10]. Similarly neutrophils and dendritic cells from mice lacking Gαq (Gnaq−/−) have deficient chemotactic responses, with the defect apparently not extending to Gnaq−/− T cells [11]. In contrast Gαq siRNA-mediated knockdown in the Jurkat T cell line enhanced migration in response to chemokine CXCL12 suggesting a repressive effect of the Gαq protein on motility [12].

In this study we have focussed on the role of Gαq and Gα11 in T cell migration mediated by the integrin LFA-1. Blocking Gαq/11 activity increased LFA-1-mediated adhesion and led to a reduction in the ability of T cells to migrate both randomly and towards chemokine. We show that this G protein family is required for the turnover of LFA-1 adhesions, has a specific role in their endocytosis and has an impact beyond its expression in the intracellular trafficking of LFA-1.

Results

Gα11 is Needed for Directed but not Random Migration

To investigate involvement of different classes of heterotrimeric G proteins in T cell migration, we first asked whether the HSB2 T cell line was able to respond to a chemoattractant by testing its migration toward CXCL12 (SDF-1α) in a Transwell assay. Transfection of T cells with a dominant negative (DN) cDNA construct of the G protein, Gα11, which is involved in chemokine-mediated chemotraction [13], caused decreased migration...
towards CXCL12 (87±4% decrease) (Fig. 1A). Placing CXCL12 in both upper and lower wells abrogated the directed movement of the T cells indicating that a chemotactic effect was being detected (data not shown). The transfection did not affect membrane expression of CXCR4, the CXCL12 receptor, compared with T cells transfected with control vector (data not shown).

Although unable to respond to the chemokine, T cells transfected with DN Gaai2 cDNA had however the same capacity as cells expressing the vector control to migrate randomly on surfaces coated with the LFA-1 ligand, intercellular adhesion molecule-1 (ICAM-1) [ICAM-1] (Fig. 1B). There was no difference in either directionality or speed of migration between DN Gaai2-treated versus vector control-treated T cells (DN Gaai2, 12.8±1.1 µm/min; control, 11.0±0.7 µm/min (mean±s.d.)).

To ask whether this distinction between directed and random migration applied more generally and to rule out autocrine chemokine stimulation, we treated T lymphoblasts with pertussis toxin (PTX) that inhibits Gaq activity by catalyzing the ADP-ribosylation of Gai proteins. PTX had significant impact on migration towards chemokines CXCL12 and CXCL10 (IP-10) as expected (% decrease: CXCL12, 71.5±6.5%; CXCL10, 56.5±1.5%) (Fig. 1C). However, as with HSB2 T cells expressing DN Gai proteins, the ability of T lymphoblasts to migrate randomly on ICAM-1 with regard to either directionality or the speed of migration was unaffected by PTX (PTX, 9.0±0.6 µm/min; control, 9.3±0.6 µm/min (mean±s.d.)) (Fig. 1D). These findings suggest that the Gai-containing heterotrimers are not utilized for random migration of T cells.

The Gq/11 Subgroup is Needed for both Random and Directed T Cell Migration

We next investigated the effect on migration of the Gq/11 subgroup of heterotrimeric G proteins whose function is insensitive to PTX [6]. DN cDNA constructs for the two major members of this group, Gq and G11, had significant impact on LFA-1-dependent migration when transfected into HSB2 T cells either singly or together. Both the extent of single cell tracking and overall speed were substantially reduced (DN Gq, 1.5±0.5 µm/min; DN G11, 3.4±0.9 µm/min; DN Gq/11, 3.8±0.6 µm/min; control, 7.9±0.7 µm/min (mean±s.d.)) (Fig. 2A).

To further confirm the role of these G proteins by a means alternative to cDNA transfection, we focused on Gq that gave the most robust siRNA knockdown. For Gq siRNA-treated HSB2 T cells, Gq protein was reduced by ~85% to a level of 16.5±1.8% of control siRNA-treated cells (mean±s.d. of n=5 experiments) (Fig. 2B). For primary T cells the average level of Gq siRNA knockdown was ~60% with Gq expression reduced to 40.0±8.9% of control siRNA (mean±s.d. of n=3 experiments). A significant decrease in single cell tracking and speed of random migration was observed with siRNA-treated primary T cells (Gq siRNA, 4.4±0.4 µm/min, control siRNA, 10.7±0.5 µm/min) (Fig. 2C).

We next examined a possible role for Gq in migration directed by chemokines. Gq siRNA-treated primary T cells displayed a decrease of 41±6% in chemotaxis to CXCL12 in a Transwell assay compared with control siRNA-treated T cells (Fig. 2D). An equivalent result was obtained when HSB2 T cells were

**Figure 1. Gai2 is needed for directed but not random migration.** (A) HSB2 T cells ± transfection with DN Gai2 or vector control cDNAs showing chemotactic response to CXCL12 (SDF-1α) or medium alone using a Transwell assay, n = 4 experiments; (B) Random migration of HSB2 T cells on ICAM-1 treated as (A): a representative experiment of single cell tracking patterns (n=15 cells per condition) and collective speed of migration (mean ± s.d.), n=3 experiments; (C) T lymphoblasts ± pre-treatment with pertussis toxin (PTX) at 200 ng/ml showing chemotactic response to CXCL12, CXCL10 (IP-10) or medium alone using a Transwell assay, n = 3 experiments; (D) Random migration on ICAM-1 of T blasts treated as (C): a representative experiment of single cell tracking patterns (n = 25 cells per condition) and collective speed of migration (mean ± s.d.), n=3 experiments.
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transfected with DN Gaq/11 and tested for chemotaxis to CXCL12. The transfected cells were reduced to the background levels of migration (Supplementary Fig. S1).

It was important to evaluate any role for Gaq/11 proteins in a shear flow assay that tests the ability of integrins to attach under conditions of mechanical stress as experienced in the circulation. The rolling and attaching behavior of Gaq siRNA-treated HSB2 T cells was assessed on chambers coated with ICAM-1 and E-selectin at a shear force of 1 dyne as previously described [14]. Both Gaq and control siRNA-treated T cells rolled normally on E-selectin and were able to attach both transiently and firmly to ICAM-1 (Supplementary Fig. S2A). The ability of Gaq siRNA-treated cells to adhere normally was further confirmed in a static adhesion assay where DN Gaq/11-transfected T cells adhered to ICAM-1 comparably to the control T cells (Supplementary Fig. S2B).

Thus the Gaq/11 proteins have a role in the random migration of T cells and also when the cells are undergoing directed migration to a chemoattractant such as a chemokine. However the G proteins appear not to influence T cell adhesion to ICAM-1 under either static or mechanical shear conditions.

DN Gaq/11 Reduction Alters the Morphology of ICAM-1-adhered T Cells

To gain further understanding of how signaling through Gaq/11 might regulate LFA-1-mediated migration, we investigated the morphology of T cells transfected with either a combination of DN Gaq/11 cDNAs or vector alone. The DN Gaq/11-treated T cells were polarized to the same extent as control T cells (DN Gaq/11, 83.5±0.7% versus control, 86±1.5%) (Fig. 3A). However, DN Gaq/11-transfected T cells...
displayed increased total cell length compared with control T cells (DN Gαq/11, 20.5±3.5 μm versus control, 13.85±3.5 μm (mean±s.d.)). Additionally, the uropods of the majority of DN Gαq/11-transfected T cells were attached to the ICAM-1-coated surface rather than elevated above it (DN Gαq/11, 81.5±2.5% versus control, 31.5±1.5%). Live cell images highlighted an abnormally attached rear of the DN Gαq/11-transfected T cells providing further evidence that T cells lacked the ability to detach correctly (Fig. 3B, Supplementary Videos S1 and S2). A lack of effect on migration of T cells transfected with WT Gαq cDNA provided further evidence that the DN cDNAs were working as expected (data not shown).

These observations indicate that T cells transfected with DN Gαq/11 cDNAs are able to move the leading edge of the cell forward but have impaired ability to detach from the substrate ICAM-1.

**Association of Gαq/11 with LFA-1 Endocytosis and Intracellular Vesicles**

An association has been made previously between the failure of LFA-1 detachment and β2 subunit mutation leading to lack of LFA-1 endocytosis [15]. It was therefore of interest to test whether there was a connection between the ability of the Gαq/11-inhibited T cells to turnover LFA-1 adhesions and endocytosis or recycling of this integrin. To investigate LFA-1 internalization biochemically, intact HSB2 T cells were surface labelled with glutathione-cleavable biotin and allowed to migrate on ICAM-1 for 40 min followed by LFA-1 immunoprecipitation and blotting for biotinylated integrin. Removal of membrane LFA-1 using glutathione, total LFA-1 could be distinguished from internalized LFA-1 [16,17]. The T cells were also treated with primaquine (PQ), which is a lysosomotropic amine that slows recycling by blocking membrane fusion of exocytic vesicles [17]. When Gαq siRNA-treated T cells were compared with control siRNA-treated cells there was a 33±4% reduction in internalized LFA-1 based on total cell biotinylated LFA-1 levels (Fig. 4A).

Confocal microscopic images of T blasts revealed a pattern of Gαq-expressing intracellular vesicular structures with highest density of immunostaining in the juxta-nuclear region of the polarized cells and trailing edge with scattered distribution towards the front of the cell (Fig. 4B). Thus Gαq not only influences LFA-1 internalization, but is also associated with intracellular vesicles. These observations provide the first suggestion that the Gαq proteins might be involved in LFA-1 recycling.

**Figure 3. DN Gαq/11 alters the morphology of ICAM-1-adhered T cells.** (A) HSB2 T cell transfected with DN Gαq/11 or vector control cDNAs showing morphology following attachment to ICAM-1 for 20 min at 37°C. Effect on polarization, cell length and cell uropod attachment to ICAM-1 (n=25 cells per sample); results expressed as mean ± s.d.; (B) Representative live cell images of ICAM-1 attached T cells following transfection with vector control cDNA (left) showing elevated uropods or DN Gαq/11 cDNAs (right) with attached trailing edge and uropods; black asterisk = leading edge, white asterisk = trailing edge; scale bar = 10 μm. doi:10.1371/journal.pone.0038517.g003
Co-localization of Gq with LFA-1 and Vesicle Markers

We used confocal microscopy to further define the association of Gq with LFA-1 and other intracellular vesicle markers. Gq co-localized with LFA-1 particularly prominently where endosomal vesicles are located in the juxta-nuclear region and trailing edge (Fig. 5). Pixel-by-pixel analysis yielded 95.4±1.8% overlap between Gq and LFA-1 (n=5 cells). Gq staining also overlapped with EEA1, a key Rab5 effector protein [18] (Overlap analysis = 94.2±4.0%, n=5 cells). However, although it was well expressed, there was essentially no overlap of Gq with Rab11, a marker of a subset of late endosomal vesicles (Overlap analysis = 12.7±3.9%, n=5 cells) and previously associated with LFA-1 recycling [16].

The GTPase Rap1 is required for the early events of LFA-1 adhesion [19] and also with its transport in intracellular vesicles [4,7,20,21]. We observed a partial overlap of Gq with Rap1 (Overlap analysis = 67.7±12.5%, n=5 cells) suggesting that Rap1 has associations beyond those with Gq.

Figure 4. Association of Gq/11 with intracellular vesicles and LFA-1 internalization. (A) Biotinylated HSB2 T cells migrating on ICAM-1 over 40 min with quantification of the effect on membrane LFA-1 internalization of transfection with siRNA Gq compared with control siRNA, n = 3 experiments; (B) Representative confocal microscopy image at substrate level of T lymphoblast polarized on ICAM-1 and fixed before staining with rabbit anti-Gq and Alexa488 goat anti-rabbit IgG; shown with Rainbow scale of graded fluorescence intensity; black asterisk = leading edge; scale bar = 10 μm;
doi:10.1371/journal.pone.0038517.g004

In summary, confocal microscopy showed that there was selectivity in immunostaining of Gq in that it overlapped with LFA-1 and with some, but not all, endosomal vesicle markers previously associated with this integrin.

Association of Gq with LFA-1 and Vesicle Markers at Plasma Membrane Level

We next used TIRF microscopy to look in closer detail at the T cell membrane where LFA-1 was in contact with ICAM-1. At TIRF level, Gq co-localized with LFA-1 in the main cell body where the integrin attached to ICAM-1 sparing the attached filopodia (Overlap analysis = 79.8±6.2%, n=5 cells). Co-localization of Gq staining with EE1 was also observed (Overlap analysis = 81.6±12.9%, n=5 cells) (Fig. 6). Thus Gq was expressed at membrane level with LFA-1 and EE1. In contrast, Rab11 and Rap1 were both poorly visible at TIRF level. As both proteins were easily imaged at epifluorescence level, the implication is that they are expressed intracellularly but away from the plasma membrane.
Figure 5. Co-localization of Gaq with LFA-1 and vesicle markers. Confocal images of T lymphoblasts attached to ICAM-1. A comparison is made of Gaq localization (green) with LFA-1 and intracellular markers of endosomal vesicles EEA-1, Rab11 and Rap1 (all red) and subsequent merged images; the images are representative of n = 4 experiments; scale bar = 10 μm.
doi:10.1371/journal.pone.0038517.g005
Figure 6. TIRF images of T lymphoblasts polarized on ICAM-1. Single cell images of T lymphoblasts viewed at ICAM-1 level by TIRF showing co-localization of Gaq expression (green) with LFA-1 and endosomal vesicle markers EEA1 (red) and merge of both colors. There is an absence of detection of Rab11 and Rap1 at TIRF level; the presented images are from the same experiment as illustrated in Fig. 5; images are representative of n = 3 experiments; scale bar = 10 μm.
doi:10.1371/journal.pone.0038517.g006
Effect of Gq/11 Reduction on Vesicle Expression and Distribution

It was relevant to ask whether Gq/11 siRNA knockdown altered the expression or distribution pattern of intracellular vesicles. When Gq/11 siRNA-treated T cells were compared with control siRNA-treated cells, it was evident that the T cells with reduced Gq/11 displayed increased expression of LFA-1 and EEA1 that were both co-expressed with Gq/11 [Fig. 7A, Table 1]. In addition, although Gq/11 only partially overlapped with Rap1, and not at all with Rab11, the staining associated with these vesicle markers was also increased in the Gq/11 siRNA-treated T cells. Therefore the reduction in Gq/11 expression had an impact not only on Gq/11-expressing vesicles, but also on vesicles with which it did not co-distribute.

Finally it might be expected that these effects of lack of Gq/11 on vesicular traffic would have an impact on membrane expression of LFA-1. Using laser scanning cytometry to examine LFA-1 expression per unit cell area, a comparison of T cells transfected with control versus DN Gq/11 cDNAs revealed ~40% reduction in expression of LFA-1 on membranes of Gq/11 compromised T cells with intracellular accumulation of recycling vesicles [Fig. 7B].

The accumulation of several types of intracellular vesicles when the level of Gq/11 is diminished is consistent with there being a general slowdown in intracellular trafficking of LFA-1 that has a knock-on effect of causing reduction in LFA-1 at membrane level.

Discussion

In this study we find that the Gq/11 class of G proteins has an essential function in the LFA-1-mediated migration of human T cells. These two G proteins are needed for a basic aspect of migration as their blockade affects both random migration and also when the T cells are undergoing directed chemokine-mediated migration through the use of G protein, Gq/11. The use of dominant negative cDNAs indicate an overlapping role for Gq/11 and Gq/11 as has been previously suggested [6,8]. We provide evidence that Gq/11 proteins participate in LFA-1 recycling and in particular that they regulate LFA-1 adhesion turnover, internalization and membrane expression. The effect on migration is in keeping with an earlier report indicating Gq/11 involvement in the LFA-1-mediated migration and invasion of a T cell lymphoma [10]. Furthermore there is increasing evidence that recycling of integrin is generally essential for successful migration of leukocytes. For example, the presence of α5β1 [22,23] and LFA-1 [16] in recycling vesicles drives neutrophil migration.

An initial observation was that blockade of Gq/11 and Gq/11 activity or Gq/11 siRNA knockdown caused excessive T cell adhesion to ICAM-1. Although the leading edge of the T cells displayed some forward motility, migration halted because of increased attaching, not at the front, but at the rear of the cell. Blocking Gq/11 activity however had no overall effect on LFA-1-mediated adhesion of T cells under either static or shear flow conditions, suggesting that the pro-adhesive phase was not affected. The evidence thus pointed to an inability of Gq/11-compromised T cells to detach or turnover their LFA-1 adhesions.

A previous report showed that mutation of the β2 subunit in the endocytosis motif prevented not only endocytosis, but also LFA-1 turnover implying a connection between the two processes [15]. Similarly we found that Gq/11 affected de-adhesion and was also required for LFA-1 internalization. This was consistent with confocal images showing the presence of Gq/11 on intracellular vesicles and co-localization with LFA-1 and EEA1, a protein associated with the GTPase Rab5 that characterizes vesicles involved in the early endocytic stage of recycling [24].

The GTPase Rap1 plays an essential early role in lymphocyte arrest on the vasculature following chemokine stimulation [19] and this is consistent with its involvement in vesicle transport as well-demonstrated in other studies [20,21,25,26]. Gq/11 only partially co-distributed with Rap1 suggesting additional roles for the GTPase. Other studies report Rap1 to be associated with EEA1, Rab5 and Rab11 [21] or alternatively on vesicles with limited EEA1 and Rab7 overlap [26]. Thus, in terms of vesicle marker expression, the pattern of Rap1 expression is distinct from but overlapping with Gq/11. It is of interest that Rap1 is also required for delivery of LFA-1 to the membrane [27] whereas we found no role for Gq/11 in this activity.

Gq/11 did not co-distribute with Rab11 that is displayed by a subset of late endosomal vesicles. This is of relevance because LFA-1 recycling has also been associated not only with Rap1, but with recycling vesicles expressing Rab11 and with trafficking of LFA-1 to the lamellipodia [16]. The data therefore support the idea that Gq/11 is associated with the initial endocytic phase of LFA-1 recycling and not with the later stages. Thus there must be heterogeneity in LFA-1-transporting vesicles with Gq/11 characterizing one set and Rap1 and Rab11, a partially overlapping and separate set respectively that are involved in the subsequent events of bringing LFA-1 to the membrane followed by exocytosis. Supporting evidence comes from a comparison between epifluorescence and TIRF observations that show both Rap1 and Rab11 to be most highly concentrated away from the level of close membrane contact of T cell LFA-1 with ICAM-1. The Rab11-dependent release of LFA-1 into membrane ruffles at the leading edge of CHO cells is in keeping with their lack of substrate contact [16].

The influence of Gq/11 on the behavior of intracellular vesicles however goes beyond the vesicles that express it, as Gq/11 siRNA knockdown affects not only EEA1-expressing vesicles on which Gq/11 is co-expressed, but also Rap1- and Rab11-expressing vesicles. These vesicle markers normally display a juxta-nuclear distribution pattern with scattered representation towards the front of the polarized T cell. In Gq/11 siRNA-treated T cells, the juxta-nuclear pattern is relaxed and this is accompanied by an increase in vesicles expressing not only LFA-1 and EEA1, but also Rap1 and Rab11. Such a “log jam” of vesicles and the reduction in membrane LFA-1. This is apparently not fully compensated for by the vesicles that normally express it, as Gq/11-expressing late endosomes also display increased LFA-1-mediated adhesion [28]. A speculative idea that Gq/11-expressing vesicles are linked in terms of function to other vesicles with later involvement in the endocytic/exocytic sequence of events involved in the intracellular movement of LFA-1 back to the membrane. An end result of the failure of normal recycling is the ~40% decrease in expression of membrane LFA-1. This is apparently not fully compensated for by a decrease in LFA-1 internalization in Gq/11 blocked cells. It was also not reflected in diminished adhesion, but rather the reverse, consistent with disturbance in LFA-1 turnover as evident from impaired uropod retraction.

Some of these activities of Gq/11 are similar to those of the Gq/12/13 class of G proteins. T cells from Gq/12/13-deficient mice also display increased LFA-1-mediated adhesion [28]. A speculation is that Gq/12/13 may also be involved in recycling of integrin as Rab11-expressing vesicles that are Gq/13-dependent are associated with an intracellular recycling compartment of T cells containing CXCR4/TCR heterodimers [29].

In summary we here define an early stage in LFA-1 recycling on T cells that is regulated by the Gq/11 proteins. Although Gq/11
Figure 7. Effect of Gαq siRNA knockdown on intracellular vesicles. (A) DIC and confocal microscopy images of HSB2 T cells on ICAM-1 showing distribution and intensity of staining of LFA-1, EEA1, Rab11 and Rap1 following transfection with either control or Gαq siRNAs; results are representative of n = 3 experiments, scale bar = 10 μm; (B) Comparison of membrane LFA-1 expression per comparable cell area in T cells treated either with control or DN Gαq/11 cDNAs.

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Table 1. Quantification of the effect of Gαq siRNA knockdown on expression of other vesicle markers.

|                      | control siRNA | Gαq siRNA | P value |
|----------------------|---------------|-----------|---------|
| LFA-1                | 705±5*        | 739±5     | 0.0014  |
| EEA1                 | 679±7         | 710±4     | 0.0018  |
| Rab11                | 696±3         | 737±10    | 0.0034  |
| Rap1                 | 662±16        | 719±8     | 0.015   |

Mean fluorescence intensity (MFI) measurements were quantified from 10 T cells per sample type for integrin LFA-1, Rab5 effector EEA1 and GTPases Rab11 and Rap1. The HSβ2 T cells were transfected with either control or Gαq siRNAs for 48 hr prior to attaching to and migrating on ICAM-1.

*Mean fluorescence intensity ± SD.

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11 has a direct role in endocytosis, there is evidence for more extended influence on an interconnected sequence of events involving other types of vesicles that traffic LFA-1 back to the T cell membrane. The presented evidence does not exclude the extended influence on an interconnected sequence of events independent of Gαq/11. A key issue for the future will be to determine the relationship between the different LFA-1-containing intracellular vesicles and the extent of their heterogeneity.

Materials and Methods

Antibodies and Reagents

MAbs used in this study are: 38, pan-LFA-1, prepared at CRUK LRI [30]; α tubulin DM1A (T6199, Sigma-Aldrich Ltd, Gillingham, Kent, UK); GTPase Rap1 (610196), endosomal vesicle markers EEA1 (610457) and Rab11 (610656) (all BD Transduction Laboratories, Oxford UK); rabbit anti-Gαq Ab (E-17) (SC-393, Santa Cruz Biotechnology Inc/Insight Biotechnology Ltd, Wembley, UK). Five domain ICAM-1Fc was produced as previously described [31].

Cell Isolation, Culture and Transfection

Peripheral blood mononuclear cells were prepared from single donor leukocyte buffy coats (National Blood Service, Tooting, London, UK); T cells were expanded as previously described and used between days 10 and 14 [31]. Primary T cells were isolated from donor leukocyte buffy coats (National Blood Service, Tooting, London, UK); T cells were expanded as previously described and re-suspended in 0.5 mg/ml EZ-link Sulpho-NHS-SS-Biotin (12131, Pierce, ThermoFisher Scientific, Loughborough, UK) at 25 x 10^6 cells/ml and incubated on ice for 1 h. After washing, 4 x 10^6 T cells in HBSS buffer were added to each ICAM-1-coated coverslip. Primaqinine diphosphate (PQ) (160393, Sigma-Aldrich Ltd) at 300 μM was added and the cells incubated for 40 min at 37°C to allow internalization of receptors. To remove membrane bound biotin, fresh glutathione buffer (46 mM glutathione, 75 mM NaCl, 1 mM EDTA, 1% BSA, 75 mM NaOH) was added and the cells incubated on ice for 30 min. Controls for biotinylation of total LFA-1 were maintained in PBS.

To analyze biotinylated LFA-1, T cells were lysed with a standard buffer containing 0.2% NP40 buffer (46 mM glutathione, 75 mM NaCl, 1 mM EDTA, 1% BSA, 75 mM NaOH) was added and the cells incubated on ice for 30 min. Controls for biotinylation of total LFA-1 were maintained in PBS.

LFA-1 Internalization Assay

This protocol was adapted from [35]. Glass coverslips (32 mm) were coated overnight with 3 μg/ml ICAM-1Fc, then blocked with 2.0% BSA. To biotinylate membrane proteins, washed T cells were re-suspended in 0.5 mg/ml EZ-link Sulpho-NHS-SS-Biotin (12131, Pierce, ThermoFisher Scientific, Loughborough, UK) at 25 x 10^6 cells/ml and incubated on ice for 1 h. After washing, 4 x 10^6 T cells in HBSS buffer were added to each ICAM-1-coated coverslip. Primaqinine diphosphate (PQ) (160393, Sigma-Aldrich Ltd) at 300 μM was added and the cells incubated for 40 min at 37°C to allow internalization of receptors. To remove membrane bound biotin, fresh glutathione buffer (46 mM glutathione, 75 mM NaCl, 1 mM EDTA, 1% BSA, 75 mM NaOH) was added and the cells incubated on ice for 30 min. Controls for biotinylation of total LFA-1 were maintained in PBS.

To analyze biotinylated LFA-1, T cells were lysed with a standard buffer containing 0.2% NP40 buffer. Immunoprecipitation using anti-LFA-1 mAb 38 and subsequent blotting were performed as previously described [36]. Biotinylated LFA-1 was revealed by blot incubation with Streptavidin-HRP conjugate (RPN1231, GE Healthcare) in PBS/0.1% Tween 20 and ECL reagent (GE Healthcare). Samples were also probed with α tubulin mAb and anti-mouse IgG-HRP Ab (GE Healthcare) to check for equivalent sample loading.

Chemotaxis

For chemotaxis assays, T cells at 5 x 10^6 cells/100 μl were allowed to migrate through 5 μm pore size Transwell insert wells coated with ICAM-1Fc as above (Corning, Acton, MA, USA). The lower well contained either 600 μl RPMI 1640/0.1% BSA alone or medium plus 10 nM CXCL10 or CXCL12 (PeproTech EC Ltd, London, UK). After 90 min of incubation at 37°C and 5% CO2, inserts were discarded and the migrated T cells were counted by flow cytometry after recovery using ice-cold 5 mM EDTA/PBS. All samples were tested in triplicate.

Video Microscopy

35 mm glass-bottom microwell dishes (MatTek Corp., Ashland, MA, US) or μ-slides VI (Ibidi GmbH, Martinsried, Germany) were coated overnight with 3 μg/ml ICAM-1Fc as above. The T cells (2 x 10^6 cells/ml in HBSS with 20 mM HEPES (HBSS) were exposed to ICAM-1 for 10 min at 37°C and images captured using an Olympus MTV3 Inverted microscope using a 20 x lens or Zeiss Axiovert 135TV Inverted microscope using a 63 x lens plus AQM® Kinetic Acquisition Manager software (Kinetic Imaging Ltd). The cells were tracked at 15 sec intervals with Motion Analysis software (Kinetic Imaging Ltd, Bromborough, UK) and data analyzed using a Mathematica notebook (Wolfram...
Uropod attachment was quantified as previously reported [37]. Briefly, individual live migrating T cells were observed using a visual assessment and scored by two observers. Analysis of the attachment status was accomplished by focus on both the T cell contact interface with ICAM-1 and the focal plane above this level.

Confocal and TIRF Microscopy

13 mm round glass coverslips or glass bottomed MatTek dishes were pre-coated with ICAM-1-Fc as above. Washed T cells (2×10^5 cells/sample) were added to coated coverslips for 30 min. Adherent cells were fixed with fresh 3% paraformaldehyde in Pipes buffer (pH8) for 5 min at RT, washed and fixed again in 3% paraformaldehyde in Borax, (pH 11, Sigma-Aldrich Ltd)[14]. Cells were then permeabilized with 0.1% Triton-X-100 for 5 min at 4°C. Autofluorescence was quenched using fresh sodium tetraborate (1 mg/ml, pH8) for 15 min at RT. Coverslips were incubated with primary mAbs overnight at 4°C, followed by Alexa488-goat anti-mouse IgG or Alexa546-goat anti-rabbit IgG (Invitrogen, Paisley, UK) for 45 min. Images were acquired on a Zeiss Laser Scanning Microscope LSM 710 or 780 using Zen software and x63 DIC oil lens.

The polarity of the T cells was determined by examining their morphology. A migrating T cell displays a spreading lamellipodium at the leading edge and an elevated uropod at the trailing edge, although HSB2 cells attach less ideally that T lymphoblasts. We have confirmed the assignments in previous studies of both leading edge (F-actin cross-linking; α-actinin localization) and trailing edge (increased α-tubulin and ICAM-1/3 distribution)[14,36,38].

TIRF images were acquired using a TIRF microscope system (Cell R, Olympus) based on an inverted microscope (IX 81, Olympus), TIRF illuminator with 488 nm and 561 nm lasers (Olympus), an objective (UAPON 150× TIRFM, NA 1.45, Olympus) and a sensitive EMCCD camera (iXon3 897, Andor) using Xcelsius software (Cascadell, Photometrics).

For quantification of the fluorescence using the microscope software, an arbitrary mean fluorescence value per designated cell area was determined. This was done by applying a filter between 500–1000 mHz to exclude both the background and saturated signals, leaving the positive signal of interest and generating the mean fluorescence intensity (MFI) ± s.d.

The extent of co-localization of different markers was analyzed using ImageJ software and JACoB analysis. Co-localization was measured using the Manders coefficient to evaluate the overlap in fluorescence.

Detection of Cell Membrane LFA-1 Using Laser Scanning Cytometry

Epitope expression and the area of spread contour of T cells mounted on ICAM-1 coverslips were calculated based on their fluorescence using a Laser Scanning Cytometer (CompuCyte, Mass, USA) and WinCyte version 3 software (CompuCyte). The technique has the advantage of allowing investigation of membrane expression of epitopes on lymphocytes that are adhered to and spread on the LFA-1 ligand ICAM-1. The approach was to allow cell attachment and migration followed first by cell fixing and labelling with anti-LFA-1 mAb 38 conjugated to AlexaFluor-488, then by permeabilization with 0.1% Triton X100 (5 min on ice) and labeling with Phalloidin-PE. The threshold level for measurement was set using the signal from Phalloidin-PE so that individual cells could be segmented and assigned an area value (microns squared). Within this area, the total integrated AF488 signal was measured by summation of the value of AF488 fluorescence for each pixel (10-bit scale per pixel). In Fig. 7C, we measured the change in AF488 measurements per average cell area of T cells treated with cDNA constructs of DN Gαq/11 compared with control cDNA. 6000 T cells were measured per coverslip.

Statistical Analysis

The migration and other assays are presented as mean±s.d. The unpaired Student’s t test was performed using GraphPad Prism software version 5 for Macintosh computers. The following significant differences are as indicated: *, P<0.05; **, P<0.01 and ***, P<0.001.

Supporting Information

Video S1 Chemotaxis of HSB2 T cells to CXCL12. Transwell assay showing the chemotactic response to CXCL12 of HSB2 T cells transfected with Gαq/11 or control cDNAs, n = 3 experiments. (EPS)

Video S2 Ineffectiveness of Gαq/11 blockade on T cell adhesion in static and shear flow assays. (A) HSB2 T cells treated with either control or Gαq siRNAs were tested at a shear force of 1 dyne using chambers coated with E-selectin alone to detect rolling cells and E-selectin and ICAM-1 together to detect both slow rolling and stable adhesion due to LFA-1 engagement; n = 3 experiments; (B) Static ICAM-1 adhesion assay of HSB2 T cells treated either with DN Gαq, DN Gzq11 or a combination of both cDNAs; results are representative of n = 5 experiments. (EPS)

Video S1 HSB2 T cells migrating on ICAM-1 after transfection with control cDNA for 24 h. T cells with trailing uropods are observed to be migrating. Each frame = 1/10 sec representing 15 s real time. (MOV)

Video S2 HSB2 T cells migrating on ICAM-1 after transfection with DN Gαq/Gzq11 cDNAs for 24 h. Note the attached uropods on T cells attempting to migrate. Each frame = 1/10 representing 15 s real time. (MOV)

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Author Contributions

Conceived and designed the experiments: LS FW PS NH. Performed the experiments: LS FW PS. Analyzed the data: LS FW NH. Contributed reagents/materials/analysis tools: LS FW PS NH. Wrote the paper: NH.

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