The N terminus of SKAP55 enables T cell adhesion to TCR and integrin ligands via distinct mechanisms

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The T cell receptor (TCR) triggers the assembly of “SLP-76 microclusters,” which mediate signals required for T cell activation. In addition to regulating integrin activation, we show that Src kinase–associated phosphoprotein of 55 kD (SKAP55) is required for microcluster persistence and movement, junctional stabilization, and integrin-independent adhesion via the TCR. These functions require the dimerization of SKAP55 and its interaction with the adaptor adhesion and degranulation-promoting adaptor protein (ADAP). A “tandem dimer” containing two ADAP-binding SKAP55 Src homology 3 (SH3) domains stabilized SLP-76 microclusters and promoted T cell adhesion via the TCR, but could not support adhesion to integrin ligands. Finally, the SKAP55 dimerization motif (DM) enabled the communoprecipitation of the Rap1-dependent integrin regulator Rap1-GTP–interacting adaptor molecule (RIAM), the recruitment of talin into TCR-induced adhesive junctions, and “inside-out” signaling to β1 integrins. Our data indicate that SKAP55 dimers stabilize SLP-76 microclusters, couple SLP-76 to the force-generating systems responsible for microcluster movement, and enable adhesion via the TCR by mechanisms independent of RIAM, talin, and β1 integrins.

Abbreviations used in this paper: ADAP, adhesion and degranulation-promoting adaptor protein; CCD, charge-coupled device; DM, dimerization motif; Grads, Grb2-related adaptor downstream of Shc; ICED, intensified CCD; LAT, linker of activated T cells; IFA-1, leukocyte function–associated antigen 1; MOT, maximum-over-time; mRFP1, monomeric red fluorescent protein; Mt1, macrophage stimulating 1; mYFP, monomeric YFP; PH, Pleckstrin homology; Rap1, regulator of adhesion and polarity in leukocytes; RIAM, Rap1-GTP–interacting adaptor molecule; SH2, Src homology 2; SH3, Src homology 3; SKAP55, Src kinase–associated phosphoprotein of 55 kD; SKAP-Hom, SKAP55 homologue; SLP-76, SH2 domain–containing leukocyte protein of 76 kD; TCR, T cell receptor; TD, tandem dimer; TRT, TagRFP-Turbo; VLA-4, very late antigen 4; VLA-5, very late antigen 5.

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hesion via immunologically relevant integrins such as very late 
Consequently, the mechanisms by which the TCR regulates ad-
Rap1-GTP–interacting adaptor molecule (RIAM), a regulator 
These data demonstrate that SKAP55 regulates T cell 
microclusters, and is required for their persistence and centrip-
Even though it is widely assumed that SKAP55 primarily acts 
Consequently, the mechanisms by which the TCR regulates ad-
L integrin leukocyte function–associated anti-
Although SKAP55 binds regulator of adhesion and polarity in leukocytes (RapL), a regulator of the αL integrin leukocyte function–associated antigen 1 (LFA-1; αLβ2), the manner in which SKAP55 engages Rap1-GTP–interacting adaptor molecule (RIAM), a regulator of integrin β chains, remains elusive (Ménasché et al., 2007). Even though it is widely assumed that SKAP55 primarily acts through its effects on integrins, we and others have shown that the TCR can function as a fast-acting adhesion receptor (Nguyen et al., 2008). Therefore, it is possible that SKAP55 also influences conjugate formation by promoting the efficient coupling of TCR and SLP-76 microclusters to the underlying actin cytoskeleton via associated adaptors, such as ADAP and RIAM (Lafuente et al., 2004; Pauker et al., 2011).

In the context of immune synapses, multiple adhesive and co-stimulatory molecules contribute to T cell activation, making it difficult to dissect the pathways operating downstream of a particular receptor. This presents a significant complication, as integrins recruited into physiological immune synapses and lipid bilayer–induced synapses (e.g. LFA-1, VLA-4) signal through ADAP and SKAP55 (Grakoui et al., 1999; Hunter et al., 2000; Mittelbrunn et al., 2004; Baker et al., 2009). Here, we use plate-bound antibodies specific for the TCR to establish that SKAP55 is an integral component of TCR-induced SLP-76 microclusters, and is required for their persistence and centripetal movement. We also show that SKAP55 regulates T cell spreading downstream of the TCR, facilitates the formation of stable contacts, and promotes adhesion via the TCR in the absence of integrin ligands. These processes require a functional SKAP55 dimer and can be supported by an artificial “tandem dimer” (TD) consisting of two SKAP55 SH3 domains coupled via a flexible linker. These data demonstrate that SKAP55 regulates cluster dynamics and TCR-based spreading and adhesion by multimerizing ADAP. However, the TD cannot support the transmission of “inside-out” signals from the TCR to β1 integrins and cannot bind to RIAM and talin, which play crucial roles in T cell adhesion via integrins. Further, we show that the deletion of an N-terminal dimerization motif (DM) within SKAP55 prevents the formation of SKAP55–RIAM–talin complexes and eliminates the recruitment of talin into the TCR-induced adhesive junctions within which SLP-76 microclusters are nucleated. Thus, we have identified distinct structural elements that enable SKAP55 to independently regulate adhesion via the TCR and the transmission of local inside-out signals from the TCR to integrins.

## Results

### The recruitment of SKAP55 into signalling microclusters is dependent on SLP-76 and ADAP

The constitutive association of SKAP55 with ADAP enables these adaptors to participate in a variety of biological processes (Wu et al., 2002; Wang et al., 2003, 2007; Burbach et al., 2008, 2011). Because all SKAP55 molecules associate with ADAP, which engages SLP-76 directly when tyrosine phosphorylated, we hypothesized that SKAP55 would function within SLP-76 microclusters (Marie-Cardine et al., 1998a; Pauker et al., 2011). Thus, we plated SLP-76–deficient Jurkat cells (J14 cells) that had been stably reconstituted with SLP-76-YFP (J14.SY cells) on stimulatory antibody (OKT3)-coated and glass surfaces that had been BSA blocked to minimize the deposition of serum components on the glass. T cells settling onto these substrates are activated via the TCR (Fig. S1 A), develop signaling microclusters, and undergo cytoskeletal rearrangements that convert the responding cells into flat adherent cells within 3–5 min. Under these conditions, endogenous SKAP55 colocalized with SLP-76 in TCR-induced microclusters (Fig. 1 A). Similarly, an exogenous SKAP55 chimera tagged with the red fluorescent protein TagRFP-Turbo (TRT) entered and co-migrated with SLP-76 microclusters (Video 1). To display the movement of the SLP-76– and SKAP55-containing microclusters, movies were compressed into maximum-over-time (MOT) images that depict persistent, mobile microclusters as radial spokes extending from the periphery to the center of the contact (Fig. 1 B). SKAP55 was cytoplasmic in SLP-76–deficient J14 cells expressing monomeric YFP (mYFP), but clustered when co-expressed with exogenous SLP-76-YFP (Fig. 1 C). Although ADAP increases the half-life of SKAP55, it is possible to express exogenous SKAP55 in the absence of ADAP (Fig. S1 B; Huang et al., 2005). Using ADAP-deficient JDAP cells, we demonstrated that the recruitment of SKAP55 into persistent and mobile microclusters also requires ADAP (Fig. 1 D). To display microcluster persistence and directionality, we created kymographs depicting lateral movement over time. In these images the long, slanted traces represent persistent and mobile microclusters, whereas shorter, vertical traces represent labile, immobile microclusters (Fig. 1 E, top). SLP-76 microclusters did not undergo sustained movements in the absence of ADAP, even when exogenous SKAP55.mCFP was present. Reconstitution with exogenous ADAP restored normal microcluster
and deriving a single composite kymograph for each condition, weighing each cell equally (Fig. S1 E). In addition, the time-averaged fraction of SLP-76.YFP intensity falling within microclusters was reduced upon SKAP55 knockdown (Table 1); this parameter reflects microcluster number, relative brightness, and survival over time (Table 1). SKAP55-deficient cells also formed less stable contacts with the stimulatory substrate over time. To quantitate this phenotype, we used an automated segmentation algorithm acting on the cytoplasmic mRFP1 signal to track contact boundaries. Regions of boundary growth (red) and retraction (blue) were defined by comparison with images captured 30 s earlier; regions that remained constant were labeled in gray (Fig. S1 F; and Videos 3 and 4). Consistent with our observations, the fluctuation of contact, defined as the mean over time of the dynamic area (red + blue) per current area (red + gray), increased after SKAP55 knockdown (Fig. S1, F and G). These changes were associated with increases in the extent and duration of periodic cycles of contact growth and retraction (Fig. S1 H; color indicates rate of growth or retraction along the cell perimeter). Because these analyses were computationally intensive, we also categorized cell boundaries as stable or unstable by blinded manual scoring.

dynamics, and enabled the comigration of SKAP55 with SLP-76 (Fig. 1 E). Thus, SKAP55 recruitment to and movement with signaling microclusters requires both SLP-76 and ADAP.

SKAP55 is required for the stabilization of SLP-76 microclusters and TCR-initiated contacts

To determine if SKAP55 influences the dynamics of SLP-76 microclusters, we performed transient knockdown experiments using a SKAP55-specific shRNA expression vector incorporating a monomeric red fluorescent protein 1 (mRFP1) reporter. J14.SY cells transfected with the knockdown vector or a control mRFP1 expression vector were isolated using a YFP+/RFP+ gate and imaged on stimulatory coverslips. The knockdown cells had fewer SLP-76 microclusters, and these structures were both labile and immobile (Fig. S1, C and D; and Video 2). Differences in microcluster persistence, displacement, and peak speed were quantified by manual microcluster tracing, which confirmed the significance of the alterations in microcluster dynamics (Table 1; ±SEM in three or more experiments). These changes were also depicted by compiling average traces for each cell, and deriving a single composite kymograph for each condition, weighing each cell equally (Fig. S1 E). In addition, the time-averaged fraction of SLP-76.YFP intensity falling within microclusters was reduced upon SKAP55 knockdown (Table 1); this parameter reflects microcluster number, relative brightness, and survival over time (Table 1). SKAP55-deficient cells also formed less stable contacts with the stimulatory substrate over time. To quantitate this phenotype, we used an automated segmentation algorithm acting on the cytoplasmic mRFP1 signal to track contact boundaries. Regions of boundary growth (red) and retraction (blue) were defined by comparison with images captured 30 s earlier; regions that remained constant were labeled in gray (Fig. S1 F; and Videos 3 and 4). Consistent with our observations, the fluctuation of contact, defined as the mean over time of the dynamic area (red + blue) per current area (red + gray), increased after SKAP55 knockdown (Fig. S1, F and G). These changes were associated with increases in the extent and duration of periodic cycles of contact growth and retraction (Fig. S1 H; color indicates rate of growth or retraction along the cell perimeter). Because these analyses were computationally intensive, we also categorized cell boundaries as stable or unstable by blinded manual scoring.

Figure 1. SKAP55 is recruited into microclusters by SLP-76 and ADAP. (A) Immunofluorescent staining for endogenous SKAP55 in J14.SY cells fixed 5 min after plating on anti-CD3 coated, BSA-blocked stimulatory coverslips. (B) J14.SY cells expressing either SKAP55.TRT (top) or TRT (bottom) were stimulated on coverslips and imaged for 5 min. MOT projections depict the trajectories of microclusters over time (n = 20). (C) MOT images of J14 cells coexpressing SKAP55.mRFP1 and either mYFP (top) or SLP-76.mYFP (bottom) (n = 3). (D) MOT images of ADAP-deficient JDAP cells coexpressing SKAP55.3×Flag.mCFP, SLP-76.YFP, and either 3×Flag.TRT (top) or TRT.3×Flag.TRT.ADAP-120 (bottom) (n = 4). (E) Kymographs depicting the lateral movements of SLP-76, SKAP55, and ADAP microclusters along a narrow region of interest spanning the center of the cell. Bars: (A–D) 10 µm; (E) 5 µm x 60 s.
This approach also revealed a significant destabilization of contact boundaries in cells lacking SKAP55 (Fig. S1, I and J).

To verify that the phenotypes observed upon transient knockdown were caused by the specific loss of SKAP55, rather than off-target effects of the hairpin, we derived SKAP55-deficient J14.SY cells (JSKAP.SY) using a lentivirally encoded SKAP55-specific shRNA. These cells were transfected with vectors encoding either mRFP1 or a hairpin-resistant SKAP55.mRFP1 chimera (Fig. 2 A). In contrast to J14.SY cells, JSKAP.SY cells produced immobile and short-lived SLP-76 microclusters (Fig. 2, B and C; Table 2; and Video 5). The reexpression of SKAP55 restored optimal microcluster dynamics, confirming that SKAP55 is an integral component of SLP-76 microclusters (Fig. 2, B and C; Table 2; and Video 6). Finally, reconstitution limited boundary fluctuation in TCR-induced contacts, and reduced the fraction of contacts scored as “unstable,” confirming that SKAP55 also regulates the junctions formed in response to solo TCR ligation (Fig. 2, D and E).

Defects in SLP-76 microcluster persistence and movement have been correlated with significant reductions in TCR-proximal signals, including calcium entry and CD69 up-regulation (Bunnell et al., 2006; Sylvain et al., 2011). Although the loss of SKAP55 clearly impacted microcluster properties and TCR-induced cytoskeletal rearrangements, the suppression of endogenous SKAP55 did not dramatically impact microcluster-induced increases in CD69 expression or Erk activation (Fig. 2, F and G).

The SKAP55 SH3 domain is necessary but insufficient for recruitment into and stabilization of SLP-76 microclusters

Consistent with the important role of ADAP in the recruitment of SKAP55 into SLP-76 microclusters (Fig. 1, D and E), an ADAP nonbinding SKAP55 SH3 domain mutant chimera (W333R; “WR”) failed to cocluster with SLP-76 when overexpressed in J14.SY cells (Fig. 3, A–C). Relative to cells expressing either a WT chimera or an mRFP1 control, cells expressing the W333R mutant exhibited short-lived and immobile microclusters (Fig. 3, B–D; Video 7; and Table 1). The SLP-76 microclusters produced in cells expressing the W333R mutant also incorporated less SLP-76, but did not show significant decreases in peak microcluster speed (Table 1). An isolated SKAP55 SH3 domain (“SH3”) behaved as a dominant-negative for microcluster dynamics even though it interacted with ADAP (Fig. 3, A–E; and Table 1). Finally, the W333R mutant and the isolated SH3 domain reduced the stability of TCR-induced contacts (Fig. 3 F). Thus, regions in the N terminus of SKAP55 are critical for its function.

The SKAP55 Pleckstrin homology (PH) domain and linker tyrosines play minimal roles in SLP-76 microcluster dynamics and contact stability downstream of the TCR

Within the central portion of SKAP55, two regions have been implicated in intermolecular interactions: a PH domain and a tyrosine-phosphorylated linker region (Wu et al., 2002; Hornbeck et al., 2004; Swanson et al., 2008; Fig. 4 A). Nevertheless, SKAP55 chimeras lacking the PH domain (∆PH) or the linker tyrosines (Y219F/Y232F/Y271F, “3YF”) entered SLP-76 microclusters (Fig. 4, A–C). Only the 3YF chimera exhibited even a mild (but significant) dominant-negative effect on microcluster dynamics or TCR-mediated contact stability (Fig. 4, D and E; and Table 1). Reconstitution of JSKAP.SY cells with mixed levels of shRNA-resistant wild-type, 3YF, ∆PH, or inositide nonbinding (R131M, PH*) SKAP55 chimeras all improved SLP-76 microcluster dynamics relative to cells expressing only 3×Flag.TRT, and all three mutant chimeras stabilized contacts in JSKAP.SY cells (Fig. 4, E and F; and Fig. S2 A; Swanson et al., 2008). SKAP55 did not recruit to the plasma membrane at surfaces outside of SLP-76 microclusters, either at or above the stimulatory coverslip, even though the phosphatidylinositol-3,4,5-trisphosphate–binding PH domain of Akt clearly labeled these membranes (Fig. 4 G). Furthermore, an isolated SKAP55 PH domain chimera was not recruited to the plasma membrane and remained distributed throughout the cytoplasm and nucleus after TCR ligation (Fig. S2 B). Thus, in our model system, the PH domain and the linker tyrosines of SKAP55 are neither necessary nor sufficient for recruitment into and stabilization of SLP-76 microclusters.

Table 1. Impact of SKAP55 mutants on SLP-76 microcluster dynamics

<table>
<thead>
<tr>
<th>SKAP55 chimera</th>
<th>Persistence</th>
<th>% Inward movement</th>
<th>Max speed</th>
<th>% SLP-76 in clusters</th>
<th>Clusters tracked per diameter</th>
<th>Total cells</th>
<th>n (experiments)</th>
</tr>
</thead>
<tbody>
<tr>
<td>mRFP1</td>
<td>210.5 ± 7.20</td>
<td>3.0 ± 0.2</td>
<td>147.7 ± 6.1</td>
<td>62.0 ± 2.8</td>
<td>15.1 ± 0.48</td>
<td>46</td>
<td>19</td>
</tr>
<tr>
<td>KD</td>
<td>115.8 ± 38.2</td>
<td><strong>0.6 ± 0.1</strong></td>
<td>**57.8 ± 8.6</td>
<td><strong>27.3 ± 6.9</strong></td>
<td><strong>12.5 ± 1</strong></td>
<td>*, ††</td>
<td>10</td>
</tr>
<tr>
<td>WT</td>
<td>215.7 ± 7.52</td>
<td>3.4 ± 0.3</td>
<td>150.6 ± 8.6</td>
<td>72.1 ± 2.3</td>
<td>17.2 ± 0.87 **</td>
<td>*</td>
<td>29</td>
</tr>
<tr>
<td>WR</td>
<td>129.3 ± 18.9</td>
<td><strong>1.3 ± 0.3</strong></td>
<td>**128.7 ± 31.9</td>
<td>37.6 ± 6.6 **</td>
<td><strong>13.6 ± 1.8</strong></td>
<td>8</td>
<td>3</td>
</tr>
<tr>
<td>SH3</td>
<td>150.5 ± 16.4</td>
<td><strong>1.4 ± 0.5</strong></td>
<td>**104.6 ± 23.4</td>
<td><strong>41.9 ± 15.4</strong></td>
<td>**9.6 ± 1.5 **</td>
<td><strong>10</strong></td>
<td>5</td>
</tr>
<tr>
<td>∆PH</td>
<td>222.9 ± 2.1</td>
<td>2.8 ± 0.2</td>
<td>154.2 ± 9.6</td>
<td>77.3 ± 2.9</td>
<td>15.3 ± 0.33</td>
<td>10</td>
<td>3</td>
</tr>
<tr>
<td>3YF</td>
<td>169.2 ± 16.4</td>
<td><strong>1.3 ± 0.3</strong></td>
<td>**153.5 ± 17.4</td>
<td>66.5 ± 5.1</td>
<td>16.4 ± 0.98</td>
<td>10</td>
<td>4</td>
</tr>
<tr>
<td>∆DM</td>
<td>175.9 ± 23.3</td>
<td>1.5 ± 0.2</td>
<td>137.7 ± 15.1</td>
<td>44.9 ± 5.2 **</td>
<td>**13.3 ± 1.5 **</td>
<td><strong>10</strong></td>
<td>3</td>
</tr>
<tr>
<td>DM</td>
<td>133.1 ± 5.9</td>
<td><strong>1.1 ± 0.1</strong></td>
<td>**101.6 ± 6.2</td>
<td>**32 ± 4.0 **</td>
<td><strong>14 ± 2</strong></td>
<td>10</td>
<td>3</td>
</tr>
<tr>
<td>TD</td>
<td>227.2 ± 11.6</td>
<td>2.5 ± 0.2</td>
<td>129.1 ± 23.8</td>
<td>73.1 ± 1.1</td>
<td>14.0 ± 0.95</td>
<td><strong>10</strong></td>
<td>3</td>
</tr>
</tbody>
</table>

SLP-76 microcluster dynamics in J14.SY cells expressing each of the indicated constructs were measured on a per cell basis by manual tracing of microcluster trajectories from SLP-76 kymographs. Values for each experiment were obtained by averaging these per cell values, weighing each cell equally. KD, knockdown.
SKAP55 is required for microcluster persistence and movement, and for contact stability. [A] Confirmation of the efficacy of SKAP55 knockdown and add-back in stable SKAP55 knockdown cells (JSKAP.SY) with or without transient reconstitution (n = 3). [B] J14.SY and JSKAP.SY cells expressing mRFP1 or SKAP55.mRFP1 were stimulated on coverslips and imaged for at least 5 min. Representative MOT images and kymographs are shown. Bars: (MOT images) 10 µm; (kymographs) 5 µm x 60 s. See Table 2 for microcluster properties and experiment numbers. [C] Composite microcluster traces for the conditions examined in B. Numbers in parentheses indicate the total number of cells examined. Line intensity corresponds to the fraction of microclusters surviving; arrowheads identify points of half-maximal microcluster dissociation. [D] Fraction of the contact area engaged in fluctuation (see Fig. S1, F and G; n = 3). [E] Fraction of cells scored as displaying unstable contacts (see Fig. S1, I and J; n = 3). [F] Surface expression of CD69 in J14.SY and JSKAP.SY cells, after normalization to a TCR-stimulated J14.SY control (n = 4). [G] Kinetics of Erk1/2 phosphorylation in J14.SY and JSKAP.SY stimulated for the indicated time points (n = 3). Error bars indicate mean ± SEM. From parental J14.SY cells (with or without mRFP1): **, P < 0.01. From JSKAP.SY (with or without mRFP1): ##, P < 0.01.

Table 2. Impact of SKAP55 mutants on SLP-76 microcluster dynamics in JSKAP.SY

<table>
<thead>
<tr>
<th>SKAP55 chimera</th>
<th>Persistence</th>
<th>μm</th>
<th>Inward movement</th>
<th>nm/s</th>
<th>Max speed</th>
<th>μm/s</th>
<th>% SLP-76 in clusters</th>
<th>μm</th>
<th>Clusters tracked per diameter</th>
<th>Total cells</th>
<th>n (experiments)</th>
</tr>
</thead>
<tbody>
<tr>
<td>mRFP1</td>
<td>103.9 ± 35.2</td>
<td>††</td>
<td>0.89 ± 0.13</td>
<td>††</td>
<td>84.04 ± 15.6</td>
<td>††</td>
<td>25.8 ± 6.8</td>
<td>††</td>
<td>11.7 ± 1.2</td>
<td>18</td>
<td>7</td>
</tr>
<tr>
<td>WT</td>
<td>235.3 ± 13.5</td>
<td>**</td>
<td>3.27 ± 0.47</td>
<td>**</td>
<td>131.1 ± 10.5</td>
<td>**</td>
<td>67.3 ± 2.9</td>
<td>**</td>
<td>15.4 ± 1</td>
<td>*</td>
<td>14</td>
</tr>
<tr>
<td>Hom</td>
<td>221.2 ± 14.8</td>
<td>**</td>
<td>3.29 ± 0.13</td>
<td>**</td>
<td>188.4 ± 25.9</td>
<td>**</td>
<td>73.7 ± 0.4</td>
<td>**</td>
<td>15.9 ± 0.57</td>
<td>*</td>
<td>10</td>
</tr>
<tr>
<td>ΔDM</td>
<td>111.3 ± 23.8</td>
<td>††</td>
<td>0.88 ± 0.09</td>
<td>††</td>
<td>74.6 ± 18.4</td>
<td>††</td>
<td>19.0 ± 7.2</td>
<td>††</td>
<td>4.8 ± 0.92</td>
<td>**, ††</td>
<td>9</td>
</tr>
<tr>
<td>TD</td>
<td>203.4 ± 20.9</td>
<td>††</td>
<td>2.95 ± 0.14</td>
<td>††</td>
<td>129.5 ± 12.6</td>
<td>**</td>
<td>65.1 ± 2.8</td>
<td>**</td>
<td>13.5 ± 1.3</td>
<td>10</td>
<td>3</td>
</tr>
</tbody>
</table>

SLP-76 microcluster dynamics in JSKAP.SY cells were measured as in Table 1. From JSKAP.SY cells expressing mRFP1: *, P < 0.05; **, P < 0.01. From JSKAP.SY with SKAP55.WT.mRFP1 add-back: †, P < 0.05; ††, P < 0.01.

for either the recruitment of SKAP55 to the plasma membrane or the entry into and stabilization of SLP-76 microclusters by SKAP55.

SKAP55 mediates the inside-out pathways that enable integrin-dependent adhesion after TCR ligation (Wang et al., 2003; Kliche et al., 2006). However the role of the SKAP55 PH domain in the transmission of these signals remains controversial (Kliche et al., 2006; Burbach et al., 2011). In the current study, the WT, ΔPH, 3YF, and R131M SKAP55 chimeras reconstituted TCR-induced adhesion to fibronectin (Fig. 4 H), confirming that neither the PH domain nor the linker tyrosines of SKAP55 are required for the activation of the predominant
fibronectin-binding integrins expressed on Jurkat T cells (α4β1/VLA-4 and α5β1/VLA-5; Seminario et al., 1998). Because the loss of SKAP55 destabilized the contacts formed in response to solo TCR ligation (Fig. 2), we also examined whether adhesion via the TCR was impaired in the absence of SKAP55 (Nguyen et al., 2008; Chapman et al., 2012). In fact, the loss of SKAP55 reduced TCR-dependent adhesion to the basal levels observed in the absence of immobilized stimulatory antibodies. Reconstitution with matched levels of shRNA-resistant wild-type, ΔPH, 3YF, and R131M chimeras significantly attenuated this defect (Figs. 4 I and S2 C). Thus, the cluster stabilizing and pro-adhesive functions of SKAP55 require the interaction with ADAP and an unidentified structural element N-terminal to the PH domain.

**SKAP55 homologue (SKAP-Hom) is functionally redundant with SKAP55 downstream of the TCR**

SKAP55 and SKAP-Hom possess similar domain structures (Fig. 5 A). Although SKAP-Hom is not expressed in Jurkat T cells, it has been observed in primary murine T cells (Marie-Cardine et al., 1998b; Jo et al., 2005). On this basis it has been suggested that SKAP-Hom cannot compensate for the loss of SKAP55 (Jo et al., 2005; Heng et al., 2008). However, when expressed in J14.SY cells, an mRFP1-tagged SKAP-Hom chimera entered and co-migrated with TCR-induced SLP-76 microclusters (Fig. 5, B and C). In addition, when expressed in JSKAP.SY cells, the SKAP-Hom chimera reconstituted normal microcluster dynamics and reduced the fraction of cells exhibiting unstable contacts (Fig. 5, D and E; Table 2; and Fig. S2 D). Furthermore, the SKAP-Hom chimera restored TCR-elicited adhesion to fibronectin and adhesion via the TCR itself. (Fig. 5, F and G; and Fig. S2 E).

Whereas our studies used SKAP55 and SKAP-Hom chimeras expressed at similar levels, the study that argued for the non-equivalence of these proteins did not evaluate their relative abundances. Our data suggest that SKAP-Hom only fails to compensate for the loss of SKAP55 in primary T cells because it is not expressed at sufficient levels (Marie-Cardine et al., 1998b; Heng et al., 2008).
The SKAP55 DM is required for recruitment to and stabilization of SLP-76 microclusters, and for adhesion to both TCR and integrin ligands

Because SKAP-Hom can substitute for SKAP55, the N-terminal DM observed in both proteins could contribute to microcluster stabilization and T cell adhesion. Secondary structure prediction and molecular modeling indicated that the DM motif of SKAP55 forms a homodimer, as in SKAP-Hom (Fig. S3, A–D; Swanson et al., 2008; Zhang, 2008; Roy et al., 2010). To test this, we created deletion mutants lacking the entire DM (ΔDM) or retaining only the DM motif (Fig. 6 A). Coimmunoprecipitations confirmed that the N-terminal DM motif of SKAP55 is both necessary and sufficient for dimer formation (Fig. 6 B). Finally, both SKAP55 and the isolated SKAP55 DM motif captured SKAP-Hom, which is consistent with the conservation of key hydrophobic residues within the dimerization interface (Fig. S3, A and E). Therefore, SKAP55 and SKAP-Hom are likely to form functional heterodimers if coexpressed in vivo.

Upon overexpression, the SKAP55 DM mutant remained cytoplasmic and weakly destabilized TCR-induced SLP-76 microclusters (Fig. 6, C–E; and Table 1). In contrast, the isolated SKAP55 DM motif potently antagonized microcluster dynamics (Fig. 6, C–E; Table 1; and Video 8). Furthermore, the isolated DM motif destabilized TCR-dependent contacts to a greater extent than the ΔDM chimera (Fig. 6 F). However, in the absence of endogenous SKAP55, an shRNA-resistant ΔDM chimera failed to restore microcluster dynamics (Fig. 6, C and E; Video 9; Table 2; and Fig. S2 F). Similarly, reconstitution with the ΔDM chimera failed to restore either TCR-induced adhesion to fibronectin or adhesion via the TCR (Fig. 6, G and H; and Fig. S2 G). Thus, the SKAP55 DM motif is required for the adhesive function of the TCR and for TCR-mediated increases in integrin adhesion. Thus, we hypothesized that the most potent dominant-negative SKAP55 chimeras, including the SH3 domain mutant (W333R) and the isolated DM motif destabilize SLP-76 microclusters by heterodimerizing with endogenous SKAP55 and preventing the multimerization of ADAP (Fig. 6 I).

A TD composed of linked SKAP55 SH3 domains stabilizes SLP-76 microclusters and promotes adhesion to TCR ligands, but not to integrin ligands

Because the SKAP55 DM motif could stabilize SLP-76 microclusters by dimerizing ADAP and increasing overall microcluster avidity or by recruiting additional effector proteins, we generated an artificial TD consisting of two SKAP55 SH3 domains linked by a 3YF linker region (Fig. 7 A). Unlike the isolated SH3 domain (Fig. 3), this chimera entered SLP-76 microclusters and had no significant impact on SLP-76 microcluster dynamics upon overexpression in J14.SY cells (Fig. 7, C and D; and Table 1). Although the TD weakly destabilized TCR-initiated contacts upon overexpression in J14.SY cells, this effect was not significant (Fig. 7 E). In reconstitution studies, the hairpin-resistant TD restored optimal SLP-76 microcluster dynamics (Fig. 7, C and D; Video 10; Table 2; and Fig. S2 H). Remarkably, reconstitution with the TD increased the stability of TCR-induced contacts and promoted adhesion via the TCR nearly as well as wild-type SKAP55, but could not support TCR-mediated increases in adhesion to the αβ, αβγ, and αβδ integrin ligand fibronectin (Fig. 7, E–G; and Fig. S2 G; Shimizu et al., 1990; Arroyo et al., 1992; Springer, 1994; Seminario et al., 1998). Thus, the dimerization of the SKAP55 SH3 domain is sufficient to support microcluster stability and adhesion via the TCR, whereas the DM motif plays a distinct and critical role in the regulation of adhesion via β integrins (Fig. 7 G).

The DM motif is required for the interaction of SKAP55 with the integrin-activating molecule RIAM and for the recruitment of talin into TCR-induced adhesive junctions

The SKAP55 DM motif regulates LFA-1 affinity via a complex incorporating RapL, macrophage stimulating 1 (Mst1), and Rap1 (Raab et al., 2010). As expected, RapL coimmunoprecipitated with full-length SKAP55 and was not captured with the ΔDM chimera (Fig. 8 A). However, this complex acts via the αL subunit, and cannot explain the ability of SKAP55 to facilitate adhesion to fibronectin. We found that SKAP55 also requires its DM motif to capture RIAM, a Rap1-dependent adaptor molecule that interacts with talin to facilitate integrin activation via a motif present in all integrin β chains (Fig. 8 A; Han et al., 2006; Ménasché et al., 2007; Watanabe et al., 2008; Lee et al., 2009). None of these integrin-activating proteins coimmunoprecipitated with the SKAP55 TD (Fig. 8 B).

In J14.SY cells stimulated through the TCR, endogenous talin entered distinct structures found alongside peripheral SLP-76 microclusters, but also accumulated in the center of the contact, where it overlapped with a centralized pool of SLP-76 microclusters (Fig. 8 C and Fig. S4 A). In JSKAP54 cells, talin clusters were more uniformly distributed, and the accumulation of talin in the center of the contact was reduced significantly (Fig. 8, C and E; and Fig. S4 B). These defects in talin localization were eliminated upon reconstitution with wild-type SKAP55, but not with the TD (Fig. 8, D and E; and Fig. S4, C and D). Because SKAP55 regulates T cell adhesion via the TCR (Figs. 4–7), we postulated that SKAP55 regulates the integrity of the adhesive junctions formed by the TCR itself. These junctions are subdomains within the plasma membrane that form intimate contacts with the underlying substrate and are substantially resistant to extraction via mechanical disruption (Harder and Kuhn, 2000; Bunnell et al., 2001, 2002). To examine whether SLP-76 and talin are retained within these junctions, we sheared away the bodies of cells fixed after stimulation on immobilized TCR ligands. The central accumulations of SLP-76 and talin observed in J14.SY cells were eliminated by this procedure, which indicates that this pool is not in intimate contact with the substrate. Nevertheless, SLP-76 and talin were retained in adherent complexes in the contact periphery and partially overlapped with one another.
Figure 4. The SKAP55 PH domain and linker tyrosines are dispensable for recruitment into and stabilization of SLP-76 microclusters, and for T cell adhesion. (A) Domain structures of the ΔPH, 3YF, R131M, and PH-alone SKAP55 chimeras. (B) J14.SY cells were transiently transfected with the indicated SKAP55.mRFP1 chimeras; expression levels were determined by Western blotting (n = 3). (C) Cells from B were stimulated, imaged, and presented as in
SKAP-Hom heterodimerizes with and is functionally redundant with SKAP55. (A) Domain structures of the SKAP55 and SKAP-Hom chimeras. (B) Cells were lysed and Western blotted to determine relative expression of the SKAP55 (WT) and SKAP-Hom (Hom) chimeras (n = 3). (C) J14.SY and JSKAP.SY cells transiently expressing mRFP1 or SKAP-Hom.mRFP1 were stimulated, imaged, and presented as in Fig. 2 B. See Tables 1 and 2 for microcluster properties and experiment numbers. Bars: (MOT and conventional images) 10 µm; (kymographs) 5 µm × 60 s. (D) Composite microcluster traces for the conditions examined in C; numbers in parentheses indicate the total number of cells examined. Line intensity corresponds to the fraction of microclusters surviving; arrowheads identify points of half-maximal microcluster dissociation. (E) Fraction of cells scored as displaying unstable contacts (n = 3). (F and G) Fractional retention on fibronectin-coated or anti-CD3-coated coverslips, as described in Fig. 4 (n = 3). Error bars indicate mean ± SEM. From parental J14.SY cells (with or without mRFP1): *, P < 0.05. From JSKAP.SY (with or without mRFP1): #, P < 0.05; ##, P < 0.01.
Figure 6. The SKAP55 DM is required for microcluster entry, microcluster stabilization, and the pro-adhesive functions of SKAP55. (A) Domain structures of the ΔDM and DM alone SKAP55 chimeras. (B) Differentially tagged SKAP55 (S1) and SKAP-Hom (S2) chimeras were coexpressed in E6.1 Jurkat cells. Immunoprecipitations were performed with anti-YFP antibody. Total lysates and immunoprecipitates were blotted with anti-YFP or anti-Flag (n = 4). (C) J14.SY
Figure 7. An artificial SKAP55 TD is sufficient for recruitment to and stabilization of SLP-76 microclusters, and for adhesion to TCR but not integrin ligands. (A) Domain structure of the SKAP55 TD chimera. (B) J14.SY cells were transiently transfected with WT and TD chimeras and blotted to confirm comparable expression levels (n = 3). (C) J14.SY and JSKAP.SY cells expressing the TD chimera were stimulated, imaged, and presented as in Fig. 2 B. See Tables 1 and 2 for microcluster properties and experiment numbers. Bars: (conventional images) 10 µm; (kymographs) 5 µm × 60 s. (D) Composite microcluster traces for the conditions examined in C; numbers in parentheses indicate the total number of cells examined. Line intensity corresponds to the fraction of microclusters surviving; arrowheads identify points of half-maximal microcluster dissociation. (E) Fraction of cells scored as displaying unstable contacts (n = 6). (F and G) Fractional retention on anti-CD3–coated or fibronectin-coated coverslips, as described in Fig. 4 (n = 3). Error bars indicate mean ± SEM. From parental J14.SY cells (with or without mRFP1): *, P < 0.05; **, P < 0.01. From JSKAP.SY (with or without mRFP1): #, P < 0.05. From JSKAP.SY with SKAP55.WT.mRFP1 add-back: †, P < 0.05.

However, SLP-76, but not talin, was retained within the adhesive junctions formed by JSKAP.SY cells. Upon reconstitution with wild-type SKAP55, but not with the TD, the retention of talin at sites adjacent to SLP-76 microclusters was restored (Fig. 8 G). These data suggest that the SKAP55 DM motif governs the recruitment of talin into TCR-dependent adhesive junctions and the recruitment of talin into a central pool that is not tethered to the stimulatory substrate.
Figure 8. The SKAP55 DM is required for binding to RapL and RIAM, and governs the recruitment of talin into TCR-induced contacts. (A and B) 3xFlag-TRT-tagged SKAP55 wild-type (WT), DM deleted (ΔDM), and TD chimeras were expressed in J14.SY cells and immunoprecipitated via the Flag epitope. Blots of total lysates and immunoprecipitates are shown (n = 3). (C and D) Images of SLP-76.YFP (blue) and endogenous talin immunofluorescence.
SKAP55 governs the distribution of SLP-76 and talin microclusters within TCR-induced contacts, but does not alter the distribution of β₁ integrins

Talin interacts with the cytoplasmic tails of integrin β-chains and promotes the conversion of integrins into high-affinity states; therefore, SKAP55 and talin might be expected to control the localization of β₁ integrins. Nevertheless, immunofluorescent stains revealed that β₁ integrin clusters were distributed throughout the contact, whether SKAP55 was present or not (Fig. 9, A–C). In contrast, the loss of SKAP55 reduced the central clustering of talin and SLP-76, and increased the appearance of these proteins at the edge of the contact (Fig. 9, A, C, and D). Remarkably, the distributions of β₁ integrin, talin, and SLP-76 were substantially exclusive of one another, with overlap primarily occurring at the margins of adjacent structures (Fig. 9, B–D). Because similar mutually exclusive arrangements have been observed for microclusters whose components clearly interact with one another (e.g., ZAP-70 and SLP-76 microclusters), these structures may represent distinct functional modules that interact with one another at their boundaries (Nguyen et al., 2008; Sherman et al., 2011).

To identify regions of potential interaction among adjacent structures, we used an automated thresholding algorithm to identify SLP-76, talin, and β₁ microclusters. Regions of pairwise “adjacency” (see Materials and methods) were pseudocolored yellow (SLP-76 near talin), magenta (talin near β₁), or cyan (β₁ near SLP-76), merged, and labeled to indicate the boundary of the contact (Fig. 9, B and C). Microcluster enrichments in the edge of the contact, the center of the contact, and the intervening “middle” region were calculated by normalizing cluster density in the region of interest by the corresponding cluster density in the entire contact (Fig. 9 D). Similarly, we calculated the fraction of each domain engaged in adjacency (Fig. 9 E). In J14.SY cells, regions of adjacency between SLP-76 and talin (yellow) were predominantly found in the center of the contact, with the remainder found in the middle region, rather than the edge of the contact. In contrast, adjacency between β₁ integrin and talin (magenta) was more evenly distributed between the middle region and the center of the contact. In the absence of SKAP55, these distributions were significantly altered, such that the regions of adjacency between SLP-76 and talin and between β₁ integrin and talin shifted toward the outer margin of the contact.

Discussion

The mechanisms by which SKAP-family adaptors are integrated into receptor proximal signaling networks are not yet well understood. Here, we show that SKAP55 is recruited into SLP-76 microclusters via ADAP, and is retained within the TCR-induced junctions that anchor T cells to stimulatory substrates. In addition, SKAP55 regulates the persistence and movement of SLP-76 microclusters, stabilizes the boundaries of TCR-induced contacts, and facilitates T cell adhesion via the TCR and via β₁ integrins. Although microcluster persistence is commonly associated with efficient T cell activation, SKAP55 was not required for TCR-dependent increases in CD69 expression or Erk activation, establishing that these outputs do not require the formation of persistent microclusters. These data require a re-evaluation of prior observations that linked microcluster persistence to the efficacy of TCR-induced Erk activation and CD69 up-regulation, and suggest that these defects were caused by the impaired recruitment or function of key effector molecules, rather than a nonspecific reduction in the cohesion of SLP-76 microclusters (Bunnell et al., 2006; Sylvain et al., 2011).

We also show that the SKAP55 PH domain and the predominant tyrosine phosphorylation sites in SKAP55 are not required for normal SLP-76 microcluster dynamics, for adhesion via the TCR, or for adhesion via β₁ integrins. Instead, these functions all require an N-terminal dimerization (DM) motif similar to that observed in SKAP-Hom (Swanson et al., 2008). The DM motifs of SKAP55 and SKAP-Hom form both homotypic and heterotypic dimers; further, contrary to prior studies, our data indicate that SKAP-Hom is functionally redundant with SKAP55 in T cells (Jo et al., 2005). Finally, we show that the DM motif influences T cell adhesion via two distinct mechanisms, involving either the oligomerization of microcluster components and the generation of adhesive junctions by the TCR, or the coupling of the DM motif to effector proteins responsible for the activation of β₁ integrins.

Based on the data presented in Figs. 3–7, we conclude that overexpressed SKAP55 mutants reduce microcluster persistence and movement to the extent that they prevent the dimerization of endogenous SKAP55 SH3 domain ligands. Consistent with this hypothesis, SKAP55 mutants do not restore normal microcluster dynamics unless capable of dimerizing endogenous ADAP (Fig. S5 A). According to this model, the dominant-negative impacts of the monovalent SKAP55 SH3 domain and the SKAP55 ΔDM mutant result from the sequestration of SH3 domain ligands from endogenous SKAP55, whereas the potent dominant-negative impacts of the full-length SKAP55 SH3 mutant and the isolated DM motif reflect their ability to perturb endogenous SKAP55 dimers (Figs. 6 I and S5 B).

The SKAP55 TD supports microcluster persistence, microcluster movement, the stabilization of TCR-induced contacts, and adhesion via the TCR. However, it does not
Figure 9. SKAP55 is dispensable for \( \beta_1 \) integrin clustering downstream of TCR ligation. (A) J14.SY and JSKAP.SY cells were stimulated on anti-CD3–coated plates and fixed after 10 min. Immunofluorescent images of endogenous \( \beta_1 \) integrin (blue) and endogenous talin (red), and direct images of SLP-76.YFP (green) are shown in greyscale and as a pseudocolored merged image \((n = 3)\). (B and C) Higher-resolution merged images of representative J14.SY (B, left) or JSKAP.SY (C, left) cells prepared as in A. SLP-76, talin, and \( \beta_1 \) integrin microclusters were identified algorithmically and used to derive regions of adjacency \((n = 3)\). The pseudocoloring scheme is indicated on the right. \((n = 3)\). Bars, 10 \( \mu \)m. (D) Enrichment of talin, SLP-76, and \( \beta_1 \) clustered areas in distinct domains of the contact \( \text{(edge, middle, and center)} \), relative to the entire contact. For D and E, data are shown \( \pm \)SD \((\text{error bars})\) for six cells acquired in three independent experiments. From parental J14.SY cells \((\text{with or without mRFP1})\): °, \( P < 0.10 \); *, \( P < 0.05 \); **, \( P < 0.01 \). (F) Diagram showing the binding sites of the fluorescent probes used in A–E.
support integrin activation downstream of the TCR, and does not interact with regulators of integrin activation, such as RIAM, talin, RapL, and Mst1. Thus, the integrin-activating ability of SKAP55 represents a distinct functional module that can be ablated without impacting the dynamics of SLP-76 microclusters. In contrast, we were unable to identify mutations that decouple the persistence and movement of SLP-76 microclusters from contact stabilization and adhesion via the TCR.

SKAP55 participates in the regulation of integrin affinity through distinct Rap1-containing complexes: one incorporates RapL and acts on αL integrins, the other incorporates RIAM and talin and acts through integrin β chains (Ménasché et al., 2007; Raab et al., 2010; Kliche et al., 2012). Our data demonstrate that the DM motif of SKAP55 is required for the association of RIAM and talin with SKAP55, for TCR-induced adhesion via β1 integrins, for the retention of talin in adhesive junctions adjacent to SLP-76 microclusters, and for the localization of talin and SLP-76 in nonadherent centralized microclusters (Fig. 10 B). In the absence of SKAP55, integrin-mediated adhesion is impaired, talin is eliminated from TCR-induced junctions, and the central clusters of talin and SLP-76 are lost. Finally, talin and SLP-76 redistribute to the outermost edge of the contact in the absence of SKAP55.

SLP-76, talin, and β1 integrins participate in interconnected complexes. Nevertheless, these structures were distinguishable and adjacent from one another. This pattern is consistent with the sizes of the complexes involved, assuming their constituents adopt extended conformations, as diagrammed in Fig. 9 F (Shaw, 2006; Kanchanawong et al., 2010; Margadant et al., 2011). However, triple adjacency was rarely observed, which suggests that complexes bridging SLP-76 to β1 integrins are not maintained for long periods of time. Instead, we suggest that SLP-76 and talin are initially recruited to the outermost edges of TCR-induced contacts through SKAP55-independent interactions with Abi/WAVE complexes (Zipfel et al., 2006; Nolz et al., 2007). Subsequently, we expect talin to interact with SLP-76 in a SKAP55- and Rap1-dependent manner, giving rise to activated clusters of β1 integrins in the regions lagging the edge of the contact (Fig. 10 B). Finally, we expect vinculin to displace SKAP55 and SLP-76 from fully activated integrins, whereas nonengaged SLP-76 and talin complexes are extracted from the cell surface and transported to the center of the contact (Fig. 10 C; Lee et al., 2013).

In contrast to the DM motif, the PH domain of SKAP55 proved dispensable for the persistence and movement of SLP-76 microclusters, for the stabilization of TCR-induced contacts, and for adhesion via both the TCR and β1 integrins (Fig. S5 C). In addition, SKAP55 was not recruited to the plasma membranes of TCR-stimulated Jurkat T cells, despite constitutively high levels of phosphatidylinositol-3,4,5-trisphosphate in these cells, as confirmed through the use of the PH domain of Akt as a positive control (Seminario et al., 2004). Our data are consistent with prior studies in Jurkat T cells, which also failed to identify a role for the PH domain of SKAP55 in TCR-induced adhesion to integrin ligands (Kliche et al., 2006). Although several studies have reported the recruitment of SKAP55 into an insoluble membrane fraction in Jurkat cells, SKAP55 may, in fact, be rendered insoluble through interactions with large signaling complexes, or through interactions with insoluble actin polymers (Ménasché et al., 2007; Burbach et al., 2008, 2011; Raab et al., 2011). Nevertheless, our observations appear to be at odds with the roles of the SKAP55 PH domain in synaptic localization and integrin activation in primary murine T cells (Burbach et al., 2011). Because the isolated SKAP55 PH domain appears to be incapable of binding the plasma membrane, we propose that this domain normally engages lipids only once SKAP55 has been recruited into microclusters via ADAP, whereupon lipid recognition by the PH domain promotes the conversion of SKAP55 into a “open” conformation that liberates the DM motif to engage integrin-activating ligands (Fig. S5 D). Whatever the source of these differences, our data indicate that the PH domain is not an integral component of the systems that activate integrins in response to TCR ligation, but may instead regulate these functions in primary T cells.

Our data suggest SKAP55 regulates microcluster dynamics, contact stability, and TCR adhesion by multimerizing ADAP, SLP-76, Gads, and LAT into higher-order complexes that couple TCR-induced microclusters to the pro-adhesive and force-generating systems of the actin cytoskeleton (Fig. 10, A and B). In their incorporation of tyrosine kinase-dependent scaffolds that impact the organization of the cytoskeleton, SLP-76 microclusters resemble focal adhesions and podosomes (Burgstaller and Gimona, 2004; Johansson et al., 2004; Evans and MatsudaIRA, 2006; Gomez et al., 2006; Block et al., 2008; Gimona et al., 2008; Ha et al., 2008; Machesky et al., 2008; Oikawa et al., 2008; Ori et al., 2008; Albige-Rizo et al., 2009; Carrizosa et al., 2009; Oikawa and Takenawa, 2009; Sage et al., 2012). Based on these similarities and on the coupling of SLP-76 microclusters to the actin cytoskeleton, the orientation of actin filaments above SLP-76 microclusters, the association of SLP-76 microclusters with adhesive structures, and the adjacency of SLP-76 microclusters to integrins, we propose that SLP-76 microclusters function as lymphocyte-specific podosomes (Bunnell et al., 2001, 2002; Nguyen et al., 2008; Bunnell, 2010; van den Dries et al., 2013). In this manner, SLP-76 microclusters may couple integrin-mediated adhesions to local actin polymerization, generating both the “downwardly directed” forces required to overcome glycosalix repulsion and the lateral shear forces required for efficient TCR mechanotransduction (Seminarin and Bunnell, 2008; Martínez-Martín et al., 2011; Wang and Reinherz, 2012).

Materials and methods

Cell lines and transfections

Jurkat T cells were maintained in RPMI-1640 (BioWhittaker) supplemented with 10% FBS, 20 mM glutamine, and 10 µg/ml ciprofloxacin. SLP-76-deficient Jurkat cells (J14 cells) were a gift of A. Weiss (University of California, San Francisco, San Francisco, CA). ADAP-deficient Jurkat cells (JADAP cells) were a gift of R. Wong (National Institutes of Health, Bethesda, MD). J14 cells stably reconstituted with SLP-76·YFP (J14.SY cells)
Figure 10. Distinct roles of SKAP55 domains in microcluster stabilization, adhesion via the TCR, and integrin regulation. (A) SKAP55-dependent multimers enable microcluster stabilization and movement, and are required for adhesion via the TCR and via integrins. Microcluster persistence requires interactions capable of joining LAT, Gads, SLP-76, and ADAP into a minimal signaling complex. Constituents of stable microclusters (e.g., ADAP), may interact directly...
have been described previously (Bunnell et al., 2006). J14.5 SY cells lacking SKAP55 (JSKAP55 SY cells) were generated by lentiviral transduction and selection in puromycin. J14.5 SY and JSKAP55 SY lines stably expressing SKAP55 chimeras tagged with a red fluorescent protein were created by lentiviral transduction and sorting for double-positive cells with matched brightness via flow cytometry. Transient transfections were performed as described previously (Bunnell et al., 2006). Human 293T renal epithelial cells were cultured in DMEM containing 10% FBS, 20 mM glutamine, 100 U/ml penicillin, and 100 U/ml streptomycin.

**Lentivirus production and lentiviral transduction**

24 h before transfection, 293T cells were replated so that on the day of transfection they were ~65–75% confluent. For each 10-cm plate, 18 µl of FuGENE 6 reagent (Roche) was added to 500 µl of serum-free DMEM for 5 min. Concurrently, 6 µg of the lentiviral expression and/or knockdown vectors was combined with 1.5 µg of the packaging plasmid psPAX2 and 0.5 µg of the pMD2.G in 40 µl of serum-free DMEM. These mixes were combined and incubated for 30 min at room temperature, and were added to 293T cells in a dropwise fashion. After 12–15 h, the transfection cocktail was replaced with fresh media, and the lentiviral supernatants were collected 66–72 h after transfection. Jurkat cells were transduced by combining equal parts rapidly dividing Jurkat cells, fresh lentiviral supernatants, and complete RPMI. For fluorescence microscopy, the efficiency of transduction was assessed in fixed cells after 48 h, and was typically 50–90%.

**SKAP55 cloning and mutagenesis**

Vectors encoding mRFP1 and TRT were obtained from R. Tsien (University of California, Davis, CA) and subcloned into “n1-type” vectors (Takara Bio Inc.) by PCR. Where specified, sequences encoding triple FLAG epitope tags (3xFlag) were subcloned 3’ to the encoded fluorescent protein. The mRFP1-n1 vector containing the monomerizing A206K mutation was modified by the addition of a triple Myc epitope tag (3xMyc) 5’ of the fluorescent protein via overlap extension PCR. Unless otherwise noted, SKAP55 and associated mutants were created by overlap extension PCR and subcloned into the mRFP1-n1 or 3xFlag-TRT-n1 vectors at the XhoI and AgeI sites. Associated mutants were created by overlap extension PCR and subcloned into the mRFP1-n1 or 3xFlag-TRT-n1 vectors at the XhoI and AgeI sites. Point mutations in the SKAP55 linker region between the PH and SH3 domains were generated by QuikChange PCR mutagenesis using the indicated primers: W333R with NS727/NS728; 3YF in a...
BCECF retention was determined. For adhesion to fibronectin, plates were treated with 0.01% poly-lysine, left uncoated or coated with 10 µg/ml fibronectin (Gibco), and blocked with 1% BSA for 1 h at 37°C. Before plating, labeled cells in 1x HBSS were left unstimulated, stimulated for 30 min with 2 µg/ml OKT3 (anti-CD3ε, BioExpress), or stimulated for 30 min with 50 ng/ml PMA. After 30 min on plates, fractional retention was determined and normalized to the PMA control. For adhesion via the TCR, unstimulated cells were plated in wells treated with 0.01% poly-lysine, left uncoated or coated with 10 µg/ml OKT3, and blocked with 1% BSA. Fractional retention was determined after a 7-min incubation in complete media (Nguyen et al., 2008; Chapman et al., 2012). Standard deviations, standard errors, and statistical significances were calculated with Excel, using a two-tailed Student’s t test for unpaired samples with similar variances.

Bioinformatics and structural modeling

The secondary structures of the SKAP55 and SKAP-Hom DM motifs were predicted using the prediction server at www.predictprotein.org (Rost and Sander, 1993, 1994; Rost, 1996). The sequences of the DM motifs of SKAP55 and SKAP-Hom across vertebrate species were aligned using the constraint-based multiple protein alignment tool COBALTI (Papadopoulos and Agapitou, 2007). The structure of the SKAP55 DM-H module (spanning M1-S213) was predicted using the I-Tasser threading server, with the existing SKAP-Hom DM-PH structure as a constraint (2OTX, chain A; Swanson et al., 2008; Zhang, 2008; Roy et al., 2010, 2012). Of five models obtained, four preserved the overall topology of the SKAP-Hom DM-PH module, and possessed C-scores ranging from ~1.10 to ~2.36. The best model is unlikely to be valid, as it perturbed highly conserved elements within the PH domain; reflecting this, the C-score for this model was very low (~4.54). All molecular views were generated using Swiss-PdbViewer (http://spdbv.vital-it.ch/); Gueck and Peitsch, 1997).

Online supplemental material

Video 1 depicts the recruitment of SKAP55.3xFlag.TRT (red) into SLP-76 microclusters upon TCR ligation. SLP-76 microcluster dynamics and boundary fluctuation in SKAP55 knockdown J14.SY (Fig. S1) in addition to methodology with the distinction of subdomains to how half of SLP-76 microclusters are defined as structures with brightness 4× greater than the cellular background, and clustered SLP-76 was calculated as the total background-subtracted intensity within the clustered area divided by the total background-subtracted intensity within the cell. The means and statistical tests shown in all figures and tables (except for Fig. 9, D and E) were calculated by compiling the means of independent experiments, each of which incorporated multiple cells. The total number of cells examined across all experiments are shown for Tables 1 and 2, all composite kymographs, and for Fig. 8 E. All data are shown as means ± SEM unless otherwise indicated. For analyses of microcluster position within the contact and for microcluster adjacency analyses, microcluster masks were developed using a segmentation algorithm sensitive to local intensity maxima. Regions of adjacency were identified by dilating the SLP-76 and talin masks by ~300 nm and defining the intersections of dilated and undilated masks as regions of adjacency. Cell boundary masks were developed using an algorithm that acts on the sum of all channels. Distinct subdomains of the contact were defined by iteratively eroding the cell boundary mask until fixed fractions of the contact area remain (“edge,” outermost 25% of the contact area; “center,” innermost 25%; “middle,” the intervening 50%). The fractions of each domain occupied by microclusters or regions of adjacency were determined, and relative enrichments were calculated by normalizing to the fraction of the entire contact occupied by the corresponding mask.

Statistical analyses

All data are presented as means ± SEM unless otherwise noted. The number of experiments is indicated in all cases unless otherwise noted. Please note that for all quantified imaging experiments the numbers of experiments and cells are presented in Tables 1 and 2. Statistical significances were calculated in Excel using a two-tailed Student’s t test for unpaired samples with similar variances.

Plate bound adhesion assays

Jurkat cells were labeled with 4 µM 2’7’-bis-(2-carboxylethyl), 5(6) carboxyfluorescein (BCECF-AM; Molecular Probes) in 1x PBS (no calcium or magnesium) for 15 min at 37°C. Labeled cells were plated at a density of 2.5 x 10^4 cells per well in 96-well glass-bottom plates. After the cells settled for the indicated times, BCECF fluorescence was read on a SpectraMax plate reader (488 ex/530 em, 515 nm cutoff). Nonadherent cells were removed by gentle pipetting in prewarmed 1x HBSS, and
References


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**Figure S1. SKAP55 stabilizes TCR-induced contacts.**

(A) Confirmation of T cell activation on stimulatory substrates. Lysates were prepared after allowing J14.SY cells to settle on anti-CD3-coated glass coverslips for the indicated time points. Lysates were blotted for phospho-Erk1/2, total Erk1/2, and γ-tubulin. (B, left) Lysates from Jurkat E6.1 cells and JDAP cells were blotted for SKAP55, ADAP, and Erk1/2. (B, right) Lysates from JDAP cells transfected with SKAP55.mRFP1 and either a 3×Flag.TRT control or 3×Flag.TRT.ADAP-120 were blotted for ADAP, SKAP55, and γ-tubulin. (C) Confirmation SKAP55 knockdown in transiently transfected and sorted cells (n = 3). J14.SY cells were transiently transfected with vectors encoding mRFP1 with or without a SKAP55-specific shRNA. Cells were sorted for mRFP1 and blotted for SKAP55 and γ-tubulin. (D) Cells from C were stimulated on coverslips and imaged for at least 5 min. MOT images and kymographs are shown. (E) Composite microcluster traces are shown; numbers in parentheses indicate the total number of cells examined. Line intensity corresponds to the fraction of microclusters surviving. Arrowheads indicate the point of half-maximal microcluster dissociation. (F) Boundary fluctuation was tracked over a 30-s running window; cells shown are from the cells above in D. For D and E, n = 3 experiments, with at least 10 cells total per condition. See Table 1 for the number of experiments and the total number of cells examined in D and E. (G) Running mean of the fraction of the contact area engaged in fluctuation (red and blue), normalized by the current area (red and gray). (H) The rate of boundary growth and retraction along the perimeter of the contact over time. (I) Scoring criteria for contact stability. Representative examples of “stable” and “unstable” contacts were drawn from J14.SY cells transiently transfected with vectors expressing an mRFP1 marker with or without a SKAP55-specific shRNA, as in C. Cell boundaries are outlined in white. Boundaries that underwent repeated cycles of rapid extension and retraction were scored as “unstable,” whereas boundaries that had minimal change in area over time were scored as “stable.” Examples of “stable” contacts were drawn from mRFP1 J14.SY cells transfected with a vector expressing the mRFP1 marker alone. Examples of “unstable” contacts were drawn from mRFP1 J14.SY cells transfected with a vector expressing mRFP1 and the SKAP55-targeting hairpin. (J) Fraction of cells scored as displaying unstable contacts. n = 4 experiments, 20 cells total per condition. Bars: (D, MOT images; and F): 10 µm; (D, kymographs; and I) 5 µm × 60 s. From parental J14.SY cells (with or without mRFP1): ***, P < 0.001. Error bars indicate mean ± SEM.
Figure S2. Relative expression levels of endogenous SKAP55 and exogenous SKAP55 chimeras in imaging and functional assays. Lysates were prepared from parental J14.SY cells and transiently transfected (A, D, F, and H) or stably transduced (C, E, and G) JSKAP.SY cells. SKAP55 expression levels were determined by Western blotting for SKAP55 (rat monoclonal; gift from S. Kliche and B. Schraven). Because this antibody is specific for the SKAP55 DM domain, the levels of the mRFP1 or 3×Flag.TRT-tagged SKAP-Hom (D and E), ΔDM (F and G), and TD (G and H) chimeras were determined by comparison to wild-type SKAP55 tagged with mRFP1 (mRFP1 blots) or with 3×Flag.TRT (Flag blots). One of at least three representative blots for each experiment are depicted; the primary figures to which these blots apply are indicated below each panel. Total protein loading was monitored by blotting for γ-tubulin.

B) J14.SY expressing the solo SKAP55 PH domain were imaged at (top) and 4 µm above (bottom) the coverslip to assess localization. Bars, 10 µm. (C) Although all exposures are taken from the same membrane, endogenous SKAP55 is separated from the rest of the blot with a thin white line as it represents a longer exposure than adjacent lanes.
**Figure S3.** Structural modeling predicts a phosphoinositide-dependent conformational switch in the DM-PH module of SKAP55. (A) Secondary structure predictions for the N termini of Homo sapiens SKAP55 (SKAP1) and SKAP-Hom (SKAP2). PROF_sec predicts secondary structure (H for α helix, L for loop); PHD_acc whether sidechains are buried (B) or exposed (e); and Rel_sec and Rel_acc the reliabilities of these predictions (most reliable, 9). Diagrams mark the α helices observed in the SKAP-Hom DM-PH structure, or in the predicted models of SKAP55. Amino acids are colored based on the properties of their side chains. In general polar and charged amino acids are shown in brighter colors (red, green, magenta), whereas hydrophobic and aromatic residues are shown in duller shades (black, dark blue, purple). Large aliphatic amino acids (leucine, isoleucine, valine) and methionine are shown in black. Proline is shown in dark purple. Nonpolar, weakly hydrophobic amino acids are shown in paler shades (alanine in dark yellow, glycine in light purple). Aromatic amino acids are shown in shades of blue or brown. Tryptophan and phenylalanine are shown in dark blue, while tyrosine and histidine are shown in cyan and brown, respectively. The small alcohol- and thiol-bearing amino acids are shown in orange (serine, threonine) and in teal (cysteine). Positively charged amino acids (arginine, lysine) are shown in bright green. Negatively charged amino acids (aspartate, glutamate) are shown in red. The polar derivatives of aspartate and glutamate (asparagine, glutamine) are shown in magenta. (B and C) Models of the N terminus of SKAP55 were generated using the I-Tasser threading server, using the existing SKAP-Hom DM-PH structure as a constraint. The four highest quality models yielded tertiary and quaternary structures comparable to those observed in SKAP-Hom. Amino acids are colored based on the properties of their side chains. In general polar and charged amino acids are shown in brighter colors (red, green, magenta), whereas hydrophobic and aromatic residues are shown in duller shades (black, dark blue, purple). Large aliphatic amino acids (leucine, isoleucine, valine) and methionine are shown in black. Proline is shown in dark purple. Nonpolar, weakly hydrophobic amino acids are shown in paler shades (alanine in dark yellow, glycine in light purple). Aromatic amino acids are shown in shades of blue or brown. Tryptophan and phenylalanine are shown in dark blue, while tyrosine and histidine are shown in cyan and brown, respectively. The small alcohol- and thiol-bearing amino acids are shown in orange (serine, threonine) and in teal (cysteine). Positively charged amino acids (arginine, lysine) are shown in bright green. Negatively charged amino acids (aspartate, glutamate) are shown in red. The polar derivatives of aspartate and glutamate (asparagine, glutamine) are shown in magenta. (D) The conformations adopted by the DM-PH linker regions in our top-scoring model are shown in red. (E) The structures of isolated PH domains of SKAP55 (PDB accession no. 1U5D: chain D), SKAP-Hom (PDB accession no. 1U5G: chain C), and the inositol-1,3,4,5-tetrakisphosphate (IP4)-bound PH domain of DAPP1 (PDB accession no. 1FAO: chain A) were fit to our top scoring model of the SKAP55 DM-PH module (gray), and colored by RMS as in B. Although the core of the PH domain is highly conserved, major differences are apparent within the loops that contact the DM motif (magenta arrows). All of the isolated PH domains display major deviations within the IP4 (magenta) contacting loop at the top left. (E) Constraint-based sequence alignments were generated for SKAP55 (SKAP1) and SKAP-Hom (SKAP2) from the indicated vertebrate species using the COBALT webserver at the National Center for Biotechnology Information. Gray boxes highlight the buried residues of the hydrophobic core, as predicted in A. Amino acids are labeled by side chain properties, as in A.
Figure S4. The SKAP55 DM motif is required for the recruitment of talin into TCR-induced SLP-76 microclusters. The intensities of SLP-76.YFP, endogenous talin, and the indicated SKAP55.TRT chimeras along linear regions of interest spanning the centers of cells (see insets) were plotted in arbitrary intensity units. Representative plots from J14.SY cells (A), JSKAP.SY cells (B), JSKAP.SY cells reconstituted with wild-type SKAP55.TRT (WT; C), and JSKAP.SY reconstituted with the SKAP55 TD (D) are shown. Line scans are representative of at least eight cells per condition over three independent experiments. Bars, 10 µm.
Figure S5. **Proposed conformational and multimeric states for various SKAP55 mutants.** (A) Based on our imaging studies, our structural modeling, and the SKAP-Hom crystal structure, we expect unphosphorylated SKAP55 to remain cytoplasmic in resting cells, and to form a closed dimer in which the phosphoinositide binding site within the PH domain is occluded by the C-terminal helix of the DM motif and the inter-DM-PH linker. We also expect that a key phosphoinositide binding loop is further deformed by packing against the adjacent DM motif. (B) All microcluster-destabilizing SKAP55 mutants lack the ability to dimerize ADAP, and the most potent dominant-negative forms of SKAP55 have the capacity to disrupt endogenous SKAP55 homodimers. (C) The SKAP55 ΔPH mutant and the SKAP55 TD both enter microclusters, have the capacity to multimerize ADAP, and stabilize microclusters, demonstrating that the lipid binding capacity of the SKAP55 PH domain is dispensable for these functions. (D) Based on the observations above, we expect that SKAP55 is recruited to the plasma membrane via its SH3 domain, which couples SKAP55 to microclusters containing ADAP and to SLP-76. Once present at the plasma membrane, tyrosine phosphorylation and/or high local phosphoinositide concentrations may drive SKAP55 into an open conformation that reveals the DM motif. Domains are abbreviated as follows: DM, dimerization motif; PH, pleckstrin homology; SH3, Src-homology 3; hSH3, helically extended Src-homology 3.
Table S2. A primer list indicating the sequences of all primers used in the creation of SKAP55 chimeras via PCR mutagenesis

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Video 1. **SKAP55 recruits and co-migrates with SLP-76 downstream of TCR ligation.** J14.SY cells expressing SLP-76.YFP (green) were transiently transfected with SKAP55.3×Flag.TRT (red) and plated on glass coverslips coated with 10 µg/ml OKT3 (anti-CD3). Frames were acquired every 2 s for 5 min by confocal microscopy (CSU-10 spinning-disc confocal [Yokogawa], Axiovert 200M stand [Carl Zeiss], 40× Plan-Neofluar oil-immersion objective lens [Carl Zeiss], and an ICCD camera [Stanford Photonics]). This video is related to Fig. 1.

Video 2. **Transient knockdown of SKAP55 impairs SLP microcluster dynamics and cell contact stability.** J14.SY cells expressing SLP-76.YFP (green) were transiently transfected with SKAP55 shRNA tagged with mRFP1 (red) and imaged on glass coverslips coated with 10 µg/ml OKT3. Frames were acquired every 2 s for 5 min by confocal microscopy (CSU-10 spinning-disc confocal [Yokogawa], Axiovert 200M stand [Carl Zeiss], 40× Plan-Neofluar oil-immersion lens [Carl Zeiss], and a CCD camera [Hamamatsu Photonics]). This video is related to Fig. S1.

Video 3. **Transient knockdown of SKAP55 impairs cell boundary stability downstream of TCR ligation.** Cell shown from Video 2 with areas of boundary growth and retraction marked in red and blue, respectively, using iVision scripts. Boundary fluctuation was calculated by dividing areas of growth (red) and retraction (blue) over total cell area during the length of the movie. This video is related to Fig. S1.
Video 4.  **J14.SY expressing control mRFP1 exhibits stable contacts downstream of TCR ligation.** Cell shown from Fig. 2 using the same methodology applied to the cell in Video 3.

Video 5.  **J14.SY stably deficient in SKAP55 (JSKAP.SY) but expressing SLP-76.YFP (green) were transiently transfected with control mRFP1 (red) and imaged on glass coverslips coated with 10 µg/ml OKT3. Frames were acquired every 2 s for 5 min by spinning disc confocal microscopy (CSU-10 spinning-disc confocal [Yokogawa], Axiovert 200M stand [Carl Zeiss], 40x Plan-Neofluar oil-immersion lens [Carl Zeiss], and an ICCD camera [Stanford Photonics]). This video is related to Fig. 2.

Video 6.  **Reconstitution of JSKAP.SY with exogenous WT SKAP55 rescues SLP microcluster movement and persistence, and restores stable contact formation downstream of TCR ligation.** JSKAP.SY expressing SLP-76.YFP (green) were reconstituted with exogenous WT SKAP55.mRFP1 (red) and imaged on 10 µg/ml OKT3-coated glass coverslips. Frames were acquired every 4 s for 5 min by spinning disc confocal microscopy (CSU-10 spinning-disc confocal [Yokogawa], Axiovert 200M stand [Carl Zeiss], 40x Plan-Neofluar oil-immersion lens [Carl Zeiss], and an ICCD camera [Stanford Photonics]). This video is related to Fig. 2.

Video 7.  **Point mutation of the ADAP-binding SKAP55 SH3 domain (W333R) impairs SLP microcluster dynamics and contact stability downstream of TCR ligation.** J14.SY expressing SLP-76.YFP (green) transiently transfected with SKAP55.W333R.mRFP1 (red) were imaged on 10 µg/ml OKT3-coated glass coverslips. Frames were acquired every 4 s for 5 min by spinning disc confocal microscopy (CSU-10 spinning-disc confocal [Yokogawa], Axiovert 200M stand [Carl Zeiss], 40x Plan-Neofluar oil-immersion lens [Carl Zeiss], and a CCD camera [Hamamatsu]). This video is related to Fig. 3.

Video 8.  **Expression of the SKAP55 DM domain fragment potently impairs SLP microcluster dynamics and contact stability downstream TCR ligation.** J14.SY expressing SLP-76.YFP (green) transiently transfected with SKAP55.DM.mRFP1 (red) were imaged on 10 µg/ml OKT3-coated glass coverslips. Frames were acquired every 4 s for 5 min by spinning disc confocal microscopy (CSU-10 spinning-disc confocal [Yokogawa], Axiovert 200M stand [Carl Zeiss], 40x Plan-Neofluar oil-immersion lens [Carl Zeiss], and a CCD camera [Hamamatsu Photonics]). This video is related to Fig. 6.
Video 9. Reconstitution of JSKAP.SY with the SKAP55 ΔDM chimera fails to rescue SLP microcluster dynamics and contact stability downstream of TCR ligation. JSKAP.SY expressing SLP-76.YFP (green) reconstituted with SKAP55.ΔDM.mRFP1 (red) were imaged on 10 µg/ml OKT3-coated glass coverslips. Frames were acquired every 3 s for 5 min by spinning disc confocal microscopy (CSU-10 spinning-disc confocal [Yokogawa], Axiovert 200M stand [Carl Zeiss], 40x Plan-Neofluar oil-immersion objective lens [Carl Zeiss], and an ICCD camera [Stanford Photonics]). This video is related to Fig. 6.

Video 10. Reconstitution of JSKAP.SY with the SKAP55 TD chimera rescues SLP microcluster dynamics and contact stability downstream of TCR ligation. JSKAP.SY expressing SLP-76.YFP (green) reconstituted with SKAP55.TD.mRFP1 (red) were imaged on 10 µg/ml OKT3-coated glass coverslips. Frames were acquired every 2 s for 5 min by spinning disc confocal microscopy (CSU-10 spinning-disc confocal [Yokogawa], Axiovert 200M stand [Carl Zeiss], 40x Plan-Neofluar oil-immersion lens [Carl Zeiss], and an ICCD camera [Stanford Photonics]). This video is related to Fig. 7.

Table S1 shows parameters indicating excitation and emission, exposure time, laser channels used, pseudocoloring, resolution, camera make, temperature, and imaging media for each image in this work are depicted. It is available as an Excel file.
iVision scripts used in image analysis and quantitation, and instructions for their use are available for download as a ZIP file.