A Trifunctional Linker for Palmitoylation and Peptide and Protein Localization in Biological Membranes

Łukasz Syga,[b] Reinder H. de Vries,[a] Hugo van Oosterhout,[a] Rianne Bartelds,[b] Arnold J. Boersma,[c] Gerard Roelfes,[a] and Bert Poolman*[b]

Attachment of lipophilic groups is an important post-translational modification of proteins, which involves the coupling of one or more anchors such as fatty acids, isoprenoids, phospholipids, or glycosylphosphatidylinositol. To study its impact on the membrane partitioning of hydrophobic peptides or proteins, we designed a tyrosine-based trifunctional linker. The linker allows the facile incorporation of two different functionalities at a cysteine residue in a single step. We determined the effect of the lipid modification on the membrane partitioning of the synthetic α-helical model peptide WALP with or without here and in all cases below; palmitoyl groups in giant unilamellar vesicles that contain a liquid-ordered (Ld) and liquid-disordered (Lυ) phase. Introduction of two palmitoyl groups did not alter the localization of the membrane peptides, nor did the membrane thickness or lipid composition. In all cases, the peptide was retained in the Ld phase. These data demonstrate that the Ld domain in model membranes is highly unfavorable for a single membrane-spanning peptide.

Introduction

The traffic of proteins to the proper localization in the cell is necessary for their function. In many instances signal sequences determine the destination of a protein, be it the insertion within a membrane or translocation into the lumen of a compartment of a cell.[1–3] Remarkably, changes of a single amino acid residue can change the localization of lipoproteins from the inner to the outer membrane of Escherichia coli and vice versa.[4] Furthermore, reaching the correct compartment or target membrane is not necessarily enough for proper functioning of the protein. Biological membranes are heterogeneous in structure and localization within a specific membrane domain has been shown to affect the function of, for example, Lymphocyte function-associated antigen 1 and Toll-like receptor 2, which are moved to more ordered domains under binding of a substrate.[5–8] The signal output of K-Ras changes when a lysine residue is changed into glutamine.[10] This modification altered the interaction of K-Ras with anionic lipids and consequently the sorting of those lipids into nanodomains.[10]

Protein palmitoylation is a reversible post-translational modification whereby one or more palmitic acid group(s) are attached to a cysteine residue (or more seldom, as serine or threonine residue), and this modification has been implicated in the localization of proteins within a given membrane.[11–14] The palmitic acid group changes the hydrophobicity of the complex and may drive its partitioning into a specific membrane domain.[14] For example, the linker for activation of T cells (LAT) is enriched in the raft phase of cell-derived vesicles when palmitoylated.[15] In cells, the doubly palmitoylated H-Ras protein is localized in a different compartment than the unpalmitoylated K-RAS.[16] In yeast, several amino acid permeases (AAPs) have a C-terminal, amphipathic α-helix that associates with the inner leaflet of the plasma membrane. In a subset of these proteins, for example the amino acid transporters Gap1 and Tat2, this C-terminal helix is palmitoylated by a palmitoyl-acyl transferase.[17] The deletion of the amphipathic α-helix does not affect the apparent localization of Gap1 and Tat2 but leads to diminished growth on non-fermentable carbon sources.[18] Overall, palmitoylation of membrane proteins is relatively widespread in biology, but the functional significance of this modification is in most cases far from clear.

Hydrophobic mismatch is also known as sorting principle for membrane proteins. When the hydrophobic part of a membrane protein or peptide and the lipid membrane have different thickness, the lipids surrounding the protein are distorted which comes with an energetic penalty.[19,20] Proteins preferentially reside in lipid domains with matching thickness, which
leads to segregation of proteins with different hydrophobic thickness.\textsuperscript{[21–24]}

WALP peptides are classical transmembrane peptide models commonly used to study membrane protein/peptide behavior in vitro\textsuperscript{[25–30]} and in silico.\textsuperscript{[31–33]} Their sequences consist of alanine and leucine repeats flanked by tryptophan residues. Series of WALP peptides with different length and sequences have been developed.\textsuperscript{[34]} Here, we use WALP derivatives to investigate the effect of palmitoylation on the localization of a hydrophobic model peptide within the lipid domains of synthetic membranes.

To study the effect of protein palmitoylation and hydrophobic matching, we designed a trifunctional linker to couple a peptide or protein to both a fluorophore and (a) palmitoyl chain(s). Trifunctional linkers and scaffolds are ubiquitous in chemistry and serve a great variety of purposes. Even the simplest linkers bearing three identical reactive groups can be used, taking advantage of stochastic coupling or clever (sub-)stoichiometric introduction of the test molecules.\textsuperscript{[36–37]} Trifunctional linkers bearing three different reactive groups are more challenging to synthesize.\textsuperscript{[38–42]} A very elegant option is a molecule based on a tri-orthogonal “click” scaffold, combining inverse electron demand Diels–Alder (iEDDA) between a cyclooctyne and a tetrazine moiety with a copper-catalyzed alkyne–azide click (CuAAC) reaction as well as maleimide coupling.\textsuperscript{[43]} The combination of two CuAAC click reactions with an aldehyde and/or activated ester coupling is an alternative option.\textsuperscript{[44]} Herein we report the synthesis of a tyrosine-based trifunctional linker in which the palmitoyl chains, fluorophore and peptide are conjugated onto one scaffold via amide, CuAAC and maleimide coupling, respectively. As membrane model system to test the partitioning of hydrophobic peptides we used phase-separating giant unilamellar vesicles (GUVs). The chosen lipid compositions separate the GUV membrane into liquid-ordered ($L_0$) and liquid-disordered ($L_d$) phases.\textsuperscript{[45, 46]} In addition, we studied the effect of palmitoylation and hydrophobic mismatch in this system. We find that the lipid modification of the hydrophobic peptide does not affect its membrane partitioning and that the $L_0$ phase is disfavored for all molecules and lipid compositions tested.

**Results**

**Synthesis of tyrosine-based trifunctional linker and characterization of palmitoylated and fluorophore-coupled peptides**

Amino acids are a good starting point for the development of a trifunctional linker, as most naturally occurring amino acids already contain three functional groups. For the trifunctional linker designed here, a maleimide was introduced on $O$-propargyltyrosine, followed by an amide coupling with phospholipid 1,2-dipalmitoyl-sn-glycero-3-phosphoethanolamine (DPPE) to mimic two palmitoyl moieties. The propargyl allows CuAAC with a fluorescent dye (Sulfo-Cy3 azide), while the maleimide undergoes a Michael reaction with an introduced cysteine in the WALP23 peptide (sequence: GCGWW(LA)$_8$LWWA; Scheme 1).

**Scheme 1.** Trifunctional linker used to conjugate 1) DPPE via amide coupling, 2) Sulfo-Cy3 azide via CuAAC, and 3) WALP via maleimide coupling.

**Scheme 2.** Synthetic route toward scaffold 5.
We developed a synthetic route starting from Boc-tyrosine methyl ester (Scheme 2). First, a propargyl moiety was installed on the phenolic-OH after which 1 was obtained in high yields (Supporting Information). Boc-deprotection followed by amide coupling with 6-maleimidohexanoic acid, using DIC as a coupling reagent, resulted in amide 3 in moderate yields. Using the Nicolaou ester hydrolysis reaction,[47] employing trimethyl tin hydroxide, the free acid (4) was obtained in high yields. In the next step, DPPE was introduced on the carboxylic acid in a two-step procedure. First, an activated ester of 4 was generated in situ, followed by rapid removal of the insoluble urea side products. The activated ester was added to the solution containing DPPE, resulting in the phospholipid-modified scaffold 5 in good yield.

The functionalization of the DPPE-modified linker 5 with Sulfo-Cy3 azide via CuAAC gave the palmitoyl-dye (PD) product 7 in 24% yield after preparative HPLC purification (Scheme 3). For control experiments, free acid 4 (without DPPE) was also labeled with Sulfo-Cy3 using the same protocol, after which control conjugate 6 was obtained in 47% yield. Subsequent conjugation of 6 and 7 with WALP followed by preparative HPLC purification afforded the WALP-dye (WD, 8) and WALP-palmitoyl dye (WPD, 9) constructs, respectively (Scheme 3).

**Partitioning of the tyrosine-based trifunctional linkers and WALP in phase-separating GUVs**

We determined the localization and partitioning of the WALP peptide with and without palmitoyl moiety in phase-separating GUVs composed of DPPC, DOPC, and cholesterol in 4:3:3 molar ratio (Figure 1A). This lipid composition results in membranes with distinct phases, with most of the DPPC and cholest-
terol in the so-called L_o phase and most of the DOPC in the L_d phase.\[46\] The constructs WALP-palmitoyl-dye (WPD; construct 9), WALP-dye (WD; construct 8), and palmitoyl-dye (PD; construct 7) were used. Each construct was imaged with Atto655-DOPE as marker of the L_o phase. The Atto 655 dye displays minimal interaction with the membrane.\[49\] The Pearson correlation coefficient for the constructs (7, 8 or 9) relative to the L_d marker was calculated to signify the preference of the modified peptide in either of the phases. A Pearson’s correlation coefficient of 1 indicates that the two signals increase and decrease identically, whereas a value of 0 indicates a random relation between the signals. A negative value would indicate anti-correlation of two signals. We also determined the ratio of the molecules for the two phases (L_o/L_d), using the mean fluorescence in each phase as a measure of the partition coefficient of the constructs. The palmitoyl lipid (PD) has a slight preference for L_o (L_o/L_d ratio of 0.71 ± 0.21), whereas the constructs with WALP (WPD and WD) partition almost exclusively in L_d (Figure 1B). To eliminate the possibility that the localization of WPD and WD in L_o is biased by aggregation of the peptide, experiments at 100-fold lower concentration of the functionalized peptides were performed. The results were the same, and clearly, the palmitoyl moiety is not sufficient to transfer the WALP peptide from the L_d to the L_o phase (Figure S1 in the Supporting Information).

Lipid acyl chain saturation, not acyl chain length, determines localization of WALP

Next, we investigated the effect of membrane thickness on the partitioning of the constructs. To this end, we varied the length of the acyl chains of the lipids, yet maintaining distinct L_d and L_o phases. We prepared GUVs composed of cholesterol plus DPPC (16:0)/DOPC (18:1), and GUVs made from cholesterol plus PC with different acyl chain composition: 16:0/16:1, 18:0/18:1, and 18:0/16:1. For these mixtures we assume that the majority of DPPC (16:0) and DSPC (18:0) is in L_d and the majority of DOPC and 16:1 PC in L_o.\[50\] Additionally, mixtures with 14:0, 14:1, and 22:0 PC lipids were tested but conditions resulting in phase-separation were not found. All the constructs co-localize with the L_o marker used, which in all cases indicates a preference for the unsaturated lipid, independent of its acyl chain length (Figure 2).

The localization of a molecule in the L_d or L_o phase of a membrane affects its lateral diffusion. Because the mobility of molecules in the L_d phase is much faster than in the L_o phase,\[45\] we determined the lateral diffusion coefficient of Atto655-DOPE in GUVs prepared from different lipid compositions. The diffusion coefficients (D) were: 1.53 ± 0.41 (n = 12), 3.11 ± 0.55 (n = 8), 1.10 ± 0.256 (n = 10), and 1.04 ± 0.154 (n = 5) \(\mu m^2/s\) for the 16:0/18:1, 16:0/16:1, 18:0/18:1, and 18:0/16:1 mixtures, respectively. These values are consistent with lipid diffusion in the L_d phase and at least an order of magnitude faster than what is expected for L_o.\[46, 51\] Thus, we conclude that in all these lipid mixtures the Atto655-DOPE localizes in the L_d phase of GUVs.

The length of WALP does not affect the membrane localization

Next, we increased the length of the WALP peptide to better fit the hydrophobic thickness of the L_d phase, which is 0.7 to 1 nm larger than in the L_o phase.\[52–54\] WALP27 is four amino acids longer than the WALP-23, which results in an increase in the length of the hydrophobic part of 0.6 nm.\[55\] We also determined the partitioning of WALP27 in the presence of up to 5 mol% of GM1, which induces tighter lipid packing and is thought to be a major component of rafts in mammalian cells.\[56\] GM1 is relatively abundant in plasma membranes of the central nervous system of mammals.\[57\] WALP27 labelled with AlexaFluor 488 (Supporting Information) co-localized with the L_o marker DiD in the phase-separating GUVs, irrespective of the presence of GM1 (Figure 3).
In fact, in thin domains by creating hydrophobic mismatch, the membrane localization of WALP27 was observed by optical microscopy. We also note that the latter experiments were carried out in uniform supported bilayers. This result was expected as even GM1, one of the defining components of rafts, needs to be complexed with cholera toxin to stain the Lp phase specifically. Adding two palmitoyl tails to the WALP peptide lowers the energy barrier for entry into Lp phase, but not enough for WALP to localize into the more ordered parts of GUVs with our tertiary lipid compositions. Hydrophobic mismatch created by changing the lipid composition of the membrane or the hydrophobic length of the WALP peptide does not alter the localization or partitioning significantly, irrespective of the presence of palmitoyl groups.

Palmitoylation has been shown to affect the membrane localization of LAT and hemagglutinin. LAT is localized in the Lp phase of giant plasma membrane vesicles, and the partitioning in Lp is diminished after depalmitoylation. However, LAT does not localize in the Lc of GUVs composed of DSPC (18:0; 33.3 mol%), DOPC (18:1; 31.7 mol%), DOPG (18:1; 1.6 mol%) plus cholesterol (33.3 mol%). In addition, palmitoylation of LAT does not affect the partitioning of the molecule in these vesicles, which is consistent with our findings on the localization of WALP with or without palmitoyl groups.

What could be the reason for the apparent inconsistency in the membrane domain partitioning of LAT and other membrane proteins or peptides? The liquid-ordered and liquid-disordered domains of membranes are qualitative descriptions of lipid ordering, and, depending on the actual lipid composition, a domain can be more, or less, ordered or disordered. We have attempted to address this point by varying the lipid composition of the membrane, while conserving microscopically observable Lc and Ld phases. We have lowered the energy barrier for entering the Ld domain by creating hydrophobic mismatch, but we always find WALP associated with Lc. We cannot rule out that the transfer from Ld to Lc is more favorable in giant plasma membrane-derived vesicles, consisting of hundreds of different lipid components, that phase separate with a smaller difference in lipid order between Lc and Lp. We also note that the angle at which WALP crosses the membrane does not vary much with the membrane thickness. In fact, in thin membranes with very high hydrophobic mismatch the peptides are no longer incorporated in the membrane rather than highly tilted. Finally, in vivo, factors such as accessible surface area can also affect the partitioning of membrane peptides and proteins; we have not investigated this aspect.

GM1, a ganglioside, is often used as raft marker and associated with the Lp phase. GM1 has been shown to interact with WALP and LAT, thereby favoring the partitioning of the peptides in the Lp phase, at least in coarse grained molecular dynamics simulations. All-atom simulations contradict these findings and show depletion of GM1 near WALP. We note that the latter experiments were carried out in uniform phospholipid bilayers rather than phase-separating membranes. GM1 could form small nanodomains inside the Lp phase, thereby preventing interaction with WALP.Clusters of GM1 have been found in cell membranes, but also in supported bilayers. In any case, direct interaction of GM1 and WALP in phase-separating membranes seems unlikely, at least in our experimental system, because they are sparsely...
separated with GM1 in the L₁ phase and WALP in the L₄ phase [82,43].

Conclusion

We present the design and synthesis of a new tyrosine-based trifunctional linker, which enables conjugation of precious protein with two functional molecules in one step. To show the potential of our modular platform we study localization and partitioning of membrane-embedded peptides. Contrary to our initial hypothesis, we find in GUVs, prepared from a variety of lipid mixtures, that a double palmitoyl moiety is not sufficient to change the partitioning of a single-membrane spanner like WALP.

Experimental Section

Materials: Lipids were obtained from Avanti Polar Lipids, Inc; 1,2-dioleoyl-sn-glycero-3-phosphocholine (DOPC; product number 850375), 1,2-dipalmitoyl-sn-glycero-3-phosphocholine (product number 850358), 1,2-dipalmitoyl-sn-glycerol-3-phosphocholine (DPPC; product number 850355), 1,2-distearoyl-sn-glycerol-3-phosphocholine (DSPC, product number 850365).

For immobilization of GUVs, we used glutaraldehyde from Sigma–Aldrich, product number 340855. APTES (3-Aminopropyl) triethoxysilane) was obtained from Sigma–Aldrich, product number 440140. WALP (GCGGW(LA)LLWAA) was purchased from Bachem. Sulfo-Cyanine3 azide (Sulfo-Cy3) was purchased from Lumiprobe. All other chemicals were reagent grade and obtained from various commercial sources. High precision coverslips (type 1.5H) were obtained from Ibidi GmbH (product no. 10812). Reactions were monitored by TLC Silica 60 (Merck Millipore), examined under UV (365 nm and 254 nm), and stained by KMnO₄, ninhydrin, vanillin or H₂SO₄ in MeOH (1 %). Flash chromatography was performed on Si60 (0.040–0.063 mm) from Merck Millipore.

H NMR conditions: 500 MHz, 45 %B over 30 min, flow: 0.5 mL min⁻¹. 1H NMR spectra were recorded on an Ascend 500 (Varian) spectrometer. TLC analysis revealed that the reaction products were of high purity. The obtained fractions were analyzed using LC–MS (ESI). Analycal HPLC (same conditions): t₁ = 22 min (broad). The pure fractions were pooled and lyophilized and the product was obtained as a purple solid (0.5 mg, 0.47 mol %). HRMS (ESI) / m/z: calculated for C₁₁₂H₁₃₄O₇N₈P: 1109.411, found 1109.412. (M–H)⁻, found 1084.662.

General procedure for labeling with Sulfo-Cy3 (Example tyrosine-based linker without DPPE (4)) (6): MaleimidoheXyl modified O-propargyloxy-l-tyrosine carboxylic acid 4 (0.42 mg, 1 μmol, and Na-ascorbate (0.6 mg, 3.0 μmol, 3 equiv) were added to a 1 mL vial and dissolved using 50 μL TFE. Sulfo-Cy3 Azide (0.83 mg, 1.33 mol %, 1.33 equiv) in 50 μL BuOH/ddH₂O 5:1 was then added. A mixture of CuSO₄ (1.2 mg, 7.5 μmol) and THPTA (5.3 mg, 12.2 μmol) in 2.79 mL ddH₂O was prepared simultaneously and 46 μL of this solution was added to the reaction vial. The mixture was stirred at RT in the dark overnight, then filtered using a 0.45 μm microfilter and purified using semi-preparative HPLC (Waters Cortecs HILIC 2.7 μm 4.6 × 150 mm column, solvent A: 0.1 %FA in ddH₂O, solvent B: 0.1 %FA in ddH₂O, gradient: 5 % B to 45 % B over 30 min, flow: 0.5 mL min⁻¹). Analytical HPLC (same conditions): t₁ = 22 min (broad). The pure fractions were pooled and lyophilized and the product (6) was obtained as a purple solid (0.5 mg, 0.47 mol %). HRMS (ESI) / m/z: calculated for C₁₁₂H₁₃₄O₇N₈P: 1109.412, found 1109.411.

Synthesis of tyrosine-based linker with DPPE labelled with Sulfo-Cy3 (7): MaleimidoheXyl (dipalmitoylglycyl-glycophosphatidyl) ethanolamide modified O-propargyloxytyrosine 5 (1.1 mg, 1 μmol, 1 equiv) was treated according to the above general procedure. The mixture was filtered using a 0.45 μm microfilter and purified using semi-preparative HPLC (XBridge C₁₈ 5 μm 4.6 × 150 mm column, solvent A: 0.1 %NH₃ in AcN, solvent B: 0.1 %NH₃ in ddH₂O, gradient: 60 % B to 5 % B over 40 min, flow: 0.5 mL min⁻¹). The obtained fractions were analyzed using LC–MS (ESI). Waters BEH C₁₈ 1.7 μm 2.1 × 50 mm column, solvent A: 0.1 %NH₃ in ddH₂O, solvent B: 0.1 %NH₃ in AcN, gradient: 90 % A to 50 % A over 8 min, to 5 % A in 1 min, total runtime: 15 min) t₁ = 11.28 min, m/z = 1782.9 (M–2H)⁻. The pure fractions were pooled and lyophilized and the product (7) was obtained as a purple solid (0.43 mg, 0.24 μmol, 24 %). HRMS (ESI) / m/z: calculated for C₁₃₂H₁₇₄O₁₇₈N₈P: 890.955 [M–3H]⁻, found 890.953.

Synthesis of WALP-Sulfo-Cy3 hybrid using Sulfo-Cy3 labelled tyrosine-based linker without DPPE (8): WALP (1.5 mg, 0.48 μmol; ≈80 % purity) was placed in a Schlenck tube, which was brought under argon atmosphere; 250 μL of a 0.94 mM solution of Sulfo-
Cy3 labeled tyrosine-based linker without DPPE (6) in TFE (0.24 μmol) was added, followed by 0.84 μL DIPEA and the mixture was stirred in the dark at RT overnight. 100 μL ddH₂O/ACN 1:1 was added, and the mixture was filtered using a 0.45 μm microfilter. The clear filtrate was purified using semi-preparative HPLC (XBridge C₁₈ 5 μm 4.6 x 150 mm column, solvent A: 0.1% NH₃ in ddH₂O, gradient: 60% B to 5% B over 40 min, flow: 0.5 mL/min). The obtained fractions were analyzed using LC–MS (ESI⁺, Waters BEH C₁₈ 1.7 μm 2.1 x 50 mm column, solvent A: 0.1% NH₃ in ddH₂O, solvent B: 0.1% NH₃ in ACN, gradient: 90% A to 50% A over 8 min, to 5% A in 1 min, total run time: 15 min); t<sub>R</sub> = 7.55 min, m/z = 1248.0 [M–4H]<sup>4+</sup>; HRMS (ESI⁺) m/z calcd for C<sub>93</sub>H<sub>135</sub>N<sub>12</sub>O<sub>15</sub>S<sub>2</sub>: 1872.438 [M–3H]<sup>3+</sup>; found 1872.440; m/z calcd for C<sub>183</sub>H<sub>252</sub>N<sub>22</sub>O<sub>30</sub>S<sub>2</sub>: 1247.956 [M–4H]<sup>4+</sup>; found 1247.960; m/z calcd for C<sub>175</sub>H<sub>228</sub>N<sub>21</sub>O<sub>29</sub>S<sub>2</sub>: 935.715 [M–5H]<sup>5+</sup>; found 935.718.

Synthesis of WALP-Sulfo-Cy3 hybrid using Sulfo-Cy3 labelled tyrosine-based linker with DPPE (9): WALP (0.24 mg, 0.24 μmol; ≈80% purity) was placed in a Schlenck tube, which was brought under Ar atmosphere; 250 μL of a 0.48 mM solution of Sulfo-Cy3 labeled tyrosine-based linker with DPPE (7) in TFE (0.12 μmol) was added, followed by 0.42 μL DIPEA and the mixture was stirred in the dark at room temperature overnight. 100 μL ddH₂O/ACN 1:1 was added and the mixture was filtered using a 0.45 μm microfilter. The clear filtrate was purified using semi-preparative HPLC (XBridge C₁₈ 5 μm 4.6 x 150 mm column, solvent A: 0.1% NH₃ in ddH₂O, solvent B: 0.1% NH₃ in ACN, gradient: 70 to 30% A over 8 min, to 5% A in 1 min, total run time: 20 min); t<sub>R</sub> = 10.82 min, m/z = 1472.7 [M–4H]<sup>4+</sup>; HRMS (ESI⁺): m/z calcd for C<sub>120</sub>H<sub>172</sub>N<sub>15</sub>O<sub>22</sub>S<sub>2</sub>: 1472.458 [M–4H]<sup>4+</sup>; found 1472.457; m/z calcd for C<sub>118</sub>H<sub>168</sub>N<sub>14</sub>O<sub>21</sub>S<sub>2</sub>: 1104.091 [M–5H]<sup>5+</sup>; found 1104.090.

GUV formation: GUVs composed of saturated lipids (DPPC, DSPC), double mono-unsaturated lipids (DOPC, 16:1 PC), and cholesterol in a 4:3:3 molar ratio were formed by electroformation. For immobilization purposes 0.1 mol% of DOPE was added to each of the mixtures, as described previously. The labelled WALP peptide together with the L<sub>d</sub> phase markers ATTO 655 DOPE, or DiD, were added to the lipid mixture in a 1:1000 molar ratio, unless stated otherwise. Atto 655 is a water-soluble, zwitterionic fluorophore coupled to a lipid that is excited in the far red and spectrally distinct from Sulfo-Cy3. Around 400 nmol of lipids, together with L<sub>d</sub> marker and WALP were spotted on a conductive indium tin oxide (ITO)-coated glass plate. After removal of the solvents under vacuum, GUVs were formed in 200 mm sucrose on the Vesicle Prep Pro (Nanion technologies) with a voltage of 1.1 V at 10 Hz for 1 h at 50 °C.

Immobilization of GUVs: GUVs were immobilized on slides modified with APTES-glutaraldehyde as described previously. In short, coverslips were cleaned in KOH and plasma cleaned. They were then modified in 2% APTES solution for 10 seconds and stored in vacuum until the day of the experiment but always within 48 h. Prior to the experiment, slides were incubated with 5% glutaraldehyde for 30 min, after which the glutaraldehyde was washed away with ddH₂O. Subsequently, the GUVs, diluted 10 times in 100 mM NaCl, were placed on the slide.

Imaging: GUVs were imaged on the Zeiss LSM 710 confocal microscope with a 40x C-Apochromat Corr M27 with NA 1.2 water immersion objective. ATTO 655 DOPE and DiD were excited with a 633 nm HeNe laser; the Sulfo-Cy3 coupled to the WALP peptide was excited with a 543 nm HeNe laser. Z-stack images of immobilized GUVs were taken. The images of both channels were separately taken to avoid cross talk.

Image analysis: The GUVs were automatically identified by detecting circles in the image. The detection of circles was done using a circle Hough transform for a range of radii, resulting in a stack of images; one image for each radius. We then created a maximum intensity projection where each pixel contains the maximum value over all images in the stack at the particular pixel location. On this projection we detect peaks by repeatedly finding the brightest pixel, which gives us the centers of the detected GUVs. The radius of each GUV corresponds to the radius on which the maximum pixel value was found when we created the maximum intensity projection (Figure S2).

After detection of the circles on the image, the non-phase-separating GUVs were filtered out. We calculated the Pearson’s correlation coefficient for the fluorescent profile of the L<sub>d</sub> marker relative to the same profile that was smoothened. Smoothening was done with a moving average filter. A high correlation indicates two separate phases, while low correlation is consistent with a single-phase vesicle. We used the correlation of 0.9 as a cut off for phase-separating vesicles. After the automatic detection all selections were manually inspected and false positives were removed. We used the smoothened profile of the L<sub>d</sub> marker to classify each intensity value as being either in the L<sub>d</sub> or L<sub>o</sub> phase based. Next, the correlation between the L<sub>d</sub> marker and target construct, and the ratio of the mean intensity of the fluorescence in the L<sub>d</sub> and L<sub>o</sub> phases, were calculated on the non-smoothened profiles (an overview of the data analysis is presented in Figure S3).

FRAP experiments: FRAP measurements were performed by imaging a small area of the membrane of the GUVs to achieve an acquisition time below 40 ms. A spot with a diameter of 1 μm was bleached at high laser intensity, after which the attenuated laser was used to record images every 40 ms for 6 s; the pre-bleaching fluorescence was obtained from five images prior to the bleach. The halftime of recovery and lateral diffusion coefficients were calculated as described previously, which is based on work of Axelrod and colleagues.

Acknowledgements
This work was supported by the Netherlands Organisation for Scientific Research (NWO): Chem-Them grant 728.011.202, an ERC Advanced Grant (ABCVolume) and Vici grant 724.013.003.

Conflict of Interest
The authors declare no conflict of interest.

Keywords: biological membranes · lipid phase separation · membrane partitioning · palmitoylation · trifunctional linker

[1] K. Yamauchi, K. Doi, Y. Yoshida, M. Kinoshita, Biochim. Biophys. Acta Bioembr. 1993, 1146, 178–182.
[2] M. Razandi, G. Alton, A. Pedram, S. Ghoshani, P. Webb, E. R. Levin, Mol. Cell. Biol. 2003, 23, 1633–1646.
[77] C. Yuan, J. Furlong, P. Burgos, L. J. Johnston, Biophys. J. 2002, 82, 2526–2535.
[78] K. Bacia, D. Scherfeld, N. Kahya, P. Schwille, Biophys. J. 2004, 87, 1034–1043.
[79] R. X. Gu, H. I. Ingólfsson, A. H. De Vries, S. J. Marrink, D. P. Tieleman, J. Phys. Chem. B 2017, 121, 3262–3275.
[80] A. Fujita, J. Cheng, M. Hirakawa, K. Furukawa, S. Kusunoki, T. Fujimoto, Mol. Biol. Cell 2007, 18, 2112–2122.
[81] M. M. Lozano, Z. Liu, E. Sunnick, A. Janshoff, K. Kumar, S. G. Boxer, J. Am. Chem. Soc. 2013, 135, 5620–5630.
[82] R. O. Duda, P. E. Hart, Commun. ACM 1972, 15, 11–15.
[83] F. Bianchi, L. Syga, G. Moiset, D. Spakman, P. E. Schavemaker, C. M. Puntes, A. B. Seinen, A. M. Van Oijen, A. Robinson, B. Poolman, Nat. Commun. 2018, 9, 501.
[84] D. Axelrod, D. E. Koppel, J. Schlessinger, E. Elson, W. W. Webb, Biophys. J. 1976, 16, 1055–1069.

Manuscript received: October 29, 2019
Accepted manuscript online: December 9, 2019
Version of record online: January 10, 2020