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The Cytosolic Phospholipase A₂α N-terminal C2 Domain Binds and Oligomerizes on Membranes with Positive Curvature

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Abstract: Group IV phospholipase A₂α (cPLA₂α) regulates the production of prostaglandins and leukotrienes via the formation of arachidonic acid from membrane phospholipids. The targeting and membrane binding of cPLA₂α to the Golgi involves the N-terminal C2 domain whereas the catalytic domain produces arachidonic acid. Although most studies of cPLA₂α concern its catalytic activity, it is also linked to homeostatic processes involving the generation of vesicles that traffic material from the Golgi to the plasma membrane. Here we investigate how membrane curvature influences the homeostatic role of cPLA₂α in vesicular trafficking. The cPLA₂α C2 domain is known to induce changes in positive membrane curvature, a process which is dependent on cPLA₂α membrane penetration. We show that cPLA₂α undergoes C2 domain-dependent oligomerization on membranes *in vitro* and in A549 cells. We found that the association of the cPLA₂α C2 domain with membranes is limited to membranes with positive curvature, and enhanced C2 domain oligomerization was observed on vesicles ~50 nm in diameter. We demonstrated that the cPLA₂α C2 domain generates cholesterol enriched Golgi-derived vesicles independently of cPLA₂α catalytic activity. Our results therefore provide novel insight into the molecular forces that mediate C2 domain-dependent membrane localization *in vitro* and in cells.

Keywords: cytosolic phospholipase A₂α (cPLA₂α); electron microscopy; Golgi; membrane bending; membrane curvature; C2 domain; oligomerization

1. Introduction

Cytosolic phospholipase A₂α (cPLA₂α) selectively cleaves phosphatidylcholine containing a *sn*-2 arachidonyl acyl chain, a critical step in the synthesis of prostaglandins and leukotrienes [1]. The analysis of cPLA₂α knockout mice revealed a marked reduction in arthritis, anaphylaxis and cerebral ischemia, among other inflammatory diseases, promoting great interest in its catalytic activity and regulation [2,3]. The cPLA₂α protein has two domains: a ~130-residue N-terminal Conserved 2 (C2) domain and a ~700-residue C-terminal lipase domain [4], the former required for localization to cellular membranes [5]. The C2 domain interacts with lipids in a Ca²⁺-dependent manner [6,7], penetrates 1–1.5 nm into the membrane [8] to enhance membrane resonance time, and selectively binds to the bioactive sphingolipid ceramide-1-phosphate [9,10]. The catalytic domain can be activated by higher cytosolic calcium levels, but C1P plays a key role in cPLA₂α localization [10,11]. In addition to its role in inflammatory signaling, cPLA₂α is also important for phagocytosis [12] and

Golgi-derived endosomal trafficking [13–15]. This homeostatic function is supported by the expression of cPLA α in a wide variety of cell types [2,3].

Several studies suggest a direct role for cPLA α in processes involving membrane curvature, including cholesterol-dependent vesicular transport from the Golgi to the plasma membrane and Golgi intercisternal tubular formations [13–15]. Recently, cPLA α was found to be necessary for Fc-mediated phagocytosis in macrophages [12]. Interestingly, this process was independent of cPLA α catalytic activity but dependent on C2 membrane binding [12]. Biophysical studies investigating how proteins generate the membrane curvature necessary for all of these processes are best understood in the context of endocytosis, exocytosis and vesicular trafficking. The molecular mechanisms responsible for this energetically unfavorable process often involve proteins with peripheral Bin-amphiphysin-Rvs (BAR) or epsin N-terminal homology (ENTH) lipid-binding domains [16]. Although both domains are responsible for inducing and stabilizing membrane curvature, they alter membrane shape via different mechanisms. BAR domains dimerize to form the intrinsically curved structure of a crescent moon, sensing local regions of membrane curvature and forming rigid protein scaffolds to bend and stabilize membrane tubules [17,18]. In contrast, the ENTH domain has a more globular structure and relies on lipid binding to induce conformational changes in an amphipathic α -helix that penetrates the membrane [19,20] and stabilizes the protein–membrane interaction [21]. The ENTH domain was later found to form oligomers on highly-curved membranes via electrostatic residues that are not involved in membrane binding [22]. A computational study found that ENTH domain oligomers on vesicles are less ordered than those found on long tubular structures, providing some insight into the molecular forces that mediate vesiculation and tubulation [18].

Although C2 domains were not initially considered able to induce membrane curvature, several recent studies have provided evidence to support this role. The first C2 domain shown to induce membrane curvature was synaptotagmin-1 [23]. We subsequently showed that cPLA α induces membrane curvature in a calcium-dependent manner, and that both calcium-binding loops must penetrate the membrane to achieve bending [24]. At least four C2 domain proteins have been shown to bend membranes, and three of them contain tandem C2A and C2B domains [23–26]. Only the C2B domain of synaptotagmin-1 is required to induce membrane curvature (22), whereas only the C2A domain is required in the case of Doc2B, although both C2A and C2B are required for SNARE-dependent vesicle fusion (25).

To gain insight into the molecular basis of membrane curvature induced by C2 domains, we compared the C2 domain of cPLA α to the well-studied ENTH and BAR domain mechanisms. We found that the C2 domain of cPLA α preferentially localizes to vesicles of high positive curvature (~50 nm in diameter), as previously reported for synaptotagmin-1 and RASAL [23,25]. Additionally, we found that the oligomerization of cPLA α *in vitro* and in A549 cells is dependent on the C2 domain, and is enhanced on vesicles with greater intrinsic curvature. This report shows that C2 domain oligomerization is used as a mechanism to overcome energetic barriers that prevent the induction and stabilization of curved membranes.

2. Materials and Methods

2.1. Materials

The lipids 1-palmitoyl-2-oleoyl-*sn*-glycero-3-phosphocholine (POPC), 1-palmitoyl-2-oleoyl-*sn*-glycero-3-phosphoethanolamine (POPE), 1-palmitoyl-2-oleoyl-*sn*-glycero-3-phosphatidylserine (POPS), 1,2-dioleoyl-*sn*-glycero-3-[(N-(5-amino-1-carboxypentyl)iminodiacetic acid)succinyl] nickel salt (DGS-NTA-Ni), 1-palmitoyl-2-(dipyrrometheneboron difluoride)undecanoyl-*sn*-glycero-3-phosphocholine (TopFluorPC), and 23-(dipyrrometheneboron difluoride)-24-norcholesterol (TopFluorChol) were purchased from Avanti Polar Lipids (Alabaster, AL, USA) and used without further purification. Nunc Lab-Tek II eight-well chambered cover glasses, the Pierce bicinchoninic acid (BCA) protein assay kit and all molecular biology enzymes were sourced from Thermo Fisher Scientific (Waltham, MA USA), with the exception of DNA ligase (New England Biolabs, Ipswich,

MA, USA). The mTurquoise2 constructs [27] were a gift from Dorus Gadella (Addgene reference numbers 36204 and 36205).

2.2. Protein Purification

The C2 domain sequence of cPLA₂ α in vector pET-28a [6] was expressed and purified as previously described [24]. E116C purification and labeling with Rhodamine Red C2 maleimide (Thermo Fisher Scientific) was carried out according to the manufacturer's protocol. Briefly, after purification with Ni-NTA resin (Qiagen, Valencia, CA, USA), the protein solution was centrifuged at 50,000 $\times g$ to remove any precipitated protein then gently mixed overnight with a five-fold molar excess of maleimide. The protein was dialyzed three times against 4 L of 20 mM HEPES buffer (pH 7.4) containing 160 mM NaCl to remove free maleimide, and the protein concentration was determined using the Pierce BCA assay. The concentration of maleimide-labeled protein was calculated using a standard curve of seven free maleimide standards prepared using free maleimide and measured on SpectaMax M5 96-well plate reader ($\lambda_{\text{excitation}} = 544$ nm, $\lambda_{\text{emission}} = 590$ nm). We achieved 20–40% labeled protein over several purification and labeling protocols.

2.3. Cloning and Mutagenesis

The EGFP-cPLA₂ α sequence in vector pEGFP-C1 was kindly provided by Dr. Charles Chalfant from the University of South Florida [11]. The EGFP-cPLA₂ α (**Figure 1A**) cassette was removed using BglII and ApaI, and was transferred to vectors pmCherry-C1 and pmEGFP-C1 (Addgene 36412), kindly provided by Dr. Benjamin Glick, University of Chicago, IL, USA. The C2 domain constructs featured a GLRS linker between the mEGFP sequence and the N-terminus of cPLA₂ α (**Figure 1A**). An EcoRI site was added to the N-terminus of the C2 domain (residues 1–128) by PCR and the cassette was transferred to vector pmEGFP-C1 using the BglII and EcoRI sites. Site-directed mutagenesis was carried out using the QuikChange II kit (Agilent Technologies, Santa Clara, CA, USA) according to the manufacturer's protocol. All constructs and mutations were confirmed by DNA sequencing.

2.4. Cell Culture

A549 cells were seeded into Nunc Lab-Tek II eight-well imaging plates at 40–50% confluency in a 50/50 mixture of Dulbecco's modified Eagle's medium (DMEM) and Roswell Park Memorial Institute 1640 (RPMI) medium without serum or antibiotics. The cells were cultivated at 37 °C in a 5% CO₂ atmosphere and were transfected using Lipofectamine-LTX and Plus Reagent (Thermo Fisher Scientific) when they reached 70–90% confluency, according to the manufacturer's protocol. TopFluor-Cholesterol (TopFluor-Chol) was prepared in a methyl β -cyclodextran (M β CD) delivery system adapted from the protocol established for dehydroergosterol [28]. Briefly, 5 mM TopFluor-Cholesterol was prepared from a chloroform stock solution, dried under nitrogen gas and resuspended in 25 mM M β CD. The mixture was sonicated for 15 min, shaken at 37 °C overnight, then centrifuged at 16,000 $\times g$ for 10 min. The soluble complex was added to A549 cells 21 h after transfection at a concentration of 50 μ M and was left in contact with the cells for 3 min before aspiration and replacement with Opti-MEM.

2.5. Confocal Microscopy

The cells were allowed to recover for 3 h after treatment and were imaged by confocal microscopy 24 h post-transfection using a Zeiss LSM 710 confocal microscope fitted with a 63 \times oil objective with a numerical aperture of 1.4. To quantify the number of cells with vesiculation, cells containing more than 20 cPLA₂ α -localized intracellular vesicles were counted versus the total number of transfected cells. Data were collected in triplicate from independent imaging wells and statistically significant differences were determined using Student's t-test.

2.6 CryoAPEX method for localization cPLA₂ α and visualization of morphological changes of the Golgi apparatus

HeLa cells were transfected with cPLA₂ α -GFP and 15 hours post transfection 10 μ M of A23187 was added to the media and cells were incubated for 30 more minutes. To observe vesiculation in these cells post treatment, cells were pelleted at 500 \times g resuspended in 20% BSA and cryofixed using a high pressure freezer (Leica, EM PACT) on copper membrane carriers (Leica). This was followed by freeze substitution (Leica, EM AFS2) in acetone in the presence of uranyl acetate and osmium tetroxide for a period of 4 days. Post freeze-substitution pellet was infiltrated with resin (Durcupan, Sigma-Aldrich) gradually (15%-30%-60%-90%-100%-100% + component C). The membrane carrier containing the pellet was then placed in a mold filled with resin and baked in the oven at 60°C for 24 hours. Copper planchets were then extracted using a razor blade and the blocks were re-embedded with more resin and baked in the oven for another 24 hours. Hardened blocks with embedded samples are then trimmed and serially-sectioned using an ultramicrotome. Serial-sections were collected on copper slot grids with formvar support (EM sciences) and imaged using a Tecnai T12 transmission electron microscope operating at 80 kV.

For localization of cPLA₂ α at high resolution, an indirect APEX2 based localization method was carried out. This method was adapted from Ariotti et al. [29]. Briefly, HEK cells were transfected with cPLA₂ α -GFP plasmid along with APEX2-csGBP plasmid (A kind gift from Dr. Rob Parton, Addgene #108874) at a 1:1 ratio using Lipofectamine 2000 (Invitrogen) and incubated for 15 hours. Cells were treated with 10 μ M of A23187 as before and then dislodged from the plates using trypsin and fixed chemically with glutaraldehyde. The pellet was then washed 3 times for 5 minutes each with 0.1 M sodium cacodylate buffer. The APEX2 peroxidase reaction was then carried out with hydrogen peroxide (in presence of 1 mg/ml 3,3'-diaminobenzamide (DAB) and in sodium cacodylate buffer). Post reaction cells were pelleted and washed pellets were subsequently subjected to the CryoAPEX method as described in Sengupta et al [30]. Briefly, cells chemically fixed with glutaraldehyde were then cryogenically fixed via high pressure freezing followed by freeze substitution in presence of osmium tetroxide in acetone. Cell pellets were then embedded in resin blocks and baked at 60°C. Thin (90nm) serial-sections were then obtained from the resin blocks using a microtome and were collected on formvar coated grids. Grids were loaded onto a Tecnai T12 TEM for image collection.

To visualize the perturbation of the Golgi structure induced by the cPLA₂ α or the C2 domain, HeLa cells constitutively expressing the Golgi cis-medial marker α -mannosidase-II-HRP (kind gift from Dr. Franck Perez, Institut Curie) were transfected with either cPLA₂ α -GFP or C2-GFP plasmids and incubated for 15 hours. Thirty minutes prior to glutaraldehyde fixation, cells were treated with 10 μ M of the calcium ionophore A23187. Cells were detached from the plate using trypsin and centrifuged at low speed to obtain a cell pellet. The pellet was then subjected to the CryoAPEX method [30,31] and processed for EM imaging exactly as above.

2.6. Cross-linking Assay

The POPC stock was dried under a stream of nitrogen and made up to 1.5 mM in 20 mM HEPES (pH 7.4) containing 160 mM KCl. The solution was gently mixed to remove dried lipid from the glass vial. To construct vesicles with different diameters, the following modifications were made to the traditional large unilamellar vesicle (LUV) extrusion protocol: the smallest vesicles were extruded 40 times through a 50-nm filter, the mid-sized vesicles were heated at 37 °C for 10 min and extruded 10 times through a 100-nm filter, and the largest vesicles were heated at 37 °C for 20 min and extruded five times through a 400-nm filter. Vesicle size was confirmed using a Delsa Nano S Particle Analyzer (Beckman Coulter, Brea, CA, USA). The number distribution was used to determine the particle size of each vesicle population in triplicate for each independent experiment. We incubated 35 μ L of the 1.5 mM POPC LUV solution with 8 μ g cPLA₂-C2 in buffer containing either 50 μ M CaCl₂ or 100 μ M EGTA for 30 min. The protein was crosslinked with 0.5 mM ethylene glycol bis(succinimidylsuccinate) (EGS; Thermo Fisher Scientific) for 5 min, then quenched with 150 mM Tris-HCl (pH 8.0) for 5 min.

The samples were separated by 12% SDS-PAGE, stained with Coomassie brilliant blue, destained, and analyzed using ImageJ software.

2.7. Giant Unilamellar Vesicle Experiments

Giant unilamellar vesicles (GUVs) were prepared as previously described [24]. The lipids in these experiments were labeled with 0.2 mol% TopFluor-PC using the lipid ratio 59.8:20:20:0.2 (POPC:POPE:POPS:TopFluor-PC). The GUVs were incubated in 20 mM HEPES (pH 7.4) containing 160 mM KCl and 50 μ M CaCl₂ to assess their stability. We then added 2 μ M cPLA₂ α and incubated the vesicles for 30 min before imaging for confocal microscopy as described above. GUVs containing protein were visualized ($\lambda_{\text{excitation}} = 488$ nm, $\lambda_{\text{emission}} = 561$ nm) at similar intensities, as determined using the intensity profile from the Zeiss software. The images were imported into ImageJ to determine the vesicle size, lipid intensity and protein intensity in triplicate for each GUV. The vesicle diameter was measured by drawing a circle around the outer diameter of the GUV and the enclosed area was analyzed for fluorescence intensity in the green and red channels, which together were used to calculate the protein-to-lipid ratio. Each vesicle was measured at three locations to obtain an average protein-to-lipid ratio. The largest GUVs contained budding vesicles, which were highly curved and therefore excluded from the intensity measurements.

2.8. Number and Brightness Analysis

The Raster Image Correlation Spectroscopy (RICS) data for Number and Brightness (N&B) analysis was collected on an Olympus FV1000 fitted with a 60 \times oil PlanApo objective with a numerical aperture of 1.42. The data were collected and exported as previously described [32] and analyzed using SimFCS v2.0. A549 cells were plated and transfected at 70–90% confluency as above, and images were acquired 24 h post-transfection. Cells exposed to ionophore were treated with 10 μ M A23187 for 30 min before imaging at a pixel dwell time of 12.5 μ s/pixel. The pixel size was set to 50 nm in photon mode as specified in the established protocol. The data were analyzed using simFCS v2.0, where the moving average was subtracted for N&B analysis. The monomer threshold was determined using mEGFP as a control with the same 12.5 μ s/pixel dwell time. These N&B settings were then applied to data collected from A549 cells transfected with mEGFP-cPLA₂ α and mEGFP-cPLA₂ α -C2. To quantify the pixel intensities of each average oligomer, colored boxes were added to the data in SimFCS v2.0, where each rectangular box corresponds to the average brightness of the monomer, hexamer, 12-mer, 18-mer and >18-mer. Each rectangular box was defined with the dimensions 250 \times 15 in the cursor window, with the exception of the >18-mer box, which was defined as 150 \times 80. The total number of pixels selected under these settings was then compiled from 11 image sets each containing 100 scans. The data were collected from two independent experiments, each independently normalized for the mEGFP control.

3. Results

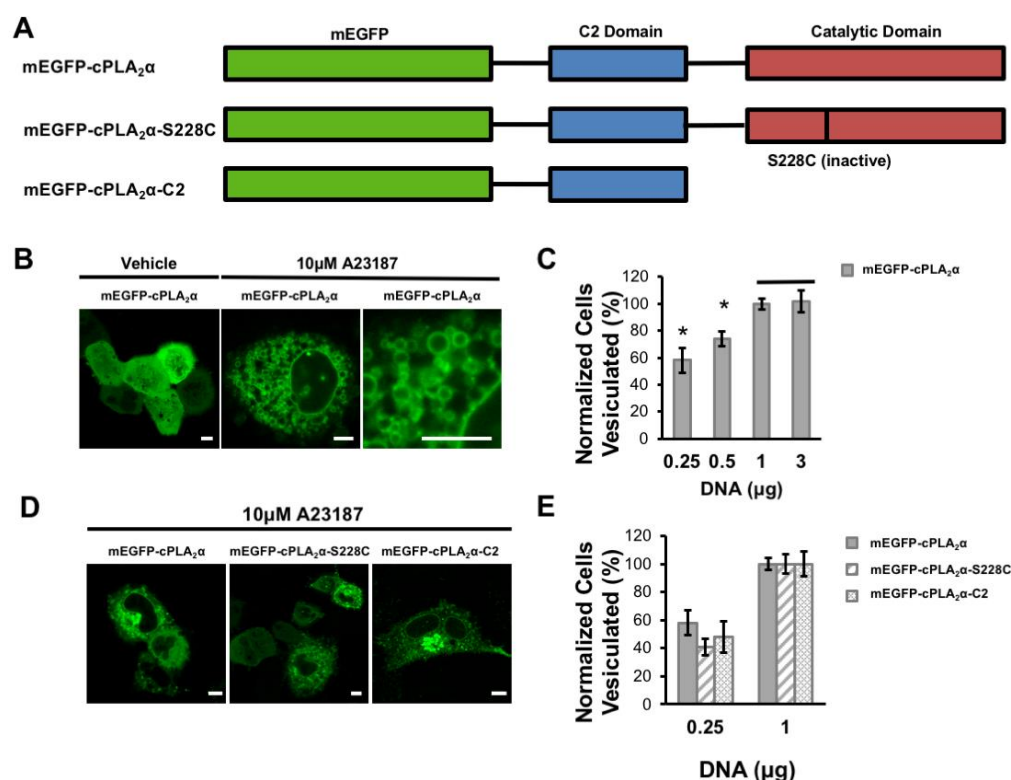
3.1. cPLA₂ α Induces Cellular Vesiculation via its C2 Domain

We investigated the ability of cPLA₂ α to induce vesiculation by transfecting A549 cells with increasing concentrations of EGFP-cPLA₂ α DNA (**Figure 1A**). To elevate the cytoplasmic calcium concentration and thus induce cPLA₂ α membrane localization, cells were treated with the calcium ionophore A23187 and imaged by confocal microscopy. As the cellular concentration of cPLA₂ α increased, the number of cells containing more than 20 cytoplasmic vesicles steadily rose until saturation was reached at 1 μ g transfected DNA (**Figure 1B,C**). These data demonstrate the number and generation of cytoplasmic vesicles are dependent upon the expression level of cPLA₂ α .

To determine the role of the cPLA₂ α catalytic and C2 domains in the induction of membrane curvature, we created constructs lacking a functional catalytic domain and tested for vesiculation in transfected A549 cells (**Figure 1A**). Either deleting the catalytic domain completely (mEGFP-cPLA₂ α -C2) or inactivating it by mutating the catalytic residue Ser²²⁸ (mEGFP-cPLA₂-S228C) caused a slight decrease in vesiculation compared to the wild-type construct in cells transfected with the lowest

concentration of cPLA₂α DNA. These data show that the catalytic domain may contribute to the formation of vesicular structures but that the C2 domain alone clearly has the ability to generate vesicles in cells (**Figure 1D,E**). At higher concentrations of cPLA₂α DNA, the constructs lacking a functional catalytic domain were capable of inducing vesiculation to the same degree as the wild-type construct (data not shown).

Figure 1. cPLA₂α induces cellular vesiculation. **A.** A schematic of the fusion constructs for the mEGFP-cPLA₂α. **B.** A549 cells were plated and transfected at 70–90% confluency with varying concentrations of the



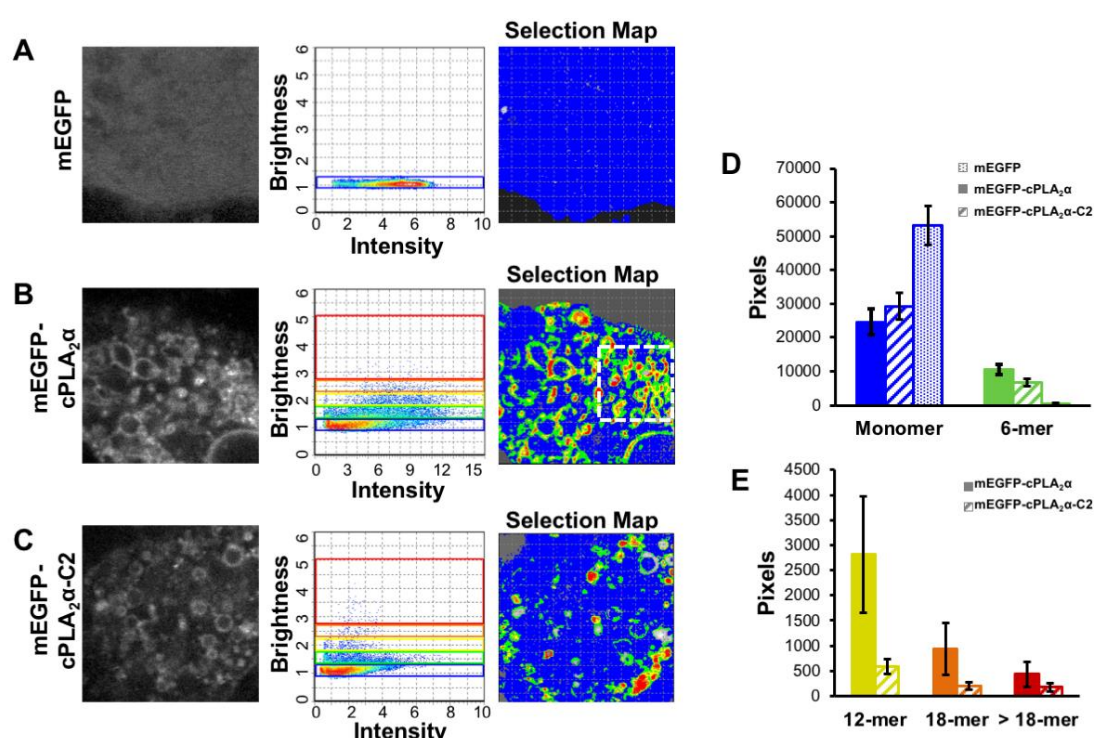
mEGFP-cPLA₂α WT or mutant construct. A549 cells were imaged 24 hours post transfection and quantified 20–30 minutes after treatment with either DMSO vehicle or 10 μM A23187. The vesiculation was defined as cells expressing mEGFP-cPLA₂α containing > 20 cellular vesicles with localized fluorescent protein. The vesiculation was normalized for the total number of cells expressing mEGFP-cPLA₂α, mEGFP-cPLA₂α-S228C or mEGFP-cPLA₂α-C2. A representative image of mEGFP-cPLA₂α transfected cells before and after treatment with the calcium ionophore A23187 or DMSO vehicle. **C.** 40–80 cells were counted in triplicate to measure the relationship between mEGFP-cPLA₂α and cellular vesiculation. Data was normalized to the 3 μg DNA average. **D.** Representative images of mEGFP-cPLA₂α, mEGFP-cPLA₂α-S228C and mEGFP-cPLA₂α-C2 after treatment with A23187. **E.** 40–80 vesiculated cells were quantified (5 replicates performed) and normalized to the 1 μg average. Error bars represent the standard error of the mean and statistics were run using a Student's t-test. Scale bars = 5 μm; * p < 0.04

3.2. cPLA₂α Oligomerizes on Membranes in A549 Cells

Next we compared the mechanism of membrane curvature triggered by cPLA₂α-C2 to that of the ENTH domain. Both domains are known to penetrate membranes [6–8,21,33] but it is unlikely that membrane penetration alone can overcome the large energetic barrier that prevents the bending of membranes into highly curved vesicles and their stabilization [16,34,35]. The ENTH domain oligomerizes on membranes and selectively binds to vesicles with positive curvature [17,19,22], so we hypothesized that cPLA₂α also oligomerizes on membranes and tested this hypothesis using N&B

analysis based on the RICS protocol in live cells using confocal microscopy [30,36]. A549 cells were transfected with mEGFP, mEGFP-cPLA₂ α or mEGFP-cPLA₂ α -C2 and imaged 24 h post-transfection. Cells were treated with A23187 to induce calcium influx, which promotes the localization of cPLA₂ α to the membrane. The oligomerization data generated using simFCS are summarized as a single image from each dataset (**Figure 2A**), the intensity versus brightness plot (**Figure 2B**), and the selection map (**Figure 2C**). The intensity versus brightness plot reveals that mEGFP generates only monomers in live cells, whereas mEGFP-cPLA₂ α and mEGFP-cPLA₂ α -C2 produce many bright pixels corresponding to large protein complexes. These larger pixels were then mapped back to the cell in the selection map, which displays the higher-order structures localized at highly curved regions inside the cell. The white dashed box in the selection map (**Figure 2B**) clearly shows that cPLA₂ α localizes and oligomerizes on highly-curved vesicles rather than larger vesicles in the same cell. Although more pronounced for the mEGFP-cPLA₂ α construct, the mEGFP-cPLA₂ α -C2 construct was also able to generate oligomers in the absence of the catalytic domain.

Figure 2. cPLA₂ α oligomerizes on cellular membranes in A549 cells. A549 cells were transfected at 70–90%



confluency with mEGFP, mEGFP-cPLA₂ α or mEGFP-cPLA₂ α -C2 for 24 hours. All cells were treated with 10 μ M A23187 for 30 minutes then imaged with confocal microscopy. **A–C.** (from left to right) A representative image of RICS data displaying the cytoplasmic localization of fluorescent constructs in A549 cells. Each intensity and brightness plot shows protein oligomerization where increased brightness corresponds to larger protein structures. The selection map displays the selected pixels from the brightness plot mapped back to the cellular morphology. **D,E.** Results were quantified through the analysis of 11 separate cellular data sets from 2 independent experiments using the simFCS software. Graphs display the number of pixels on the y-axis and the size of EGFP-tagged protein on the x-axis (monomer, 6-mer, 12-mer, 18-mer and >18-mer). Results are plotted for EGFP (dot filled), EGFP-cPLA₂ α (solid filled), and EGFP-cPLA₂ α -C2 (hash filled).

To quantitate these results, 11 separate datasets were collected, normalized and analyzed for oligomerization (**Figure 2D,E**). We found that mEGFP-cPLA₂ α consistently generated more protein oligomers than mEGFP-cPLA₂ α -C2. The deletion of the catalytic domain reduced the enzyme's ability to form a vast number of vesicles, and may have contributed to the slight reduction in cPLA₂ α oligomerization, further supporting a potential role for the catalytic domain in this process. The

quantitative data also provide evidence that the C2 domain plays an important role in the formation of oligomers, given the presence of oligomers in the cells transfected with mEGFP-cPLA₂ α -C2, which completely lack the catalytic domain. Based on the N&B data, we propose that the C2 domain is likely to drive oligomerization in these cells.

3.3. cPLA₂ α -C2 Oligomerizes on Lipid Vesicles

We investigated the role of the cPLA₂ α -C2 domain in more detail using the molecular cross-linker EGS to covalently trap protein oligomers for analysis by SDS PAGE [37]. To determine whether oligomers could be detected, purified cPLA₂ α -C2 in the presence of calcium with or without POPC liposomes was allowed to react with EGS for 5 min (**Figure 3B,C**). We found that cPLA₂ α -C2 forms both trimers and larger protein complexes (with more than 14 subunits).

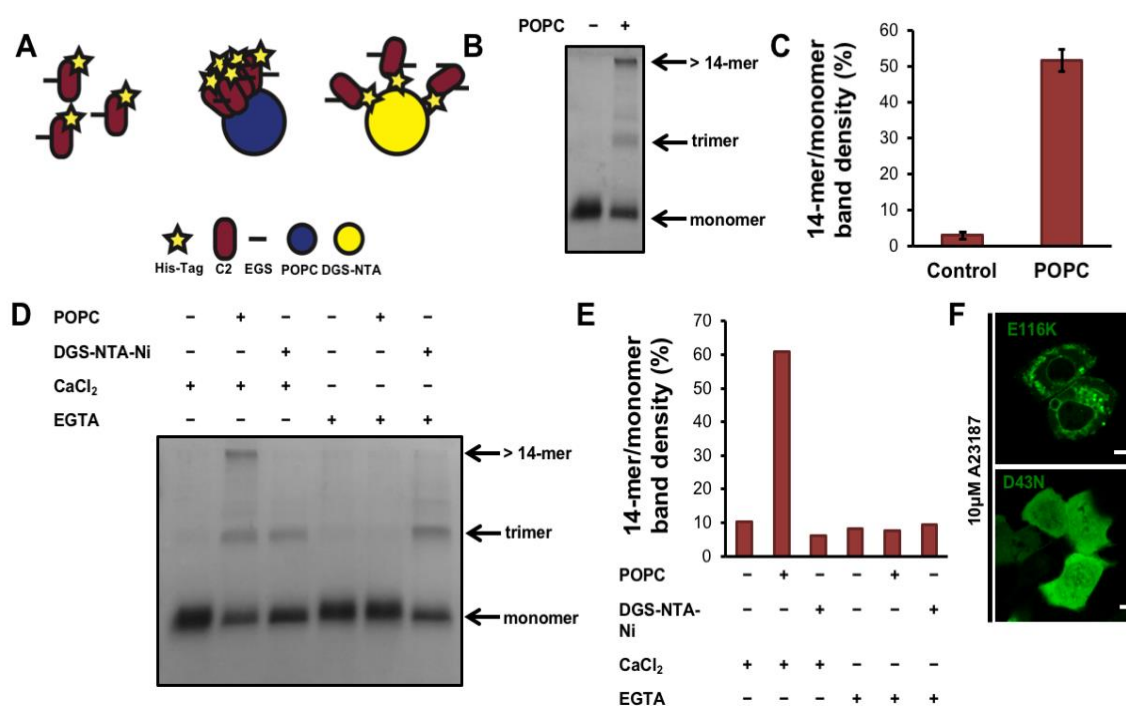


FIGURE 3. The cPLA₂ α C2 domain oligomerizes on lipid vesicles. **A**, schematic of the crosslinking assay displaying the possible experimental outcomes. **B**, 35 μ L of 1.5 mM POPC LUVs were incubated with 8 μ g of cPLA₂ α -C2 in 20 mM HEPES (pH 7.4), 160 mM KCl and 50 μ M CaCl₂ for 30 minutes. The protein was crosslinked using 0.5 mM EGS for 5 minutes, then the reaction was quenched with 150 mM Tris (pH, 8.0) for 5 minutes. The samples were run on 12% SDS-PAGE, stained with coomassie blue, destained for 120 min, and analyzed with ImageJ. **C**, Quantification of crosslinking experiments was completed in triplicate and normalized by dividing the >14-mer band density to the monomer band density as determined with ImageJ. **D**, POPC or DGS-NTA-Ni lipids were incubated with buffer either containing 50 μ M CaCl₂ or 100 μ M EGTA to chelate calcium. Each mixture was resolved using SDS-PAGE, stained with coomassie blue and destained. **E**, A representative quantification of D, which was performed independently in duplicate. Data was normalized as stated in C. **F**, A549 cells were transfected at 70-90% confluency with either mEGFP-cPLA₂ α -E116K or mEGFP-cPLA₂ α -D43N and imaged 24 hours post transfection. Cells were treated with 10 μ M A23187 for 30 minutes and representative images are shown.

To control for random diffusion within membranes and the restriction of the C2 domain to two dimensions, we designed an experiment using DGS-NTA-Ni lipids, which recruit His₆-tagged proteins to membranes. Liposome-bound proteins are restricted to two dimensions, in contrast to proteins in solution, which can move in three dimensions. The cPLA₂ α -C2 His₆ tag was used to recruit the protein to membranes in a nonspecific manner (Figure 3A,D,E). These results clearly showed that, in the presence of calcium and POPC liposomes, EGS traps cPLA₂ α -C2 in a specific oligomer with at least 14 subunits. In comparison, the DGS-NTA-Ni control experiments generated a nonspecific trimer band, which can be attributed to an artifact of the protein diffusing within the membrane during the short incubation with EGS. Quenching the calcium with EGTA abolished the POPC-dependent 14-mer but not the nonspecific trimer, confirming these results. Taken together, these data support the cellular N&B experiment showing that cPLA₂ α oligomerizes on membranes via its C2 domain in a calcium-dependent manner.

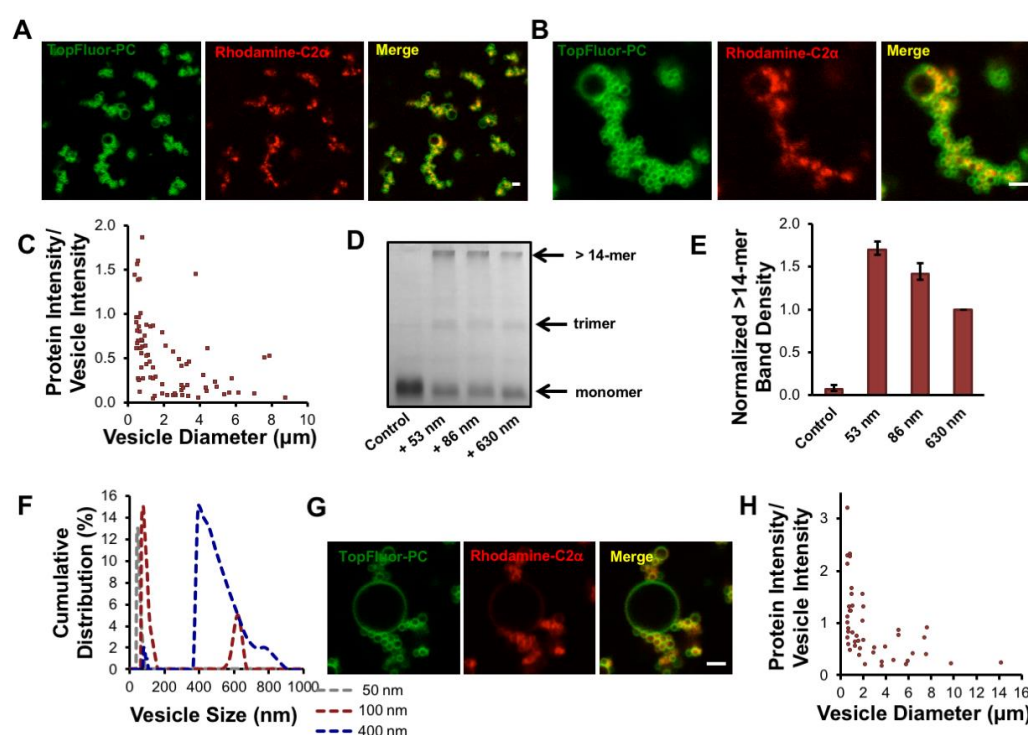


Figure 4. cPLA₂ α preferentially binds to highly curved membranes. **A–B**, TopFluorPC labeled GUVs with the lipid ratio (59.8:20:20:0.2) (POPC:POPE:POPS:TopFluorPC) were incubated with 2 μ M cPLA₂ α -C2-E116C labeled with Rhodamine Red® C₂ Maleimide (Rhodamine-C2 α) for 30 minutes then imaged with confocal microscopy. **C**, Protein intensity bound to lipids was normalized to the vesicle intensity in triplicate for vesicles ranging from 500 nm to 15 μ m in size as specified in the methods section. Vesicle size and intensity values were measured using ImageJ. **D**, The crosslinking experiment was repeated as stated in Figure 3B with POPC vesicles in buffer containing 20 mM HEPES, 160 mM KCl, 50 μ M CaCl₂, pH 7.4. **E**, Band density of the band > 14-mer was quantified from D using ImageJ and normalized to the > 14-mer band density for 630 nm vesicles. **F**, The number distribution of the vesicles used in D and E as measured with dynamic light scattering. **G**, 2 μ M cPLA₂ δ -C2 labeled with Rhodamine Red® C₂ Maleimide (Rhodamine-C2 δ) was incubated with GUVs as stated in A. **H**, Quantification was completed as stated in C. Scale bars are 2 μ m and error bars represent the standard error of the mean.

3.4. cPLA₂ Selectively Binds to and Oligomerizes on Membranes with Increasing Positive Curvature

To determine the mechanism of membrane bending by cPLA₂ α , we investigated the relationship between membrane binding and oligomerization *in vitro*. To visualize cPLA₂ α -C2 by confocal microscopy, we introduced a point mutation at E116 to provide a thiol group for labeling with the

reactive fluorophore Rhodamine Red C2 maleimide. The E116C mutation had no effect on the localization of cPLA₂ α or its ability to form intracellular vesicles (**Figure 3F**). To visualize membrane curvature induced by cPLA₂ α -C2, we incubated POPC:POPE:POPS:TopFluorPC GUVs with cPLA₂ α -C2-E116C-Rhodamine (Rhodamine-C2). The labeled C2 domain clearly induced membrane curvature, but selectively localized to vesicles with a small diameter (**Figure 4A,B**). To quantify this effect, we measured the protein and lipid content of more than 80 vesicles, each based on more than 20 images (**Figure 4C**). The results showed that Rhodamine-C2 preferentially localized to GUVs less than 2 μ m in diameter.

Given the refractive index limitations of confocal microscopy, we were unable to collect data for GUVs smaller than 500 nm in diameter. We hypothesized that cPLA₂ α not only binds more efficiently to highly-curved vesicles, but also undergoes more effective oligomerization in this setting. To determine whether the curvature-sensing trend continued for liposomes smaller than 500 nm in diameter, and to confirm our observation that oligomerization was enhanced on vesicles in A549 cells, cPLA₂ α -C2 oligomerization was measured using the EGS cross-linking assay with vesicles averaging 53 nm, 86 nm and 630 nm in diameter. The average vesicle size was measured by dynamic light scattering. In addition, using the apparent K_d and the surface area of the cPLA₂ α protein and liposomes, we calculated an occupied surface area far lower than the 20% coverage needed to induce curvature by membrane crowding [35]. These calculations revealed less than 7% surface area variation among the various vesicle populations, which cannot explain the large fold-change observed in this assay. We observed a significant difference ($p < 0.05$) in the degree of cPLA₂ α -C2 oligomerization between 630-nm vesicles and both the 53-nm and 86-nm vesicles (**Figure 4D,E,F**). A reproducible difference in oligomerization was also observed between the 53-nm and 86-nm vesicles, although the difference was not statistically significant ($p = 0.052$). To determine if C2 domains from other cPLA₂ isoforms can induce and/or sense membrane curvature, we expressed, purified and labelled the C2 domain of cPLA₂ δ , which selectively localized to regions of positive curvature as shown in **Figures 4G and H**.

3.5. cPLA₂ α Induces Vesiculation from the Golgi in Cholesterol-rich Vesicles

The cPLA₂ α protein consistently localizes to the highly-dynamic structure of the Golgi tubular and vesicular network [5,14,38] so we investigated the morphology of the Golgi body in A549 and HeLa cells transfected with the cPLA₂ α construct. As markers, we used the Golgi-localized fusion constructs mTurquoise2-Golgi [27] (**Figure 5**) and GOLPH3-GFP [39] (**Figure 6**). We found that the mCherry-cPLA₂ α fusion protein localized to the Golgi (**Figures 5 and 6**) and induced vesiculation in both A549 and HeLa cells (**Figure 5A**). The same activity was observed for the construct mCherry-cPLA₂ α -C2, showing that the C2 domain alone is capable of both localizing to the Golgi and inducing vesiculation (**Figure 5B**). To control for the overexpression of cPLA₂ α and potential nonspecific ER or nuclear localization and membrane bending, we expressed the markers mTurquoise2-ER and mTurquoise2-HA [27] but observed little co-localization in A549 cells (**Figure 5A**). These results, together with previous reports describing cPLA₂ α membrane trafficking [13,14], support our hypothesis that cPLA₂ α -dependent vesiculation originates from the Golgi.

An alternative cholesterol-dependent mechanism for cPLA₂ α -dependent membrane bending has been proposed based on a series of elegant cell-based experiments [13,15]. To determine whether these results translate into our experimental system in A549 cells, we treated the cells with TopFluor-Cholesterol (TopFluor-Chol), a fluorescent derivative of cholesterol that has similar phase transition properties to native cholesterol and is trafficked in a similar manner [40]. We found that cells treated with calcium ionophore generated cytoplasmic vesicles containing TopFluor-Chol co-localized with mCherry-cPLA₂ α or mCherry-cPLA₂ α -C2 (**Figure 5B**). These data support our hypothesis that cPLA₂ α -induced vesiculation occurs via a cholesterol-dependent mechanism in A549 cells and may be induced by the cPLA₂ α C2 domain.

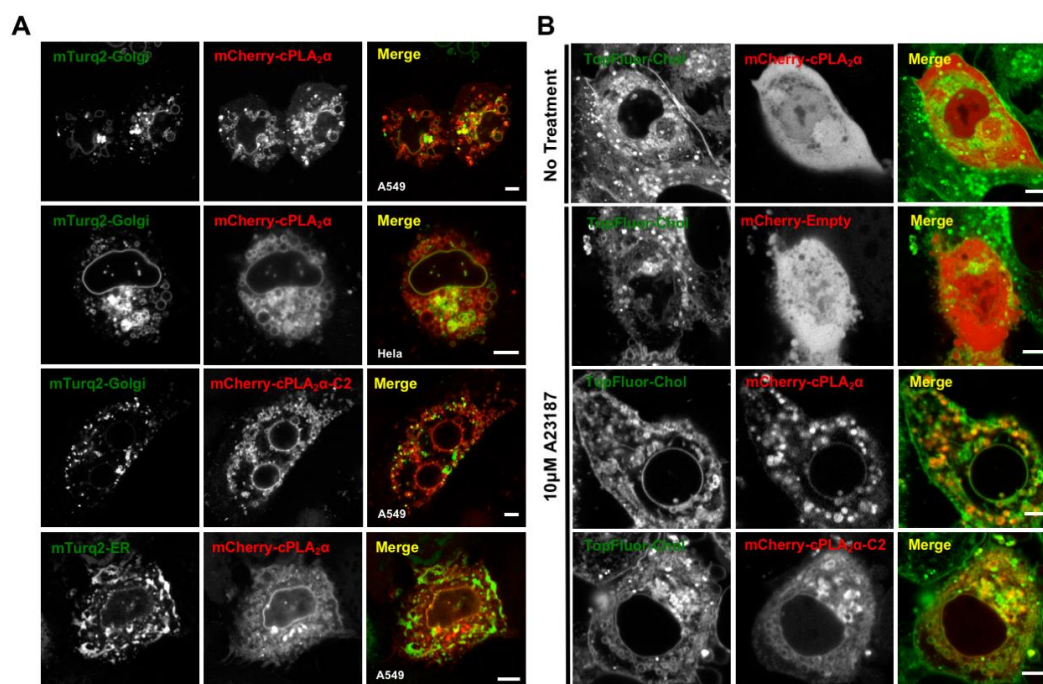


Figure 5. cPLA₂α vesiculates Golgi membranes and induces vesiculation in cholesterol enriched membranes. **A**, A549 or HeLa cells were transfected with either mTurquoise2-Golgi or mTurquoise2-ER and mCherry-cPLA₂α or mCherry-cPLA₂α-C2 for 24 hours, treated with 10 μM A23187 for 30 minutes and imaged with confocal microscopy to analyze cellular localization. **B**, A549 cells were transfected with mCherry-Empty (mCherry-lacking a fusion protein), mCherry-cPLA₂α or mCherry-cPLA₂α-C2 for 21 hours, then treated with 50 μM TopFluorChol (from the MβCD complex) for 3 minutes. Fresh medium was applied and the cells were incubated at 37 °C for 3 hours. Cells were then treated with 10 μM A23187 for 30 minutes and imaged for vesicle localization. All scale bars are 5 μm and the images were selected as representative images of the data collected.

3.6. CryoAPEX method for Transmission Electron Microscopy visualization of cPLA₂α localization

In order to gain more detailed insight into cPLA₂α localization and vesicle formation, we imaged HeLa cells expressing cPLA₂α-GFP co-expressed with a conditionally stable APEX2-GFP (csGBP-APEX2) binding nanobody [41] (**Figure 7**). The conditionally stable APEX2 allows for identification of protein localization following the conversion of the DAB substrate to precipitation of a DAB polymer, which is locally deposited [42]. HeLa cells expressing cPLA₂α-GFP and treated with calcium ionophore (**Figure 7A**), exhibited extensive vesicular structures that at high magnification (**Figure 7B and C**) demonstrate size heterogeneity and a lack of density within the vesicular structures. The indirect cryoAPEX was next applied using the aforementioned anti-GFP nanobody (csGBP-APEX2), which detected

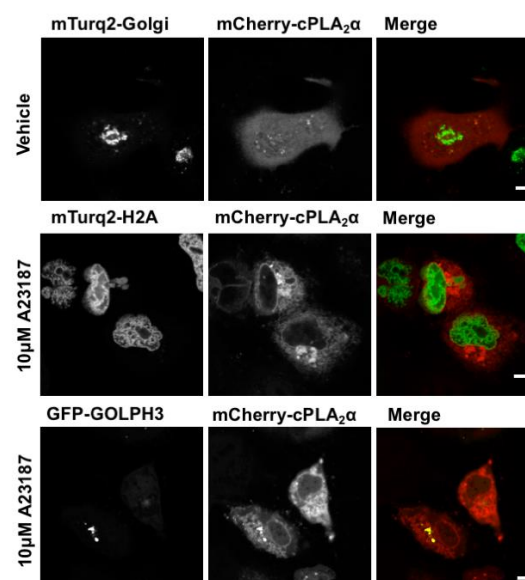


Figure 6. cPLA₂α localization with Golgi and nuclear markers. A549 cells were transfected with mCherry-cPLA₂α and the Golgi marker mTurquoise2-Golgi (top panel), mCherry-cPLA₂α and nuclear marker mTurquoise2-HA (middle panel), and mCherry-cPLA₂α and the Golgi marker GFP-GOLPH3 for 21 hours, then treated with 10 μM A23187 for 30 minutes and imaged for vesicle localization. Representative images before or after A23187 treatment are shown.

the APEX2 specific staining density corresponding to cPLA₂α-GFP around these vesicular structures (**Figure 7D-I**). Further, these stained vesicles were often found to be closely associated with mitochondria (**Figure 7G-I**, yellow arrow; red dots = mitochondria). A membrane bound structure resembling that of Golgi complex was also stained with APEX2 specific osmium, (**Figure 7H**, blue arrowhead), in agreement with cPLA₂α localization to the Golgi complex previously presented herein and in previous studies [5,14,38].

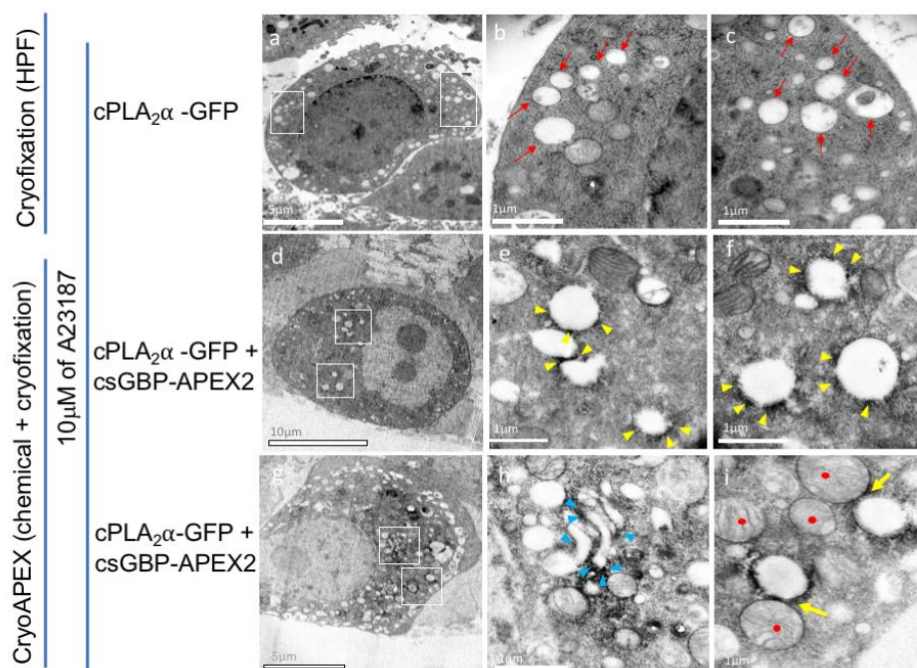


Figure 7. Cells ectopically expressing cPLA₂α in the presence of calcium ionophore exhibit extensive vesicular structures with detectable presence of cPLA₂α on vesicles and Golgi. **A**, Cryogenically fixed (HPF) HeLa cells expressing cPLA₂α when exposed to 10 μM A23187 results in the accumulation of vesicular structures in the cytoplasm. At higher magnification of the areas (**A**, white boxes) these vesicles show lack of density within and exhibit size heterogeneity (red arrows, **B** and **C**). **D**, Indirect cryoAPEX using an anti-GFP nanobody (APEX2-csGBP) tagged with APEX2 protein detected density corresponding to cPLA₂α-GFP in the cytoplasm at lower magnification. **E**, At higher magnifications the APEX2 specific osmium staining was apparent around these vesicles (**E** and **F**, yellow arrowheads) indicating the concentration of cPLA₂α in consonance with confocal imaging presented earlier.

The cryoAPEX method was also used to investigate changes to the Golgi apparatus following an increase in cytosolic calcium levels in cells ectopically expressing cPLA₂α-GFP or the cPLA₂α-C2-GFP protein constructs (**Figure 8**). For these purposes a HeLa stable cell line constitutively expressing the Golgi cis-medial marker α-mannosidase-II-HRP [43] was used to probe changes in appearances of the Golgi. Expression of cPLA₂α-GFP and an increase in the cytoplasmic calcium levels led to extensive dispersion of the Golgi from its typical perinuclear location (**Figures 8A-F**). At higher magnification, the dispersed Golgi appears to be mini-stacks with extensive herniation and vacuolization of the cisternae (**Figures 8E and F**, orange arrows). Similarly, in cells ectopically expressing the isolated cPLA₂α C2 domain, a clear dispersion of the Golgi was detectable (**Figure 8G**). At higher magnification, these dispersed Golgi appear to have almost completely lost cisternal structure with wide spread vesiculation of the ministacks (**Figures 8H and I**, orange arrows). In agreement with cell imaging presented above, either the C2 domain or full-length cPLA₂α were sufficient to disrupt host cell Golgi architecture and increase vesicular formation in cells, where vesicles were enriched with the presence of cPLA₂α.

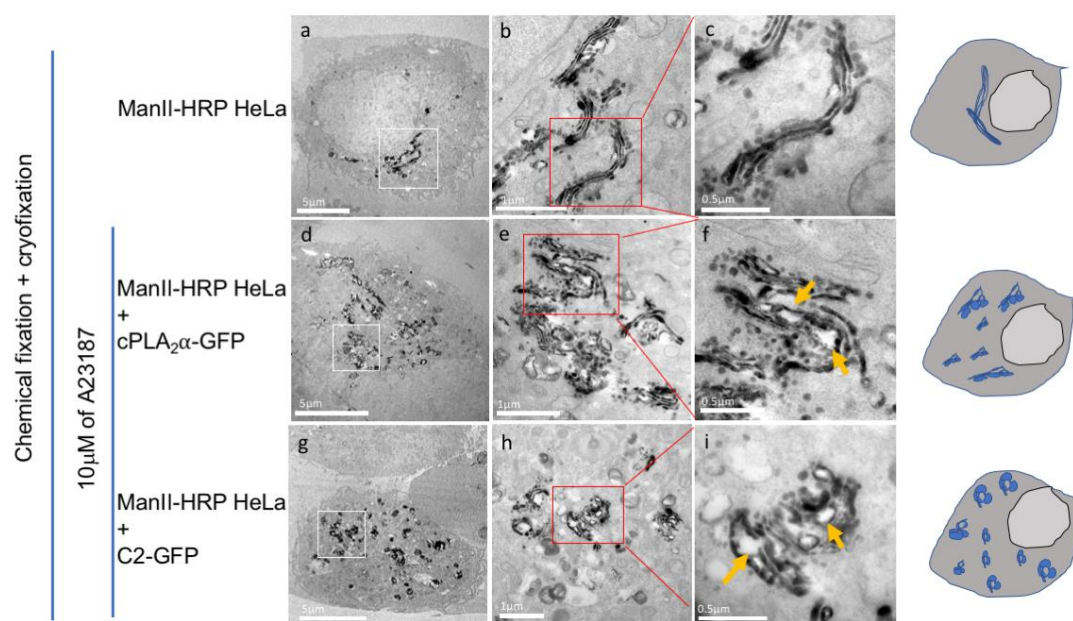


Figure 8. Ectopic cPLA $_{2\alpha}$ and/or C2 domain expression in the presence of A23187 induces vacuolization, fragmentation and dispersion of the Golgi apparatus. **A–C**, A HeLa stable cell line expressing mannosidase-II-HRP was used to image changes in Golgi apparatus morphology. A hybrid chemical-cryo fixation method was employed to demonstrate a typical perinuclear Golgi appearance and high quality of preservation of Golgi architecture in untreated control cells (**B** is a magnified image of **A** and **C** a magnification of the Golgi stack within red box in **B**). **D–F**, Ectopic expression of cPLA $_{2\alpha}$ in cells expressing the Golgi marker shows dispersion of Golgi from its typical perinuclear location. At higher magnification (**E** and **F**), these dispersed Golgi appear to be mini-stacks with extensive herniation and vacuolization of the cisternae (**E**, orange arrows). **G–I**, In cells ectopically expressing isolated cPLA $_{2\alpha}$ C2 domain, a clear dispersion of Golgi is visualized. At higher magnification, these dispersed Golgi appear to have almost completely lost cisternal structure with wide spread vesiculation of the ministacks (**H** and **I**, orange arrows). Cartoons of cells at the end of each row of image are provided to help summarize these results.

4. Discussion

We investigated the role of the C2 domain in the membrane curvature induced by cPLA $_{2\alpha}$ in order to gain insight into the underlying molecular mechanisms. We found that cells transfected with mEGFP-cPLA $_{2\alpha}$ showed pronounced vesiculation after treatment with the calcium ionophore A23187 (**Figure 1**). Although cPLA $_{2\alpha}$ is known to form tubules, and this process is dependent on its catalytic activity [15], cPLA $_{2\alpha}$ has also been observed to promote vesiculation in HeLa cells [13]. However, we are the first to show that this process can occur in live cells expressing cPLA $_{2\alpha}$ lacking a functional catalytic domain (**Figure 1**). We observed some tubulation (data not shown), but cells containing a vast number of cytosolic vesicles were the predominant phenotype (**Figures 1, 5 and 7**). To explore the molecular forces contributing to C2 domain-dependent membrane curvature in more detail, we used N&B analysis to measure oligomerization in real time. We observed cPLA $_{2\alpha}$ oligomerization in A549 cells, but also found that the cPLA $_{2\alpha}$ -C2 construct lacking the catalytic domain was also able to induce vesiculation and undergo oligomerization in cells, albeit to a less degree than the wild-type construct (**Figure 2**). By analyzing multiple datasets, we found that localization and oligomerization were concentrated at cellular regions featuring a high degree of curvature.

We therefore hypothesized that cPLA $_{2\alpha}$ can sense curvature and preferentially undergo oligomerization on highly-curved vesicles. Our *in vitro* experiments confirmed these results, given that cPLA $_{2\alpha}$ -C2 preferentially localized and induced curvature on vesicles ~50 nm in diameter, rather than those with diameters of ~80 or ~600 nm. To determine the physiological relevance of these

findings, we investigated cPLA α -induced membrane bending in the context of Golgi localization and cholesterol trafficking, finding that cPLA α and cPLA α -C2 localized to Golgi-derived vesicular membranes that were rich in cholesterol. These results are consistent with earlier findings [13,15], confirming the physiological relevance of membrane curvature induced by the C2-domain. Golgi-derived COPI and COPII vesicles are similar in size and curvature to the preferential targets for cPLA α -C2 membrane curvature and oligomerization [44]. Considering other reports suggesting the role that the catalytic domain plays in the generation of tubulation in cells, it is tempting to hypothesize that the C2 and catalytic domains work together to maintain a balance between vesicles and tubules to define the structure of the Golgi membrane.

Compared to other lipid-binding domains that can bend membranes, cPLA α -C2 is unique because it contains a C2 domain that penetrates membranes to a depth of 1–1.5 nm [8] in addition to a catalytic domain that generates lysophospholipids. The α -helix of the epsin ENTH domain penetrates the membrane to a depth of 0.2–0.5 nm [33] whereas most of the C2 domain lipid-binding surface penetrates into the membrane. We previously confirmed that membrane bending by cPLA α -C2 was dependent on deep membrane penetration using a series of hydrophobic mutants lacking the ability to penetrate or bend the membrane in several model lipid systems [24]. Unlike other lipid-binding domains that induce membrane curvature, the cPLA α catalytic domain converts phosphatidylcholine with an *sn*-2 arachidonyl chain to lysophosphatidylcholine and arachidonic acid. The production of lysophosphatidylcholine and release of arachidonic acid generates cone-shaped lipids, which are known to induce positive membrane curvature [44]. Our cell-based assays confirmed the importance of catalytic activity to membrane bending (**Figure 1**). In addition, we found evidence that supports the hypothesis that the C2 domain senses curvature and oligomerizes on the membrane to contribute to the generation of membrane curvature (**Figures 2–4**).

Our results indicate the following mechanism for cPLA α -induced membrane curvature (**Figure 9**). There is a 70–300 kcal/mol energetic barrier that must be overcome to induce and stabilize substantial curvature [16]. Therefore, we propose that cPLA α senses local regions of curvature and preferentially binds to these curved regions when calcium influx occurs within the cytoplasm. Targeting likely requires C1P in the Golgi, because basic residues in the β -groove greatly reduce localization [10,11]. It is therefore plausible that these regions are C1P-enriched in A549 and HeLa cells. The binding of cPLA α not only stabilizes the newly-curved membrane, but also allows the C2 domain to penetrate deeply into the hydrocarbon core of the bilayer to destabilize and bend the membrane. The stronger affinity for highly-curved membranes recruits additional cPLA α to the membrane, allowing the C2 domain to form oligomers and induce further membrane curvature. In addition to the actions of the C2 domain, the moment cPLA α arrives at the membrane the catalytic domain begins to generate the conical lysophosphatidylcholine and releases arachidonic acid from the membrane, promoting positive curvature. To our knowledge, this is the first curvature-inducing mechanism of its kind, with potential cooperation between a lipid-metabolizing domain and a lipid-binding domain.

Membrane curvature-inducing domains generate and stabilize curvature via complex mechanisms. The epsin ENTH domain was shown to bind PI(4,5)P $_2$ in the plasma membrane [20], causing a conformational shift that allows it to penetrate the membrane with its amphipathic α -helix [19]. The importance of membrane penetration is difficult to isolate from the experimental findings because mutating the membrane-penetrating hydrophobic and aliphatic amino acids also reduces the lipid-binding affinity of the domain [21,24]. Two recent studies used a model system with the synthetic lipid analog DGS-NTA-Ni [34,35], which interacts with His $_6$ -tagged proteins independently of membrane penetration. Both reports cast doubt upon the importance of membrane penetration by the epsin ENTH domain in the generation of membrane curvature. Although this is an incredibly powerful system to recruit proteins to lipid membranes, the experiments assume the biophysical properties of this long, bulky, charged head group behave like native lipid head groups. Considering the biophysical evidence showing that conical lipids are susceptible to the generation of spontaneous positive curvature [45] and the fact that the structural properties of DGS-NTA-Ni have not been

compared to more biologically-relevant lipids, these findings should be verified in a more biologically-relevant system.

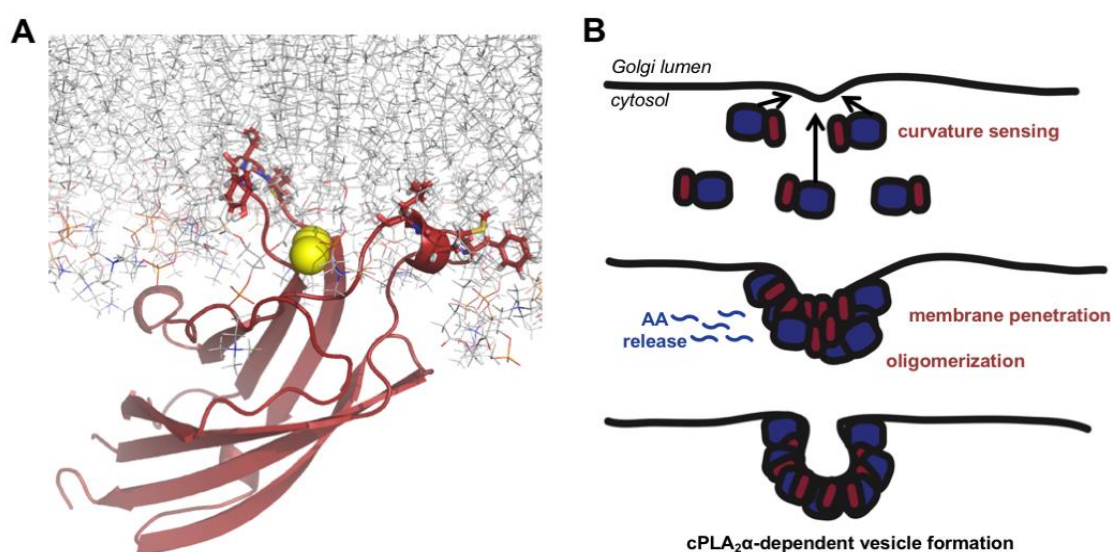


Figure 9. Mechanistic hypothesis of cPLA₂α induced membrane curvature changes, curvature sensing and vesicle formation. **A**, cPLA₂α-C2 (PDB 1CJY) shown penetrating into a POPC bilayer. The structure of the C2 domain is displayed as a ribbon in red, the hydrophobic penetrating residues are shown as red sticks and the POPC molecules are shown as lines. The sticks and lines are colored so that the hydrogen atoms are light grey, nitrogen atoms are blue and oxygen atoms are light red. **B**, A schematic of the current model for the generation of cPLA₂α-induced membrane curvature with contributions from membrane penetration, protein oligomerization and lipid metabolism of acyl chains at the *sn*-2 positions to produce arachidonic acid (AA) and lysophospholipid.

We provided the first evidence for C2 domain-dependent membrane bending based on a penetration-dependent mechanism [24]. We also showed that membrane penetration by calcium-binding loops 1 and 3 (previously shown to penetrate 1–1.5 nm into the membrane) promote the generation of membrane curvature, and both loops were essential for this process. Others have shown that the calcium-binding loops synaptotagmin-1 domains C2A and C2B penetrate the membrane, yet only the C2B domain induces curvature [23]. Recently, Doc2B was also shown to generate membrane curvature, but only the C2A domain is strictly necessary [25]. The difference in structure-function relationship between these proteins suggests that the C2 domains must be able to adopt different conformations that are capable or incapable of inducing membrane curvature. It is tempting to hypothesize that these C2 domains may also oligomerize on the membrane to stabilize membrane curvature. Oligomerization may help these C2 domains overcome the energetic barrier to form vesicles and tubules, while the tandem C2 domain may serve other purposes such as the regulation of membrane bending via protein-lipid or protein-protein interactions that contribute to the protein's overall function in cells. In support of this hypothesis, the recent structure elucidation of the cPLA₂α C2 domain bound to phosphatidylcholine and calcium contained three C2-domains in the asymmetric crystal unit [46]. Moreover, two asymmetric crystal units contained a total of six C2 domains, which demonstrated PC-binding increased C2 domain packing to form a tube-like structure. The authors of this seminal study suggest this crystal structure packing supports the notion of C2-induced positive membrane curvature changes (**Figure 9**), which couldn't previously be well visualized by crystal structures available for the non-lipid bound cPLA₂α C2 domain [7,47]. This recent crystal structure of the lipid bound C2 domain also supports the lipid-induced oligomerization [46] we have detected *in vitro* and in cells with the C2 domain and cPLA₂α.

The membrane penetration residues of the epsin ENTH domain were recently shown to play another role in the generation, stabilization and fission of vesicles. In contrast to the BAR domain, which stabilizes membrane curvature by generating rigid protein scaffolds [17,48], membrane penetration by the ENTH domain induces vesicle fission by destabilizing the vesicle neck [17]. This effect was enhanced by increasing the size of the membrane-penetrating hydrophobic residue [17]. Interestingly, enhancing the hydrophobicity of the membrane-penetrating loops in a simple system containing only synaptotagmin-1 causes the protein to generate vesicles less than 10–20 nm in diameter, suggesting that, like the epsin ENTH domain, membrane penetration by C2 domains may also promote vesicle fission independently, and future experiments should explore this possibility [23].

The cPLA₂ α protein was shown to localize to the Golgi, primarily the *trans*-Golgi network [14,38], which occurs in response to calcium influx and selective binding to C1P [9–11]. The relevance of cPLA₂ α membrane bending in terms of its cellular function is explored in several recent reports, supporting a role for cPLA₂ α -mediated membrane vesiculation via its catalytic activity. Experiments based on RNAi and acyltransferase inhibitors established a direct relationship between cPLA₂ α and the production of lysophosphatidylcholine [13]. Others have linked the catalytic activity of cPLA₂ α to the generation of Golgi-derived tubules and vesicles, suggesting that there may be a dual role for this enzyme in the maintenance of Golgi structure and trafficking [14,15]. Multiple studies have established a relationship between cPLA₂ α -dependent Golgi structures and cholesterol-enriched membranes, in agreement with our findings [12,15].

Finally, cPLA₂ α is known for its non-redundant role in the production of prostaglandins and eicosanoids in murine models of arthritis, asthma and cerebral ischemia [2,3]. The analysis of cPLA₂ α knockout mice revealed that the animals were infertile but otherwise showed no major defects. If cPLA₂ α has an important function in the maintenance of the Golgi structure and Golgi-derived endosomal trafficking, it is unclear how the cPLA₂ α knockout mice survive. Other cPLA₂ isoforms may compensate for the absence of cPLA₂ α and maintain its homeostatic functions. Such redundancy in endocytic signaling was recently confirmed when cPLA₂ ϵ was implicated in clathrin-independent endosomal trafficking, which was dependent on its catalytic activity [49]. Although few reports have considered the importance of the C2 domain in membrane bending induced by cPLA₂ α and cPLA₂ ϵ , we have shown that membrane penetration by the cPLA₂ α C2 domain and its subsequent oligomerization play a key role in this process. Our preliminary data shows that the cPLA₂ δ C2 domain also bends membranes and senses curvature (**Figure 4G and H**). It is possible that the cPLA₂ ϵ C2 domain also bends membranes, and this should be investigated in the future. Taken together, these recent findings suggest that the cPLA₂ α isoforms contribute to redundant cPLA₂ α -dependent membrane remodeling capabilities and prevent the cPLA₂ α knockout animals from showing appreciable symptoms in the absence of cPLA₂ α .

5. Conclusions

This study provides new insight into the generation of membrane curvature by C2 domains based on the analysis of cPLA₂ α *in vitro* and in cells. We found that the cPLA₂ α C2 domain oligomerizes and senses membrane curvature, preferentially targeting vesicles with a high degree of positive curvature. Given that these vesicles are comparable to those derived from the *trans*-Golgi network, this targeting is consistent with the cellular localization and *in vivo* function of cPLA₂ α . The selective targeting and oligomerization of cPLA₂ α on membranes of positive curvature is supported by studies showing that cPLA₂ α is involved in Golgi tubulation and vesiculation [12, 14]. We provide evidence for a new class of membrane-bending enzymes, where lipid asymmetry and C2 domain penetration and oligomerization may work together or independently to maintain the membrane structure of the Golgi. Our proposed oligomerization mechanism should be tested for other C2 domains that induce membrane curvature alone despite the presence of tandem C2 domains in the protein.

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preparation, K.E.W., R.V.S.; writing—review and editing, K.E.W., J.P., R.S., R.V.S.; supervision, R.V.S.; project administration, R.V.S.; funding acquisition, K.E.W., R.V.S.

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