EL PAPEL DEL DIACILGLICEROL EN EL TRÁFICO DE MEMBRANAS EN LA ZONA ENTRE EL RETÍCULO ENDOPLASMÁTICO Y EL COMPLEJO DE GOLGI

Tesis presentada por Inés Fernández Ulibarri
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Anexo
Diacylglycerol Is Required for the Formation of COPI Vesicles in the Golgi-to-ER Transport Pathway

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DIACYLGlycerol is necessary for trans-Golgi network (TGN) to cell surface transport, but its functional relevance in the early secretory pathway is unclear. Although depletion of diacylglycerol did not affect ER-to-Golgi transport, it led to a redistribution of the KDEL receptor to the Golgi, indicating that Golgi-to-ER transport was perturbed. Electron microscopy revealed an accumulation of COPI-coated membrane profiles close to the Golgi cisternae. Electron tomography showed that the majority of these membrane profiles originate from coated buds, indicating a block in membrane fission. Under these conditions the Golgi-associated pool of ARF GEF was reduced, but there was no effect on the binding of coatamer or the membrane fission protein CBP3/BARS to the Golgi. The addition of 1,2-diocanoyl-sn-glycerol or the diacylglycerol analogue phorbol 12,13-dibutyrate reversed the effects of endogenous diacylglycerol depletion. Our findings implicate diacylglycerol in the retrograde transport of proteins from Golgi to ER and suggest that it plays a critical role at a late stage of COPI vesicle formation.

INTRODUCTION

Recent observations from several laboratories indicate that membrane lipids regulate intracellular membrane transport, particularly in distal stages of the secretory pathway. Diacylglycerol (DAG) is a simple and small sized signal-transducing lipid which among other functions is necessary for protein transport from the Golgi complex to the cell surface both in yeast and in mammals. Thus, in budding yeast phosphatidylinositol (PI)-transfer Sec14p protein directly regulates DAG homeostasis in the Golgi complex and protein secretion (Bankaitis et al., 1990; Keum et al., 1997; Hulspas et al., 2000). In mammals, the reduction of DAG levels at the Golgi caused by the depletion of Nbs2 (a peripheral Golgi protein containing a PI-transfer domain) inhibits post-Golgi protein transport (Litvak et al., 2005). DAG acts in the trans-Golgi network (TGN) as a membrane acceptor for specific proteins such as the protein kinase C (PKC) family member PKD/ PKCe (Potke et al., 1996; Lijedahl et al., 2001; Baron and Malhotra, 2002), and Hnun13 (Speight and Silverman, 2005). PKD together with PKCδ, the trimeric G-protein subunits β/γ (Diaz Anel and Malhotra, 2005), and phosphatidylinositol-4 kinase IIβ (Hauesser et al., 2005) directly participate in the post-Golgi transport of plasma membrane proteins containing basolateral sorting information (Yeaman et al., 2004). On the other hand, Hnun13, through the recruitment of Rab34, participates in the Golgi-lysosome protein trafficking (Speight and Silverman, 2005). DAG also promotes the Golgi membrane targeting and activation of other C1 domain-containing signaling molecules such as other PKC isoforms (PKCγ, PKCe, and PKCδ; Maisel et al., 2006; Lehle et al., 1995; Wang et al., 1999, respectively) and Ras guanine nucleotide-releasing proteins (RasGRPs; Caloca et al., 2003), whose potential involvement in Golgi-associated transport functions remains unexplored.

The aforementioned Golgi-associated transport events linked to DAG levels can be envisioned in the framework of the DAG-phosphatidic acid (PA) interconversion. Thus, DAG is formed by phosphatidic acid phosphohydrolases (PAPs)—also known as lipid phosphate phosphatases (LPPs), and PA results from the activity of the DAG-consuming kinases (DAGKs). Although there are many DAGK isoforms, only DAGKδ and DAGKδ have been localized to biosynthetic compartments such as the TGN (Akesson et al., 2005) and the endoplasmic reticulum (ER; Nagaya et al., 2002), respectively. To date only the PAP2b isoform has been located in the Golgi complex but in a cell-type-dependent manner (Ciocca and Morris, 1999). PA is formed by de novo synthesis from glycerolaldehyde-3-phosphate or dihydroxyacetone-phosphate and acylCoAAs and

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DAG and the ER–Golgi Membrane Trafficking

Although the molecular details of its Golgi targeting are unknown, a combination of interactions between transmembrane proteins and the COPI coat and lipids has been postulated (Antony et al., 1997; Bigay et al., 2003; Mesmin et al., 2007).

Here, we test the hypothesis that DAG regulates membrane trafficking at the ER–Golgi interface. We used a variety of pharmacological compounds that compromise cellular DAG production. Briefly, we found that the decrease of Golgi-associated DAG levels inhibits retrograde (Golgi-to-ER) but not anterograde (ER-to-Golgi) protein transport, reducing the ARF-GAP1 pool in the Golgi complex and increases the amount of COPI-coated buds. These findings indicate that DAG participates in the fusion of COPI transport carriers derived from early Golgi compartments.

MATERIALS AND METHODS

Reagents, Antibodies, and Plasmids

Brefeldin A (BFA), fumonisin B1 (FB1), O-phenyl-C(5.2.1.0)6-ethyl dothiorcarbamoyl potassium salt (D689), 2-diacyl-sn-glycerol (DOG), phenol 12-methoxy-13-aracne (PMA), phenol 12,13-di-riboflavin (PDR), apo-AIV, AGIV, AGIV-C, PDAI, anti-β-tubulin, anti-FLAG monoclonal antibodies, and TRITC (tetramethylrhodamine isothiocyanate-phalloidin were purchased from Sigma (St. Louis, MO). Larsson (B. nordacaulis), propolisol, and trofortol were from Calbiochem (San Diego, CA). Rabbit polyclonal antibodies against the KDEL receptor (KDEL), galactosyltransferase (Gat), and mannose-6-phosphate receptor (M6P) were kindly provided by the late H-D. Stöhr (University of Göttingen). E. Berger (University of Zurich, and K. Moremen (University of Georgia, Athens), respectively. Mouse monoclonal antibodies to giantin, mCOPI, and mARF were provided by H-P. Haure (Biorecherche, Basel), F. Wieden (University of Heidelberg), and M. Brenner (Institute Curie, respectively. mAB to mBAR was both provided by A. Luzia (Concorzio Monte Nago Sud CMN, Cerno, Italy) and purchased from BD Transduction Laboratory (San Diego, CA). Secondary antibodies conjugated to Cy3- or fluorescein isothiocyanate (FITC)-labeled fragments were from Jackson Immunolaboratories (West Grove, PA). Plasmids encoding EGFP-C1–BARs and EGFP-ARF-GAP1 were from I. Merola (Consorzio per le Informazioni Scientifiche, Madrid) and H. G. Gad (CMN, Chieti, respectively). Unless otherwise stated, all other chemicals were from Sigma.

Cell Lines and Cell Culture

COS-1, NRK-Vero, and HeLa cells, including stable HeLa cells that constitutively express YFP-C1–BAR or GST-FLAG-TRI2 (a gift of V. Maltby, University of California, San Diego, CA), were cultured in DMEM (Invitrogen, Paisley, United Kingdom) containing 10%–20% of fetal calf serum (FCS) (GIBCO/BRL, Invitrogen, Paisley, United Kingdom). HeLa spinner cells were cultured in RPMI 1640 (Biochrom, Berlin, Germany) containing 7.5% FCS. All culture media were supplemented with sodium pyruvate (1 mM), glutamine (25 mM), penicillin (100 U/mL), and streptomycin (100 μg/mL). Cells were grown in a humidified incubator in 5% CO2 at 37°C.

Isolation of Golgi Membranes

Golgi fractions from HeLa cells were prepared by a modification of the method established by User et al. (1983). Cells were plated on coverslips and cultured in serum-free medium. After 48 h, the medium was replaced with fresh medium containing 10% FCS and 10 μm nocodazole, and the cells were exposed to 1 μm calpeptin for 30 min, washed with PBS (10 min at 500 g), and then resuspended in the buffer (250 mM sucrose in 10 mM Tris-HEC, pH 7.4) by ultrasonication. The homogenate was then centrifuged at 10,000 rpm for 10 min. The supernatant was finally adjusted to 10 μM Tris-HEC, pH 7.4, and EGT (1 mM, final concentration). Twenty milligrams of protein was used for each experiment. The supernatant was centrifuged at 100,000 rpm for 1 h. The pellet was then washed with 10 mM Tris-HEC, pH 7.4, and the protein concentration was determined.

Diacylglycerol Content

Golgi membranes isolated from control and propanolol-treated cells were extracted in glass tubes with chloroform/methanol (CHCl3/H2O, 2:1, v/v, with 0.01% Na2SO4) and analyzed by high performance liquid chromatography (HPLC) (Hich and Drey, 1985). To determine the diacylglycerol content in these lipid extracts, an accurate conversion to [3H]phosphatidic acid by diacylglycerol kinase was performed as described (Fiers et al., 1987). Chloroform extracts (800 μl) of isolated Golgi membranes (50 μg) or 1-n-octanol-2-chloroethyl ether-glycerol

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(Sigma) samples (30–500 pmol) were evaporated under a gentle stream of nitrogen, and the dried lipids were solubilized in 20 μl of 7.5% octyl-β-D-glucoside, 5 μM cardiolipin, and 1 mM dioleoylphosphatidylethanolamine acid (DETPAPC) by sonication in a bath (50–60 Hz) for 30 s, after incubation for 10 min at room temperature. To this lipid solution, we added 50 μl of 100 mM imidazole/HCl buffer, pH 6.5, containing 100 mM NaCl, 25 mM MgCl₂, and 2 mM EDTA, and then 10 μl of fresh 20 mM diisothitethidium (DITT) in 1 mM DETRAPC, 10 μl of a 100 μg/ml proteinase K solution (Calbiochem) solution (0.25 mg/ml) in 20 mM imidazole/HCl buffer, pH 6.5, containing 2 mM DETRAPC. The reaction was started by adding 10 μl of 100 mM imidazole/HCl buffer, pH 6.5, containing 1 mM DETRAPC, 10 μl of ATP, and 0.06 μg of the p39, p43, p19, and p12/ATP (Amersham Pharma Biotech, Piscivannay, NJ) cocktail, and was carried out for 30 min at room temperature. Reactions were stopped by addition of 0.2 ml of water and chloroform, in order to split two phases. The lower (chloroform) phases were washed with chloroform-saturated methanol/water (1:1), evaporated under nitrogen, dissolved in 20 μl of chloroform/methanol (1:1), and developed on silicagel 60 thin-layer chromatography plates (Merck, Darmstadt, Germany) using the solvent systems: hexane/ethyl acetate/methanol/water (100:60:16:8) vol/vol/vol/vol, or air-dried. [3H]Phospholipid acid was quantified using Phosphorimage (Molecular Dynamics, Sunnyvale, CA) and NIH Image software.

Transient Transfections

Cells were grown to 70–80% confluence and then transfected either with EGF-pcDNA3 or FGF-AR-FLAG-APF using the Effectene transfection method (Qiagen, Valencia, CA) according to the manufacturer’s instructions. Unless otherwise indicated, experiments were carried out 12–16 hr after transfection. Cells expressing EGF-pcDNA3 or FGF-AR-FLAG-APF for each microscopy were treated with cycloheximide (100 μg/ml) 60 min before the assay.

YSV-G Infection and YSV-G Transport Assay

Experiments were carried out as previously indicated (Vakilzadeh et al., 1998).

Immunofluorescence and Quantitative Image Analysis

Indirect immunofluorescence assays were carried out using the following antibody dilutions: anti-EGF, 1:100; anti-FGF, 1:100; anti-FLAG, 1:500; anti-GFP, 1:100; anti-MAP-2, 1:100; anti-HA, 1:500; anti-p53, 1:50; anti-anti-GFP, 1:50; and anti-anti-FLAG, 1:50. Immunofluorescence images were taken on a Leica TCS NT confocal microscope (Leica, Heerbrugg, Switzerland). The images were processed using Image J software. To quantify cytoplasmic fluorescent punctate structure containing KDEL, right-side gastric scale immunostained images were set at an arbitrary threshold value of 0. For each cell, the number of stained structures (defined as being smaller than 600 pixels) over threshold was scored covering the total cytoplasmic area.

Time-Lapse Fluorescence Conical Microscopy

Time-lapse fluorescence confocal microscopy experiments were carried out using a Leica TCS-3D laser-scanning confocal spectral microscope (Leica Microsystems Heidelberg, Manhatten, Germany) with Argon and HeNe lasers attached to a Leica DMIRE2 inverted microscope equipped with an incubation chamber and a temperature-controlled stage. For visualization of GFP images were acquired using a PL APO 63× oil immersion objective lens (NA 1.2, 63×, water immersion; Zeiss, Thornwood, NY), a high-speed 1024 line, reciprocating beam splitter RSP 500, and an emission range detector: 500–610 nm and the confocal pinhole set at 0.45 Airy units. Images were acquired at 30-s intervals for 1–2 hr, and optical sectioning was necessary to capture the whole signal. The excitation intensity was attenuated to 5% of the halogen power to avoid significant photobleaching. Image treatment and movie assembly were performed using the Image Processing Leica Confo. Software. PMMA (200 rpm) was added to DEMEM after the first frame, and images were recorded every 10 s. Then, after the forty-first frame, DOG (3 μM) or Fura2 (250 μM) was mixed with Fura2. Propranolol (60 μM) and DOG (5 μM) were added to DEMEM after the first frame. Cells were preincubated with DOG (6 μM, 15 min) and then mixed with propafenol and images were recorded every 10 s. Fura2 (2 μg/mg ml), prostate (60 μM), or Fura2 together with propranolol was added to the DEMEM in the same conditions, but to this case images were acquired every 10 s. Films and time series of fluorescent images taken from films were processed using Immunflu. Image J software.

Electron Microscopy, Electron Tomography, and 3D Modeling

For transmission electron microscopy (TEM), Vero, NRK, and Hela cells were rapidly fixed with 1.5% glutaraldehyde in PIPES buffer (0.1 M, pH 7.4) containing 2% and 18% sucrose and 2% and 18% glucose (2 ml) for 10 min at 37°C. Cells were then gently scraped, pelleted at 1000 x g for 10 min, rinsed in PIPES buffer (3 x 5 min), and postfixed with 1% (wt/vol) OsO₄, 1% (wt/vol) KCl, and 50% (vol/vol) in PIPES buffer for 1 h at room temperature in the dark. Cells were then treated for 5 min with tissue acid (0.3%) in PIPES buffer, rinsed in distilled water, block-stained with 1% uranyl acetate in 70% ethanol for 1 h, dehydrated with graded ethanol solutions, and finally embedded in Epon plastic resin (EMS, Hatfield, PA). Ultrathin sections (0.6–700 nm) thick were stained with lead citrate and observed on a JEOL 1010 electron microscope (Peabody, MA). Micrographs of randomly selected areas were obtained with a Gatan digital camera (Fuessen, CA) at the same final magnification (50,000 x or 80,000 x) and analyzed using point-counting procedures. The stereological parameters were determined using standard procedures. The minimum sample size of each stereological parameter was determined by the progressive mean technique (confidence limit of 5%). The results were expressed as means ± SD and compared using Student's t test.

For electron tomography and 3D modeling, sections (250 nm) of chemically fixed, Epon-embedded NRK cells were transferred to formvar-coated copper slot grids. Collodial gold particles (10 nm) were added to one side of the grid as markers to align the series of tilted images. Tile series of representative Gogli stacks were automatically recorded (Zwaan et al., 2002) at 200 kV using a Tecnai20 electron microscope (FEI/Philips Electron Optics, Eindhoven, The Netherlands equipped with a slow-scan CCD camera (TemCam F24, TVIPS (Thiet Video and Image Processing System), Gauting, Germany) and a motorized goniostat. Recording was made with Serial 3D software package; FIB at a final magnification of 14,000 x. Every specimen was tilted about two orthogonal axes from −45° to 45° at 1° intervals, resulting in two datasets of 121 microtomizations digital images. Images were then aligned using the program package IMOD (Kremer et al., 1996), and a tomogram was computed from each tilt series. The two single-axis tomograms were merged into one (Mammoto, 1997), and the tomographic dual-axis reconstruction was interpreted and modeled using IMOD software.

Statistical Analysis

For statistical computation and estimation of significance, we used the online software GraphPad (San Diego, CA; www.graphpad.com). Control and differently treated cells were run through unpaired ANOVA and, when appropriate, Student's t test.

RESULTS

Both Propanolol and U73122 Reduced DAG Levels in the Golgi Complex

To study the role of DAG in protein transport at the ER-Golgi interface, we examined a range of pharmacological agents (Figure 1) that had been reported to decrease DAG levels in a wide variety of cell types. These compounds are as follows: 1) Propanolol, which inhibits FAP and therefore prevents dephsophorylation of PA to DAG (Pappu and Hausser, 1983; Roberts et al., 1998; Baron and Malhotra, 2002); 2) D609, which inhibits PC-specific PLC (Schütze et al., 1992; Exton, 1994) and SNS (Scherber and Hanman, 1998); 3) U73122, which inhibits PPI-PLC (Blaasdale et al., 1990; Thompson et al., 1991; Jun et al., 2004); and 4) FBL, which inhibits ceramide synthase and thus de-activates SM synthase of substrate and lowers DAG (Wang et al., 1991; Wu et al., 1995; Merrill et al., 2001). First, we examined whether these compounds perturb the organization and dynamics of microtubular and actin cytoskeletons, because an efficient ER-Golgi interface membrane trafficking is dependent on the integrity of both cytoskeletons (Murfish and Pessey, 2004; Egea et al., 2006). NRK and Vero cells treated with propanolol (60 μM/30 min), U73122 (6 μM/30 min), D609 (500 μM/30 min), or FBL (25 μg/ml/24 h) showed microtubule and actin cytoskeleton organization (Supplementary Figure 1A) and dynamics (Supplementary Figure 1B, C and D) that was indistinguishable from control. However, D609 blocked the reconstitution of microtubules (Supplementary Figure 1B) and actin filaments (unpublished data) that was expected after the respective removal of nocodazole and latrunculin B. Consequently, we ruled out the use of D609.

We then examined the effects of propanolol, U73122, and FBL on the DAG pool in the Golgi complex. We used the concentrations stated above, so that the cytoskeleton would not be compromised. We used 1) the inactive mutant form of PDK (PKD-K618N/PKD-KD), 2) a biochemical assay to
measure DAG levels in Golgi fractions isolated from treated cells, and/or (3) the DAG-dependence localization of the CI domain of PKCδ in the Golgi (see below). With respect to the former approach, it is known that DAG is sufficient and necessary for the recruitment of PKD to TGN membranes (Maeda et al., 2001). Thus, the HeLa stable cell line expressing GST-flag-PKD-KD was treated with propanolol, U73122, or FB1. After 15 min of treatment with propanolol (Figure 2, C and D), U73122 (Figure 2, E and F), or FB1 (unpublished data; see Baron and Malhotra, 2002), PKD-KD was redistributed from the Golgi to the cytoplasm. Moreover, PKD-KD returned to the Golgi when propanolol (Figure 2, E and F), U73122, or FB1 (unpublished data) was washed out. We also measured DAG in Golgi membranes isolated from HeLa cells treated with propanolol or U73122. Both propanolol and U73122 decreased DAG levels to ~45% of control values (Figure 2B). In addition, FB1 (as well as propanolol and U73122) induced the complete redistribution of the GFP-C1b domain of PKCδ from the Golgi to the cytoplasm (Supplementary Figure 3B and see below). This is indicative of a robust decrease of the DAG pool in the Golgi caused by FB1 treatment. Therefore, propanolol, U73122, and FB1 diminished Golgi-associated DAG levels without altering the organization and dynamics of actin or microtubular cytoskeleton. This validates their use in examining the potential involvement of DAG in membrane trafficking at the ER-Golgi interface.

Propanolol and U73122 Blocked the Retrograde But Not Anterograde Membrane Transport

To assess whether the maintenance of DAG levels in the Golgi is required for ER-Golgi interface membrane trafficking, we examined the ER-to-Golgi transport of VSV-G protein. Cells were infected with the tsO45 VSV mutant, which

![Diagram](image)
at nonpermissive temperature (40°C) was retained at the ER (Supplementary Figure 2A). When cells were transferred to permissive temperature (32°C), VSV-G was transported to the plasma membrane (Supplementary Figure 2C) crossing the Golgi complex (Supplementary Figure 2B). When VSV-infected cells were treated with propanolol, U73122, or F1, VSV-G transport from the ER to the Golgi was unaltered (Supplementary Figure 2, E, H, and K, respectively). In accordance with these results, neither propanol nor U73122 (unpublished data) nor F1 (Supplementary Figure 3) affected the normal reassembly of the Golgi in BFA-washed-out cells. Interestingly, the VSV-G post-Golgi transport to the plasma membrane was blocked only in propanol- and F1-treated cells (Supplementary Figure 2, F and L, respectively) but not in those cells treated with U73122 (Supplementary Figure 2D).

Next, we examined the effect of low DAG in the Golgi on Golgi-to-ER transport. When propanolol, U73122, or F1 was added successively to BFA, the Golgi disassembly occurred normally (unpublished data). Conversely, when BFA was added either at the same time as, or just after, the pretreatment with propanolol or U73122, the redistribution of Golgi markers (Figure 3, A–D) to the ER was blocked. Strikingly, F1 had no effect on the normal Golgi disassembly produced by BFA (Supplementary Figure 3A). Thus, unlike F1, propanolol and U73122 perturb the Golgi-to-ER membrane flow. To confirm this result in a more physiological setting, we examined the subcellular distribution of the KDELr; KDELr mediates the return to the ER of ER-resident proteins that have escaped to the Golgi. At steady state, KDELr was observed both in the Golgi and in numerous punctate cytoplasmic structures, which represent tubulovesicular structures that are continuously cycling between the ER and the Golgi (Figure 3E). Any modification of this distribution reflects an alteration in the retrograde or anterograde traffic rates (Lewis and Pelham, 1992). In Vero cells treated with propanolol (Figure 3F) or U73122 (Figure 3G), KDELr staining was reduced in cytoplasmic fluorescent punctate structures (Figure 3H). Similar morphological features were also observed in NRK and HeLa cells (unpublished data). Moreover, morphological alterations were more robust in propanolol-treated than in U73122-treated cells (compare quantitative analysis shown in Figures 3, D and H). Cells treated with F1 did not show any alteration in the subcellular distribution of KDELr (unpublished data). Taken together, our results indicate that only DAG pool(s) altered by propanolol and U73122 seem to be required for retrograde (Golgi-to-ER) but not for anterograde (ER-to-Golgi) membrane trafficking.

It has been postulated that the inhibition by propanolol of PAP/LP and the inhibition by U73122 of PI-PLC may reduce different molecular species of DAG (Carrasco and Merida, 2004). Therefore, we examined whether propanolol or U73122 have an additive or synergetic effect on the Golgi-to-ER protein transport. Cells were treated with lower concentrations of propanolol and U73122 that do not alter BFA-induced Golgi disassembly (unpublished data) or the subcellular distribution of KDELr (Supplementary Figures 5, A and B). When propanolol and U73122 were added together there was an inhibition of the BFA-induced Golgi-to-ER membrane backflow (unpublished data) and a change in the subcellular distribution of the KDELr (Supplementary Figure 4C). These findings were indistinguishable from those observed for each compound used separately at higher

Figure 3. Propanol and U73122 block the BFA-induced Golgi disassembly and alter the steady-state staining pattern of the KDEL receptor. (A–D) Vero cells were treated with BFA (5 μg/mL) for 20 min alone (A), with propanolol (60 μM) plus BFA (propanolol was added 5 min before BFA; B), or U73122 (6 μM) plus BFA (U73122 was added 5 min before BFA; C). Cells were then processed for immunofluorescence microscopy using monoclonal anti-CTR433 to visualize the Golgi complex (see inset in A for control cells). Both propanol (B) and U73122 (C) blocked the BFA-induced disassembly of the Golgi complex (A). Quantitative analysis of these results is shown in D (E–H). The steady-state subcellular distribution of KDEL receptor (KDELr) using anti-KDELr polyclonal antibodies was also examined in control and propanol (60 μM) or U73122 (6 μM) treated Vero cells. Both propanolol and U73122 treatments induced a significant change in the steady-state staining pattern of the KDELr: the fluorescent cytoplasmic KDELr-containing punctate structures are no longer seen. These observations were quantified, as shown in H. Statistical significance, **p ≤ 0.01 and ***p ≤ 0.001. Bar, 10 μm.
concentrations (Figure 3, F and G). Next, when cells were coimmunoprecipitated with the usual working concentrations of propanol (60 µM) plus U73122 (6 µM), the change in the subcellular distribution of KDELr lasted longer than when the two agents were used separately (120 vs. 60 min). Similarly, coimmunoprecipitation resulted in a more persistent inhibition of BFA-induced Golgi (60 vs. 30 min). Overall, these results indicate that different pools of DAG participate in Golgi-to-ER membrane trafficking.

**Propanol and U73122 Perturbed the BFA-induced Formation of Tubules from Golgi Membranes**

Next, we analyzed whether the inhibition of the BFA-mediated redistribution of Golgi membranes to the ER by propanol and U73122 is the result of the inhibition of BFA-induced coatomer dissociation. We examined the kinetics of dissociation of coatomer from Golgi membranes in the presence of BFA using anti-β-COP antibodies (Supplementary Figure 5). Propanol or U73122 added just before or at the same time as BFA did not inhibit the BFA-induced dissociation of coatomer from Golgi membranes (Supplementary Figure 5, H and K). The distribution of β-COP was affected neither by propanol nor U73122 (Supplementary Figure 5, C and D). After the dissociation of coatomer and ARF1 from Golgi membranes (Klausner et al., 1992), BFA promotes the formation of Golgi-derived tubules that finally fuse to the ER. Next we examined whether propanol and U73122 impair the Golgi tubulation induced by BFA. We used time-lapse images of Hela cells expressing YFP-tagged GalTase recorded during the treatment with propanol or U73122 plus BFA (Figure 4). As expected (Schiroy et al., 1997), cells treated with BFA alone showed numerous thin Golgi-derived tubules, which after a few minutes irreversibly fused with the ER, leading to the disappearance of Golgi fluorescence (Figure 4A; Supplementary Video 1). Propanol not only reduced the density of BFA-induced tubules emerging from the Golgi but also increased their diameter (compare Figure 4A, panel 7 with 4B, panel 10, arrow; also compare Supplementary Video 1 with Supplementary Video 2). Moreover, the few thick tubules produced by BFA in the presence of propanol grew in length but failed to fuse with the ER, with most returning to the Golgi (white arrow in Figure 4B; Supplementary Video 2). U73122-treated cells also showed a significant slowing-down of the BFA-induced Golgi tubulation process but tubules were similar to those seen after BFA treatment alone. As observed in propanol-treated cells, they also remained in the cytoplasm for longer (unpublished data). Hence, the decelerated Golgi disassembly induced by BFA in propanol- or U73122-treated cells was not caused by an alteration in the kinetics of coatomer dissociation from Golgi membranes. Rather, both agents interfered with the formation and the progress of Golgi-derived tubules and/or their subsequent fusion with the ER.

**DOG and PDBu prevented the Propanol or U73122-induced Inhibition of Retrograde Transport of KDELr**

To establish a direct link between the effects of propanol or U73122 on ER–Golgi interface membrane trafficking and the decrease of DAG pool in the Golgi, we examined whether these trafficking alterations would be prevented by the exogenous re-supplementation of the DAG pool. We used short acyl chain DOG and the DAG analogue PDBu. Control experiments demonstrated that neither DOG (5 µM) nor PDBu (250 nM) altered the actin or microtubule cytoskeleton (unpublished data). We next checked that DOG and PDBu are indeed incorporated into Golgi membranes. We took advantage of the fact that DAG pools are recognized by proteins that contain a conserved sequence of 50 amino acids, the so-called C1 domain (Colón-González and Kazanietz, 2006). This is the case of PKCβ, whose C1b domain behaves as a sensor of DAG (Quest et al., 1994). When cells were transfected with the GFP-C1b domain and treated with phorbol myristate acetate (PMA), a hydrophobic DAG analogue that it is preponderantly incorporated into the plasma membrane, the GFP-C1 domain in the Golgi (Figure 5, B and E) was reduced (Figure 5A), because it was quickly redistributed to the plasma membrane (Figure 5, C and F; Supplementary Video 3) as previously reported in other cell types (Carrasco and Merida, 2004). Less than 20% of Golgi-associated GFP-C1b domain fluorescence in PMA-treated cells remained at the Golgi after 5–10 min of PMA treatment (Figure 5A). At longer times, the fluorescence rose very slowly (Figure 5A; Supplementary Video 3). On this basis, we added DOG or PDBu at the moment at which the Golgi associated GFP-C1b fluorescence was the lowest (between 5 and 10 min after PMA treatment). We expected to see a

![Figure 4](image)

**Figure 4.** Propanol impairs both the formation of normal BFA-induced Golgi-derived tubules and their subsequent fusion to the ER. Time series of fluorescent images taken from films of HeLa cells constitutively expressing YFP-GalTase during the Golgi disassembly induced by BFA (5 µg/ml; A) or propanol (60 µM) plus BFA (B). BFA induced the formation of thin YFP-GalTase-containing tubules emerging from the Golgi (5- and 7-min frames). Subsequently, tubules fused with the ER, giving rise to the characteristic ER-like shining pattern (10-min frame). In contrast, propanol pretreatment prevented BFA-induced Golgi disassembly (B). After 25 min of propanol plus BFA treatment, the Golgi was still clearly visible (B) and a representative large, thick tubule emerging from the bottom of the Golgi was seen to grow and then retract into the Golgi. Videos corresponding to frames shown in A were obtained from Supplementary Video 1 (YFP-GalTase HeLa cells plus BFA) and those shown in B were from Supplementary Video 2 (YFP-GalTase HeLa cells propanol plus BFA).
Figure 7. DOG and PDBu prevent the propanol-induced alteration of the subcellular distribution of the KDELr. Vero cells were treated for 1 h with DOG (3 µM B), PDBu (250 nM C), propanol (60 µM D), DOG plus propanol (E), or PDBu plus propanol (F). Thereafter, cells were fixed and stained for KDELr. As shown in Figure 5, at steady state, the KDELr was localized in the Golgi and in numerous punctate cytoplasmic structures (A). This staining pattern was not altered by DOG (B) or PDBu (C) treatments. Propanol decreased the fluorescent punctate cytoplasmic structures, revealing a more Golgi-like staining pattern (D). When DOG (E) or PDBu (F) was added with propanol, the resulting subcellular distribution of the KDELr was practically indistinguishable from control (A). (G) Quantitative analysis of the percentage of fluorescent punctate cytoplasmic structures in each experimental condition (A–F). Statistical significance: *p < 0.05, **p = 0.01, and ***p < 0.001. Bar, 10 µm.

tested whether DOG or PDBu prevented the alterations caused by propanol (Figure 7) or U73122 (unpublished data) in the retrograde protein trafficking. Cells were simultaneously incubated with DOG or PDBu plus propanol or U73122, and the subcellular distribution of KDELr was examined. As shown in Figure 7, the staining pattern of KDELr in DOG or PDBu plus propanol-treated cells was apparently indistinguishable from control (compare Figure 7, E and F, with 7A). Neither DOG nor PDBu alone altered the KDELr distribution (Figure 7, B and C). DOG (Supplementary Figure 6) and PDBu (unpublished data) also significantly counteracted the inhibition of BFA-induced Golgi disassembly in propanol- or U73122-treated cells. Overall, our results show that exogenously added DAG efficiently compensates for the decrease in endogenous DAG in the Golgi and prevents the alterations in Golgi-to-ER membrane traffic induced by propanol and U73122.

**DOG and PDBu Prevented Cisterne Swelling and the Abnormally High Density of Golgi-associated Buds Produced by Propanol and U73122**

We examined the ultrastructure of the Golgi complex in Vero (Figure 8), NRK (Figure 9), and HeLa (unpublished data) cells treated with propanol and U73122 despite that by immunofluorescence the Golgi complex remained apparently unaltered (Figure 2). Conventional TEM analysis indicates that propanol (Figures 8B and 9B) and U73122 (Figure 8C) both induce fragmentation of Golgi cisternae, whereas propanol treatment also results in cisternal swelling. Notably, both agents gave rise to numerous coated membranes in close vicinity of Golgi cisternae, which, judged by their ultrastructure and localization, carried a COPI coat (Figures 8B and 9B, propanol, arrowheads and insets; Figure 8C, U73122, arrowheads; Table 1). In control cells, these Golgi-associated circular profiles were almost undetectable (Figures 8A and 9A; Table 1). In conventional TEM analysis of ultrathin (50–70 nm) sections, circular membrane profiles cannot be assigned unequivocally to free transport carriers (vesicles) because they might also correspond to cross-sectional membrane tubules or buds. However, such an analysis is possible using thicker sections (~250 nm) and electron tomography. Tomograms of propanol-treated cells (Supplementary Video 7) clearly indicated that cisternae were swollen and carried an abnormally high number of membrane buds attached to the cisterna through a narrow neck (see contoured structures in Figure 9C). 3D models of these tomograms confirmed the presence of numerous nascent transport carriers that appeared to be arrested before membrane fission (vesicles colored in red in Figure 9D, 1–3; Supplementary Video 8) and that carried a characteristic electron-dense fuzzy COPI coat (Figures 8B and 9B, arrowheads and insets, and 9C; Supplementary

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Video 7). Next, we tested whether DOG and PDBu prevented these Golgi ultrastructural alterations. Thus, DOG or PDBu were added 10 min before propanolol and, after 15 min of treatment, cells were processed for TEM. The Golgi ultrastructure in DOG plus propanolol- or U73122-treated cells (Figure 8E and F, respectively) was indistinguishable from that of control cells (Figure 8A). Similar results were obtained with PDBu (unpublished data). Importantly, neither DOG alone (Figure 8D) nor PDBu alone (unpublished data) produced any alteration in the Golgi organization. Stereological analysis (Table 1) indicates that propanolol increased the Golgi membrane surface area (as expected in a swelling process), whereas both propanolol and U73122 increased the density of per-Golgi located round profiles. In contrast, there were no significant differences in any stereological parameter when control cells were compared with cells treated with DOG plus propanolol (Table 1). Overall, the ultrastructural analysis strongly suggests that propanolol and U73122 interfere with the fission process of Golgi-derived COPI-coated transport carriers resulting in an abnormally high number of Golgi-associated budding profiles. Moreover, this apparent arrest in membrane fission can be prevented by DOG and PDBu pretreatments.

Figure 8. Propanolol and U73122 induce a high density of COPI buds, which is counteracted by DOG and PDBu. Control (A), propanolol (60 μM, B), and U73122 (6 μM, C) treated Vero cells were fixed and processed for conventional transmission electron microscopy (TEM). Normal Golgi stacks contained tightly attached 4-6 flat cisternae with a small number of peri-Golgi tubulovesicular profiles (A). Propanolol (B) and U73122 (C) treatments increased the number of peri-Golgi vesicular elements around swollen cisternae in the case of propanolol (B) or smaller cisternae in the case of U73122 (C). Both treatments induced vesicle-budding profiles containing an electron-dense coat that is characteristic of the COPI complex (arrowheads in B and C, and inset in B). Cells treated with DOG alone (3 μM, D) or pre-treated with DOG before propanolol (E) or U73122 (F) treatments showed a Golgi organization that was indistinguishable from control (A). Bar, 200 nm.

The Decrease of the Golgi-associated DAG Pool Reduced ARFGAPI But Not CIBP3/BARS in Golgi Membranes

Recent studies stress the importance of ARFGAPI and CIBP3/BARS in COPI vesicle formation (Yang et al., 2005). In an attempt to examine functional coupling between DAG and CIBP3/BARS, Vero cells were first treated with propanolol and then permeabilized with streptolysin O (SLO) to remove most of the nuclear and cytoplasmic pools of CIBP3/BARS and facilitate its detection at the Golgi (Supplementary Figure 7A). Neither propanolol (Supplementary Figure 7B) nor U73122 (unpublished data), nor both agents added together decreased the Golgi-associated CIBP3/BARS pool (Supplementary Figure 7C). Next, we tested the Golgi-localized protein ARFGAPI, which controls the formation of the COPI-coated transport carriers at the ER-Golgi interface (Yang et al., 2002; Bigay et al., 2003; Lee et al., 2005) and whose activation seems to be partially dependent on DAGs (Antony et al., 1997). As expected, GFP-ARFGAPI was almost exclusively seen in the Golgi (Figure 10A). The expression of GFP-ARFGAPI did not alter the Golgi localization of either β-COP or CIBP3/BARS (unpublished data). We then monitored the dynamics of GFP-ARFGAPI by in vivo
Figure 9. Electron tomography reveals that propanolol arrested COP-coated transport carriers during fission from Golgi cisternae. Untreated (A) and propanolol (60 μM)–treated NRK cells were processed for TEM. As observed in Vero cells (Figure 9), propanolol induced cisternae swelling, and COP-coated vesicular profiles both closely localized and attached to cisternae. The latter is easily seen because of the formation of a narrow neck between the transport carrier and the cisterna (arrowheads). Two representative COP-coated budding vesicles are shown in the inset. (C) Consecutive 6-nm-thick virtual slices extracted from the tomogram. (D) 3D modeling generated by manual segmenting of the tomographic data shown in C. Cisternae are shown in blue, COP-coated round profiles attached to cisternae in red and fully isolated vesicles in green. D2 panel is the same as D1, but it has been laterally rotated 45° about the X axis. D1 panel is an enlargement of a zone shown in the adjacent other two panels, to show a better view of the numerous vesicles attached (red) to the lateral rims of cisternae (blue). Original tomogram plus segmented contours together with the modeled data derived from the 3D reconstruction can be viewed in Supplementary Video 7 and 8, respectively. Videos allow better visualization of the connections between COP-coated vesicles and cisternae in propanolol-treated cell. Bar, 200 nm.

confocal microscopy. Propanolol reduced GFP-ARF6AP1 in the Golgi by ~50% (Figures 10, B and C; Supplementary Video 9). U73122 treatment led to a milder reduction (unpublished data). Pretreatment with D6C significantly offset this decrease (Figure 10, B and C; Supplementary Video 10). D6C alone did not alter the Golgi localization of GFP-ARF6AP1 (Figure 10, B and C). Therefore, data indicate that D6C directly participates in the functional recruitment of ARF6AP1 to the Golgi.

DISCUSSION

The current study shows that a decrease in DAG at the Golgi affects retrograde (Golgi-to-ER) but not anterograde (ER-to-Golgi) membrane transport. Reducing Golgi DAG decreases the dynamic interaction of ARF6AP1 with Golgi membranes and causes a blockade in the formation of COPI-coated vesicles. Our experimental evidence is based on the use of propanolol and U73122, two compounds that are known to diminish cellular DAG content. We demonstrate that both drugs significantly reduce Golgi-associated DAG levels, and, in addition, that PKD-KD and the C-IMP57 domain (two established reporters for DAG) redistribute from the Golgi to the cytoplasm. It is important to note that propanolol and U73122 were used at relatively low concentrations (60 and 6 μM, respectively), lower than the usual concentrations used in pharmacological studies (Stiles et al., 1984). Our conclusion that a decrease in DAG impairs retrograde transport is supported by the finding that both D6C and FDBU counteract the effects of propanolol and U73122 treatments.

Table 1. Stereological analysis of the Golgi complex in NRK cells

<table>
<thead>
<tr>
<th>Treatment</th>
<th>V_{Golgi} (%)</th>
<th>S_{Golgi} (μm^-1)</th>
<th>N_{Golgi} (μm^-2)</th>
<th>N_{Golgi} (μm^-2)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Control</td>
<td>36.7 ± 3.2</td>
<td>16.0 ± 3.0</td>
<td>267.0 ± 33.3</td>
<td>1.1 ± 0.4</td>
</tr>
<tr>
<td>Propanolol</td>
<td>40.7 ± 3.0</td>
<td>20.2 ± 4.0</td>
<td>592.8 ± 45.0***</td>
<td>4.0 ± 1.0**</td>
</tr>
<tr>
<td>U73122</td>
<td>38.2 ± 1.2</td>
<td>17.4 ± 1.5</td>
<td>496.3 ± 57.9***</td>
<td>3.0 ± 0.7**</td>
</tr>
<tr>
<td>D6C</td>
<td>27.1 ± 2.0</td>
<td>15.8 ± 1.2</td>
<td>296.0 ± 34</td>
<td>1.0 ± 0.6</td>
</tr>
<tr>
<td>D6C + propanolol</td>
<td>28.1 ± 3.3</td>
<td>17.1 ± 2.0</td>
<td>301.0 ± 40</td>
<td>1.3 ± 0.6</td>
</tr>
<tr>
<td>D6C + U73122</td>
<td>37.3 ± 2.7</td>
<td>16.1 ± 1.9</td>
<td>281.0 ± 62</td>
<td>1.1 ± 0.4</td>
</tr>
</tbody>
</table>

* V_{Golgi} volume density.
* S_{Golgi} surface density of cisternae.
* N_{Golgi} numerical density of peri-Golgi vesicle profiles.
* N_{Golgi} number of Golgi buds per μm².
* Statistical significance: *p < 0.05, **p < 0.01, ***p < 0.001.
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Figure 10. Propanol decreased GFP-ARFGEF1 in the Golgi complex. COS-1 cells were transiently transfected with a plasmid coding for GFP-ARFGEF1, which co-localizes with the Golgi marker CTR25A (A, asterisks indicate transfected cells). (B) Golgi-associated GFP fluorescence measurement from ARFGEF1 of transfected cells after propanol (80 μM) or DOG (3 μM) plus propanol treatments. Propanol lowered the amount of ARFGEF1 in the Golgi by ~50% for at least 30 min (Supplementary Video 9). DOG pretreatment significantly mitigated this reduction (Supplementary Video 10) and DOG alone did not affect the Golgi-associated fluorescence of ARFGEF1 (unpublished data). Bar, 10 μm. (C) Quantitative analysis of the Golgi-associated GFP-ARFGEF1 fluorescence measured in cells (n = 8) after 5 min of each treatment. Statistical significances, **p < 0.01 and ***p < 0.001.

DAG and Membrane Traffic at the ER–Golgi interface

Our results of the ER-to-Golgi VSV-G transport and the Golgi reassembly after the BFA washout indicate that the early anterograde (ER-to-Golgi) protein transport is not dependent on the DAG pool(s) decreased by propanol, U73122, or FBL. Conversely, unlike BFA, both propanol and U73122 impair retrograde (Golgi-to-ER) protein transport, as shown by the delay in the BFA-induced Golgi disassembly and by the consistent change in the subcellular distribution of the KDELr, which led to a Golgi-like staining pattern. This is indicative that KDELr is retained in the Golgi. Importantly, DOG or PDBU, which are incorporated to the Golgi, prevented the propanol/ U73122-induced morphological alterations, which strongly indicates that such alterations were caused by the reduction of the Golgi-associated DAG pool(s). It is tempting to speculate that propanol, U73122, and FBL all reduce Golgi-associated DAG, but they probably affect different DAG pools, explaining why propanol has more profound effects on Golgi-to-ER traffic than U73122, whereas FBL reduces Golgi DAG without any measurable effect on Golgi-to-ER traffic. This hypothesis can also be extrapolated to late Golgi compartments because VSV-G post-Golgi transport is blocked by FBL but not by U73122, suggesting that as at the ER–Golgi interface, different DAG pools participate in formation of TGN-derived transport carriers. Therefore, it would be very informative to find out whether transport carriers derived from different Golgi compartments (cis- and trans-TGN) are specifically associated with different molecular species of DAG. In turn, this could also determine the particular fission molecular machinery recruitment at each Golgi compartment required to generate specific transport carriers (see below). In any case, we cannot exclude other possibilities to explain the different membrane trafficking sensitivity to these agents such as that the same DAG species are present at several Golgi compartments but in different membrane contexts (for instance, different rate of cholesterol and/or other neighbor lipids) and/or that the targeted enzymes are merely localized in different Golgi compartments.

Role of DAG in the Fission of COPI Transport Carriers

Ultrastructural analysis of the Golgi architecture in propanol/ U73122–treated cells clearly shows the absence of COPI-coated vesicle profiles next to Golgi cisternae. Electron tomography and 3D modeling showed a preponderance of COPI-coated vesicle buds, which indicates that the decrease of Golgi-associated DAG levels caused by propanol and U73122 impairs the membrane scission of COPI-coated transport carriers from the cisterna. The numerous budding profiles seen in treated cells are consistent with the postulated role of DAG as a lipid participating in neck formation in a Golgi-derived vesicle or tubule (Shemesh et al., 2003), regardless whether originating from the TGN (Bard and Malhotra, 2006) or from an early Golgi compartment (our results here). This structural role is assigned on the basis of the fact that DAG has a much smaller holo group than other lipids turning into a lipid with a pronounced cone shape. Consequently, DAG reduces the lipid head group packing and creates membrane insertion sites, allowing peripheral membrane proteins (such as ARFGEF1, see below) to access the central, hydrophobic portion of the bilayer, where they may subsequently trigger the generation of membrane curvature (Nie and Randazzo, 2006). Thus, a reduction in DAG levels of Golgi membranes would be expected to result in a more tightly packed membrane surface, and reduce the efficiency of, or even inactivate, the molecular machinery required to induce membrane fission. What may mark the difference between the TGN and the early Golgi-derived transport carrier formation is the different type of DAG generated in each compartment and, consequently, the fission-associated molecular machinery recruited to each site. In accordance with this postulate, we could explain the different membrane trafficking results obtained using FBL in the TGN (where it blocks post-Golgi protein transport; Baron and Malhotra, 2002) or at the ER–Golgi interface (no alteration; present results). The latter suggests that the DAG
DAG and the ER-Golgi Membrane Trafficking

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