3-28-2005

Targeting of Arf-1 to the Early Golgi by Membrin, an ER-Golgi SNARE

Akira Honda

Omayma S. Al-Awar

Jesse C. Hay
University of Montana - Missoula, Jesse.Hay@umontana.edu

Julie G. Donaldson

Let us know how access to this document benefits you.

Follow this and additional works at: https://scholarworks.umt.edu/biosci_pubs

Part of the Biology Commons

Recommended Citation
Honda, Akira; Al-Awar, Omayma S.; Hay, Jesse C.; and Donaldson, Julie G., “Targeting of Arf-1 to the Early Golgi by Membrin, an ER-Golgi SNARE” (2005). Biological Sciences Faculty Publications. 171.
https://scholarworks.umt.edu/biosci_pubs/171

This Article is brought to you for free and open access by the Biological Sciences at ScholarWorks at University of Montana. It has been accepted for inclusion in Biological Sciences Faculty Publications by an authorized administrator of ScholarWorks at University of Montana. For more information, please contact scholarworks@mso.umt.edu.
Targeting of Arf-1 to the early Golgi by membrin, an ER-Golgi SNARE

Akira Honda,1 Omayma S. Al-Awar,1 Jesse C. Hay,2 and Julie G. Donaldson1

1Laboratory of Cell Biology, National Heart, Lung, and Blood Institute, National Institutes of Health (NIH), Bethesda, MD 20892
2Division of Biological Sciences, University of Montana, Missoula, MT 59812

Arf and Rab family GTPases regulate membrane traffic in cells, yet little is known about how they are targeted to distinct organelles. To identify sequences in Arf-1 necessary for Golgi targeting, we examined the localization of chimeras between Arf-1 and Arf-6. Here, we identify a 16-amino acid sequence in Arf-1 that specifies Golgi targeting and contains a motif (MXXE) that is important for Arf-1 binding to membrin, an ER-Golgi SNARE protein. The MXXE motif is conserved in all Arfs known to localize to the Golgi and enables Arf-1 to localize to the early Golgi. Arf-1 lacking these 16 aa can still localize to the late Golgi where it displays a more rapid Golgi-cytosol cycle than wild-type Arf-1. These studies suggest that membrin recruits Arf-1 to the early Golgi and reveal distinct kinetic cycles for Arf-1 at early and late Golgi determined by different sets of Arf regulators and effectors.

Introduction

A fundamental problem in membrane traffic in the biosynthetic and endocytic pathways is how organelles maintain their distinct composition of proteins and lipids in the face of continuous addition and removal of membrane. This is accomplished in part by the recruitment of cytosolic protein complexes, motors, and other components responsible for receiving and producing transport vesicles at the organelle. GTPases of the Rab and Arf families play key roles in regulating the recruitment of these protein complexes and influencing membrane lipid composition on distinct organelles (Munro, 2002), but how Rabs and Arfs target to specific organelles remains unclear.

Arfs are expressed in all eukaryotes and function in various membrane trafficking events and in the maintenance of organelle structure (Moss and Vaughan, 1995; Chavrier and Goud, 1999). There are six mammalian Arfs, and Arf-1 and Arf-6 are the least similar in amino acid sequence and the best-characterized members of the Arf family. Arf-1 is primarily localized to the Golgi complex where it regulates the binding of cytosolic coat proteins, including coat protein I (COPI), adaptor protein 1, and Golgi-localized, γ-ear–containing, Arf-binding proteins (GGA) to Golgi membranes (Bonifacino and Lippincott-Schwartz, 2003; Nie et al., 2003) and thus serves to regulate membrane traffic in the ER-Golgi system (Lippincott-Schwartz et al., 1998). Arf-6, by contrast, localizes to the plasma membrane and a membrane recycling system at the cell periphery (Donaldson, 2003).

An important characteristic of Arf-1 is that the inactive protein (Arf-1-GDP) is largely cytosolic, whereas the activated protein (Arf-1-GTP) is membrane bound. Arf proteins are all myristoylated and it has been postulated that Arf-1-GDP initially docks on the membrane through this myristoyl moiety before encountering the guanine nucleotide exchange factor (GEF) that catalyzes exchange of GTP for GDP (Antonny et al., 1997). Arf-1-GTP associates more tightly with the membrane and can then recruit coat proteins to the membrane until it encounters a GTPase-activating protein (GAP) that stimulates GTP hydrolysis and dissociation of Arf-1-GDP from the membrane.

In biochemical assays, all Arf proteins share common effector functions including: activation of phospholipase D (Liang et al., 1997) and phosphatidylinositol 4-phosphate 5-kinase (Honda et al., 1999), recruitment of COPI to membranes (Liang and Kornfeld, 1997), and binding to GGA (Takatsu et al., 2002). Yet in cells, Arfs have distinct functions and localizations. Arf-1 localizes to the Golgi complex, regulates the assembly of coat proteins onto membranes and mediates traffic in the ER-Golgi system (Bonifacino and Glick, 2004). Arf-6 localizes to the endosomal/plasma membrane system and not the Golgi and thus has no effect on regulating the assembly of COPI onto the Golgi complex in vivo (Peters et al., 1995).
Thus, it is through organelle-specific targeting that Arf proteins attain their unique cellular functions.

In this study, we were interested in identifying amino acid residues in the Arf-1 sequence that determine its specificity for Golgi targeting and distinguish it from other Arf proteins, especially Arf-6. Because Arf proteins are highly conserved in structure (Goldberg, 1998; Pasqualato et al., 2001), we followed an approach that has been used by us and others, generating chimeric Arfs by exchanging amino- and carboxy-terminal portions of Arf-1 and Arf-6 and expressing them in cells (Liang et al., 1997; Jones et al., 1999; Al-Awar et al., 2000). As a result of this study, we identified a short sequence in Arf-1 containing a Golgi targeting signal, and in the sequence we identified a motif (MXXE) that is critical in vitro and in vivo for Arf-1 binding to membrin, an ER-Golgi SNARE protein. Because the MXXE motif enables Arf-1 to localize to the early Golgi, we suggest that membrin is an Arf-1 receptor at the early Golgi.

Results

Identification of the Golgi targeting sequence in Arf-1

A comparison of human Arf-1 and Arf-6 is shown in Fig. 1A where identical amino acid residues are shaded in gray and positions of the α-helices and β-sheets derived from structural studies (Amor et al., 1994; Menetrey et al., 2000) are indicated. To identify sequences in Arf-1 that are necessary for its Golgi localization, chimeric proteins of Arf-1 and Arf-6 were constructed and their localization was examined in COS-7 cells. Full-length Arf-1 localized to the juxtanuclear...
region in a pattern similar to that of galactosyltransferase (GalT)-GFP, a chimera of GFP and the transmembrane domain of a Golgi resident enzyme, GalT (Fig. 1 B, Unt). The Golgi localization of Arf-1 was also observed when cells were treated with nocodazole, a microtubule-disrupting drug that causes Golgi fragmentation (Fig. 1 B, +Nz). On the other hand, in cells overexpressing Arf-6, Arf-6 localized primarily to the plasma membrane, although some juxtanuclear labeling near the Golgi region was also observed (Fig. 1 C, Unt). This juxtanuclear staining was clearly not the Golgi because Arf-6 did not label the Golgi fragments after nocodazole treatment (Fig. 1 C, +Nz).

As summarized in Fig. 1 D, all the chimeras that included amino acids 101–116 of Arf-1 localized to the Golgi (Fig. 1 D, 1-1-6, 6-1-1, and 6-1-6). On the other hand, 1-6-6 and 6-6-1, which lacked this sequence did not localize to the Golgi (Fig. 1 D). Most strikingly, Arf-6-1-6, the chimera containing amino acid residues 101–116 of Arf-1 inserted into the Arf-6 sequence (Fig. 1 D), clearly localized to the Golgi, even after nocodazole treatment (Fig. 1 E), although some plasma membrane labeling was also observed. These results show that residues 101–116 of Arf-1 are sufficient to target Arf-6 to the Golgi. However, we observed that Arf-1-6-1, which contains amino acids 97–112 of Arf-6, also localized to the Golgi (Fig. 1 D), indicating that additional sequences in the amino- and carboxyl-terminal halves of Arf-1 could together confer Golgi localization. We made similar observations with these Arf chimeras expressed in HeLa and NRK cells (unpublished data).

**Arf-6-1-6 and Arf-1-6-1 are activated by a BFA-sensitive GEF and inactivated by a GAP on the Golgi membrane**

An important characteristic of Arf-1 is that the inactive, GDP-bound protein is in the cytosol whereas the active, GTP-bound protein is membrane bound, and cycling of Arf-1 between its activated and inactivated states is critical for Arf-1 function. When cells are treated with brefeldin A (BFA), a fungal toxin that inhibits Arf-GEFs that are associated with the Golgi complex (Jackson and Casanova, 2000), Arf-1 dissociates from Golgi membranes because activation of Arf-1 by GEF is inhibited, whereas GAP continues to inactivate Arf-1. To examine whether Arf-6-1-6 and Arf-1-6-1 can serve as substrates for GEFs and GAPs on the Golgi membrane like Arf-1, the dissociation of these Arf chimeras from the Golgi after addition of BFA were compared with that of Arf-1. In untreated COS-7 cells, clear Golgi localizations of Arf-6-1-6-GFP and Arf-1-6-1-GFP were observed (Fig. 2, Unt). After addition of BFA, both Arf-6-GFPs dissociated from the Golgi as rapidly as Arf-1-GFP (Fig. 2, BFA 2 min). These results show that both Arf-6-1-6 and Arf-1-6-1 can be inactivated through GTP hydrolysis by the GAP on the Golgi membrane. Furthermore, it suggests that activation of Arf-6-1-6 and Arf-1-6-1 is catalyzed by a BFA-sensitive Golgi GEF because neither Arf chimeras bound to the Golgi in the presence of BFA. Similar observations were made in HeLa cells (unpublished data).
This result confirmed that residues 101–116 of Arf-1 are sufficient by itself to target to the Golgi, because GFP alone localized to the cytosol and never showed juxtanuclear localization (unpublished data). Moreover, in cells expressing GFP-Arf-1(101–116) at a higher level and showing juxtanuclear localization of the GFP fusion protein, the distribution of GM130, a Golgi matrix protein, was clearly different than in untransfected cells. In untransfected cells, GM130 localized to interconnected, ribbon-shaped elements (Fig. 4 C, inset I). This pattern was also observed in Arf-1-GFP–transfected cells (not depicted). In contrast, in cells showing juxtanuclear localization of GFP-Arf-1(101–116), the distribution of GM130 was changed into punctate structures (Fig. 4 C, inset II). Moreover, high level expression of GFP-Arf-1(101–116) caused COPI to dissociate from the Golgi complex (Fig. 4 D). These results suggest that overexpressed GFP-Arf-1(101–116) competes with endogenous Arf-1 for binding to the Golgi, and inhibits Arf-1 regulation of maintenance of Golgi structure and recruitment of COPI onto the Golgi complex.

Arf-1, but not Arf-1-6-1, binds to membrin on Golgi membranes

In an attempt to identify the receptor on Golgi membranes that specifically recognizes 101–116 of Arf-1, we considered membrin on Golgi membranes.
potential candidate receptors. Recently, Rein et al. (2002) showed that SNAREs may act as an Arf receptor on membranes in yeast. Using in vitro binding assays, they showed that Arf1p directly binds Bet1p, Sec22p, and Bos1p, SNAREs that function in transport pathways between the ER and the Golgi. The association with Bet1p is independent of the nucleotide bound to Arf1p (Rein et al., 2002), suggesting that the SNARE recruits Arf1p-GDP to membranes where the exchange of GDP to GTP, and thus the activation of Arf1p, takes place.

To test the possibility that those SNAREs act as Golgi membrane receptors for Arf-1 in mammalian cells, we coexpressed rbet1, sec22b, membrin, and syntaxin5, which are the mammalian homologues of Bet1p, Sec22p, Bos1p, and Sed5p, respectively, with Arf-1-GFP in HeLa cells. As reported (Hay et al., 1996, 1998), rbet1, membrin, and syntaxin5 mainly localized to the Golgi whereas sec22b localized to the ER. We noticed that, although Arf-1 generally colocalized with all of the Golgi-localized SNAREs (not depicted), Arf-1 localization was tightly coincident with membrin (Fig. 5 E), raising the possibility that Arf-1-GFP was directly binding to the overexpressed membrin and that membrin may be serving as an Arf-1 receptor in vivo.

To investigate whether membrin specifically interacts with Arf-1 and could be the basis for Golgi targeting of Arf-1, we used in vitro binding experiments. Arf-1 was expressed in E. coli as His6-tagged proteins where the amino-terminal 17 aa were replaced by the His6 affinity tag. We incubated affinity-purified Arf proteins with HeLa cell lysate expressing myc-membrin in the presence of GDP. Assuming that the interaction between Arf-1 and its receptor would not be strong, we used a cross-linking reagent to cross-link the proteins bound to Arf. As shown in Fig. 5 (A and C), membrin efficiently bound to Arf-1 in the presence of the cross-linker. However, Arf-1-6-1, which lacks residues 101–116 of Arf-1 yet still localizes to the Golgi (Fig. 1 D), did not bind to membrin. Furthermore, when 110M and 113E (110^MXXE^113) were substituted with corresponding residues of Arf-6, the Arf-1 mutant failed to bind membrin (Fig. 5, B and D). We know that these mutations do not affect the general conformation of His6-Arf-1, because both His6-Arf-1-6-1 and His6-Arf-1M110I,E113D bound to the VHS-GAT domain of GGA as well as wild-type Arf-1 in the presence of GTPyS (Fig. S1, A and B, available at http://www.jcb.org/cgi/content/full/jcb.200409138/DC1). Moreover, circular dichroism (CD) spectra of these Arf-1 mutants were essentially identical to that of Arf-1 (Fig. S1 C). Although we could detect binding of detergent-solubilized membrin to His6-Arf-1, we could not obtain binding using recombinant membrin (unpublished data). This might indicate that other proteins or membrane lipids are re-
quired for the interaction. Together, these results demonstrate that Arf-1-GDP binds membrin, and the association with membrin requires the MXXE motif of Arf-1.

Having demonstrated that Arf-1 can specifically bind to solubilized membrin, we examined more carefully the extent of colocalization of Arf-1 and membrin in intact cells. In HeLa cells, we observed a high degree of colocalization of Arf-1 and membrin (Fig. 5 E). However, colocalization of Arf-1-6-1 with membrin was partial and some membrin-positive structures were clearly devoid of Arf-1-6-1 (Fig. 5 E, inset, arrowheads). We observed similar immunolocalization results in NRK cells where we quantified the amount of colocalization (see Materials and methods), and found that 80% of Golgi-associated Arf-1 colocalized with membrin whereas only 41% of Golgi-associated Arf-1-6-1 colocalized with membrin (Fig. 5 F). Importantly, if we mutated Arf-1-6-1 such that it now contained the MXXE motif, 75% colocalization between Arf-1-6-1 and membrin was now observed (Fig. 5 F). We also observed near complete colocalization of membrin with GFP-Arf-1(101–116) (unpublished data). These results suggest that Arf-1 can bind to membrin in vitro and in vivo but requires the MXXE motif. Arf-1-6-1, on the other hand, does not interact with membrin and thus must localize to the Golgi by an alternative mechanism.
The finding that Arf-1 could bind to membrin, both in cells and in vitro binding assays, suggested that Golgi-associated membrin could act as the initial receptor for Arf-1-GDP before GEF-catalyzed nucleotide exchange. If this is true, it is possible that overexpression of membrin would partially protect Arf-1 from release from Golgi membranes during BFA treatment. When Arf-1 or Arf-1-6-1 was expressed alone in COS-7 cells, a significant amount of Arf dissociated from the Golgi within 2 min after BFA addition (Fig. 2, BFA 2 min). However, if membrin was coexpressed with Arf-1, Arf-1 labeling of the Golgi was still apparent after 2 min of BFA addition (Fig. 6 A). Even after 4 min, Golgi localization of Arf-1 was still prominent in membrin-transfected cells (Fig. 6 A, cell marked with arrowhead), whereas the bulk of the Arf-1 was dissociated in cells not coexpressing membrin (Fig. 6 A, cell marked with arrow). This association of Arf-1 with membrin was lost as Golgi membranes redistributed into the ER (see below). On the other hand, in Arf-1-6-1–transfected cells, overexpressed membrin did not protect the dissociation of Arf-1-6-1 from the Golgi by BFA (Fig. 6 A), suggesting that the 16 aa of Arf-1 including the MXXE motif were required for this effect. Overexpression of membrin did not affect COPI dissociation after BFA addition (Fig. 6 B), indicating that “protection” of Arf-1 dissociation did not lead to GDP loading onto Arf-1. Because rbet1 and syntaxin5 also showed Golgi localization in mammalian cells, we examined whether overexpression of rbet1 or syntaxin5 would protect Arf-1 from dissociation by BFA. As shown in Fig. 6 C, regardless of the level of expression, neither rbet1 nor syntaxin5 affected the distribution of Arf-1 after BFA addition, indicating that overexpression of these SNAREs did not retain Arf-1 at the Golgi in COS-7 cells. We made similar observations in HeLa cells and quantified the amount of Arf-1 and Arf-1-6-1 associated with the Golgi before and after BFA in cells coexpressing these ER-Golgi SNAREs (Fig. 6, D and E). In untreated cells, ~17% of total cellular Arf-1 was associated with the Golgi and this dropped to 6% after 2 min BFA (Fig. 6 D, control). In cells expressing membrin however, Arf-1 associated with the Golgi drops only to 12% after BFA (Fig. 6 D, +membrin). On the other hand, neither rbet1 nor syntaxin5 expression affected the distribution of Arf-1 after BFA addition (Fig. 6 D, +rbet1 and +syntaxin5). In Arf-1-6-1–transfected cells, dissociation from the Golgi by BFA was similar in all cases and not affected by expression of any SNARE (Fig. 6 E). Together, these results indicate that membrin can specifically recruit Arf-1-GDP to Golgi membranes and transiently “protect” Arf-1-GDP from BFA-induced dissociation. Furthermore, that it is Arf-1-GDP that is binding to membrin is supported by the observation that Arf-1 Q71L did not colocalize with membrin in cells (unpublished data).

**Arf-1 and membrin colocalize on COPI-coated transport structures between the ER and Golgi**

Having demonstrated that membrin appears to represent an initial Arf-1-GDP binding site on Golgi membranes, we wondered where the interaction occurs. Membrin is involved in the membrane transport pathway between the ER and the Golgi complex (Hay et al., 1997). Arf-1 also has been shown to function in this system (Dascher and Balch, 1994; Ward et al., 2001). These findings raise the possibility that both proteins might interact on transport structures from the ER to the Golgi. Discerning Arf-1 localization on peripheral, incoming ER to Golgi transport structures was difficult due to the Arf-1 presence in the cytosol. Therefore, we examined the distribution of membrin and Arf-1 during recovery from BFA in NRK cells, a process that involves rapid and massive anterograde membrane transport from the ER, resulting in reformation of the Golgi complex (Lippincott-Schwartz et al., 1990). After 30 min of BFA treatment, Arf-1 was cytosolic, whereas membrin localized to small, peripheral structures (Fig. 7 A, BFA) that colocalized with ERGIC53/p58 (unpublished data) and thus were ER exit sites (Tang et al., 1995; Ward et al., 2001). 10 min after BFA wash out, Arf-1 now colocalized with membrin on scattered peripheral structures (Fig. 7 A, WO 10 min). β-COP was also distributed on those structures, indicating that Arf-1 was activated and recruited COPI onto the structures (Fig. 7 B). After 15 min of recovery, most of the membrin and Arf-1 colocalized on larger juxtanuclear structures, although some small, peripheral structures were still observed (Fig. 7 A, WO 15 min). Arf-1-6-1 also showed cytosolic distribution in BFA-treated cells similar to Arf-1 (Fig. 7 A, BFA). However, 10 min after BFA wash out, the distribution of Arf-1-6-1 was still cytosolic, whereas membrin was observed on peripheral structures (Fig. 7 A, WO 10 min). Although some Arf-1-6-1 weakly colocalized with membrin on the juxtanuclear structures after 15 min of recovery, a major part of Arf-1-6-1 was still cytosolic and some membrin-positive transport structures were clearly devoid of Arf-1-6-1 (Fig. 7 A, WO 15 min, inset, arrowheads). After a 20-min recovery, Arf-1-6-1 could be observed to colocalize with membrin on the fully reassembled, juxtanuclear Golgi complex (Fig. 7 A, WO 20 min). Similar recruitment of Arf-1, but not Arf-1-6-1, to reforming Golgi structures was observed in COS-7 cells (unpublished data). The delay in recruitment of Arf-1-6-1 to the reforming Golgi did not slow Golgi recovery because endogenous Arf-1 could be recruited. Together, these results demonstrate that these 16 aa and the MXXE motif of Arf-1 allow Arf-1 recruitment to membrin-containing transport structures bound for the Golgi complex.

**Arf-1-6-1 localizes to the trans-Golgi, but not to the cis-Golgi, and is regulated differently from Arf-1**

Because Arf-1-6-1 did not associate with reforming Golgi during BFA wash out (Fig. 7 A), we wondered how and where Arf-1-6-1 is recruited to the Golgi. The Golgi complex can be divided into cis- and trans-sides, shown to have distinct functions (Bonifacino and Glick, 2004). Golgi-specific BFA resistance factor 1 (GBF1) and BFA-inhibited GEF (BIG) 1/2 are Arf-GEFs known to localize mainly to cis- and trans-elements of the Golgi, respectively, and limited overlap between the distribution of GBF1 and BIG1 has been observed (Yamaji et al., 2000; Kawamoto et al., 2002; Shinotsuka et al., 2002a,b; Zhao et al., 2002). Indeed, double staining of NRK cells with antibodies for GBF1 and BIG1 confirmed the feasibility of dis-
Distinguishing the distributions of these Arf-GEFs at the light microscopy level (unpublished data). To identify more specifically the distributions of Arf-1 and Arf-1-6-1 in the Golgi complex, we compared their distributions to the localizations of GBF1 or BIG1. The distribution of Arf-1 overlapped extensively with that of GBF1 with nearly superimposable images (Fig. 8 A). By contrast, Arf-1-6-1 overlapped less with GBF1 (Fig. 8 A). Quantifying the extent of colocalization revealed that 82% of the Golgi-associated Arf-1 colocalized with GBF1 whereas only 38% of the Golgi-associated Arf-1-6-1 colocalized with GBF1 (Fig. 8 B). On the other hand, Arf-1-6-1 seemed to colocalize more with BIG1 at the trans-Golgi than did Arf-1 (59% and 38% overlapping, respectively; Fig. 8, C and D). Importantly, mutagenesis of Arf-1-6-1 to include MXXE shifted the colocalization of Arf-1-6-1MXXE back to that observed with Arf-1, 72% colocalized with GBF1 (Fig. 8 B) and 38% colocalized with BIG1 (Fig. 8 D). These results demonstrate that Arf-1-6-1 localizes mainly to the trans-Golgi, and not to the cis-Golgi. Because the distribution of membrin was almost identical to that of GBF1, whereas membrin did not colocalize well with BIG1 (unpublished data), these results suggest that interaction with membrin may be required for Arf-1 to localize to the cis-Golgi.

Although our data suggest that Arf-1 binding to membrin is the mechanism for recruitment of Arf-1 to the early Golgi, it is possible that Arf-1 is recruited to the cis-Golgi through direct
interaction and activation by GBF1. Arf-1-6-1 might not bind
to the early Golgi because it cannot interact with GBF1 due to
its Arf-6 sequence. Indeed, some Arf-GEFs may recognize
subtle folding differences between Arf-1 and Arf-6 explaining
their selectivity for different Arfs (Macia et al., 2001). To ex-
amine whether Arf-1-6-1 can be activated by GBF1, we mea-
sured the amount of GTP-bound Arf-1 and Arf-1-6-1 in cells
overexpressing HA-tagged GBF1 (see Materials and methods).
As shown in Fig. S2 (available at http://www.jcb.org/cgi/
content/full/jcb.200409138/DC1), overexpressed GBF1 activated
Arf-1-6-1, although not to the same extent as Arf-1, suggesting
that Arf-1-6-1 can be activated by GBF1 in cells.

In addition to GEFs, distinct GAPs may regulate Arf-1 at
the Golgi in mammalian cells (Cukierman et al., 1995; Miura et
al., 2002). It is likely that distinct GEFs and GAPs regulate Arf-1
at cis- and trans-elements of the Golgi complex. Having dem-
onstrated that Arf-1-6-1 localizes mainly to the trans-Golgi, and
not to the cis-Golgi, we wondered if Arf-1-6-1 is regulated dif-
ferently from Arf-1. FRAP is a powerful technique to examine
the kinetics of dissociation and association of Arf-1 at the Golgi
in live cells (Vasudevan et al., 1998; Presley et al., 2002). Be-
cause the kinetics reflect GAP and GEF activities on Arf-1, we
examined the FRAP of the Golgi region in Arf-1-GFP- and Arf-
1-6-1-GFP–transfected cells. Representative FRAP kinetic data
are shown in Fig. 9 A. The recovery of Arf-1-GFP fluorescence
showed kinetics ($t_{1/2} = 20$ s) similar to previous studies (Presley
et al., 2002). By contrast, the recovery kinetics of Arf-1-6-1-
GFP ($t_{1/2} = 10$ s) was much more rapid, indicating that Arf-1-6-1
spends less time on the Golgi per cycle than Arf-1. Because
Arf-1-6-1 primarily localizes to the late Golgi (Fig. 8), the dif-
ference in the FRAP data for Arf-1 and Arf-1-6-1 suggests that
Arf-1 cycling at the trans-Golgi might be faster than at the cis-
Golgi. We hypothesized that failure to bind to membrin at
the early Golgi leads to Arf-1-6-1 being activated and inactivated
at the late Golgi with more rapid kinetics. To test this, we mea-
sured the FRAP kinetics of Arf-1-6-1MXXE-GFP and observed
that Arf-1-6-1MXXE-GFP now exhibited FRAP kinetics ($t_{1/2} =
20$ s) identical to that of wild-type Arf-1 (Fig. 9 A).
Discussion

We have identified a 16–amino acid region in Arf-1 that is necessary and sufficient for Arf-1 targeting to the early Golgi. These 16 aa include helix α3 (Fig. 1 A) and contains a motif (MXXE) that is found in all Arfs known to associate with the Golgi complex, and in all eukaryotes examined. Membrin, an ER-Golgi SNARE, binds Arf-1-GDP via the helix α3 and is responsible for recruiting Arf-1 to the early Golgi. An Arf-1 mutant lacking this region (Arf-1-6-1) cannot bind membrin and does not localize to the early Golgi although it does associate with the late Golgi through other means that require both amino- and carboxyl-portions of the protein. Although SNAREs are believed to function in membrane fusion events (Hay, 2001; Bonifacio and Glick, 2004), our results show an additional role of membrin as a membrane receptor for Arf-1 at the Golgi. Because Bos1p, the yeast homologue of membrin, has also been shown to interact with Sar1p, a component of the coat protein II (COPII) coat (Springer and Schekman, 1998), membrin recruitment of Arf-1 might coordinate the exchange of Sar1/COPII to Arf-1/COPI coats on incoming, pre-Golgi structures.

The first suggestion that ER-Golgi SNAREs could recruit Arf-1 came from in vitro binding studies in yeast (Rein et al., 2002) showing that nonmyristoylated, Δ17Arf1p-GDP could bind directly to GST fusion proteins of Bet1p, Sec22p, and Bos1p. In that study, Arf1p binding to Bet1p was stronger than to Bos1p and, curiously, required the presence of an Arf-GAP protein, Glo3p, to prime the SNAREs (Rein et al., 2002). Our study shows that membrin, but not rbet1, sec22b or syntaxin5, can bind specifically to full-length, myristoylated Arf-1 through the MXXE motif in mammalian cells. Because our cells express mammalian ArfGAP1, it is possible that this endogenous GAP could function in vivo to prime membrin for Arf-1 binding. Interestingly, the proximal region of helix α3 makes contact with ArfGAP1 in a co-crystal of Δ17Arf1p-GDP and the GAP domain of ArfGAP1 (Goldberg, 1999), raising the possibility that the recruitment of Arf-1 to the early Golgi by membrin might also involve ArfGAP1. Because yeast Arf1p also contains MXXE, and can be recruited to Golgi when expressed in mammalian cells (unpublished data), this motif may be used for Golgi targeting in yeast cells. Indeed, evidence that the α3 region in yeast promotes Golgi recruitment of Arf-1 comes from a genetic study that identified amino acid residues in the distal portion of helix α3 as an intragenic suppressor of a dominant lethal mutation (Click et al., 2002).

The other class of Golgi membrane proteins that have been suggested to serve as Arf-1 receptors are the abundant p23 and p24 family proteins. The p23 protein was shown by chemical cross-linking to bind directly to Arf-1-GDP, but not to Arf-1-GTP, in vitro and the interaction site was mapped to the carboxyl-terminal 22 aa (Gommel et al., 2001). Although this interaction was also observed in an in vivo study examining fluorescence resonance energy transfer between p23-CFP and Arf-1-YFP (Majoul et al., 2001), it may not represent the interaction that targets Arf-1-GDP specifically to the Golgi. We did not detect a Golgi targeting motif in the last 22 aa of Arf-1 because Arf-6-6-1, which lacked the 16–amino acid sequence and the amino-terminal half of Arf-1 but contained Arf-1 sequence from 117–181, did not localize to the Golgi (Fig. 1 D). Our data suggest that membrin serves as a specific receptor for Arf-1-GDP. However, it does not preclude an interaction of Arf-1-GDP with p23 proteins either simultaneously or subsequently during the interaction cycle of Arf-1 with Golgi membranes.

Arf proteins are highly conserved both in sequence and in structure with nearly identical switch I and II regions (Goldberg, 1998; Pasqualato et al., 2001). Helix α3 is positioned on the “backside” of the molecule, on the opposite side of the GTP binding pocket. It alone appears to contain sufficient information for Golgi targeting (Fig. 4) and presumably membrin binding. In the context of the Arf-1 protein, the MXXE motif in helix α3 appears to be required for Golgi targeting. We do not know...
whether the M or E make direct contact with membrin, but they are necessary for Arf-1 binding to membrin.

We propose that in the ER-Golgi system, membrin recruits Arf-1-GDP to the membrane subsequent to the release of the COPII coat (Fig. 9 B, I). Arf-1-GDP is then activated by GBF1, the early Golgi GEF, and Arf-1-GTP can then recruit coatomer or other effectors and Arf-GAP, leading to GTP hydrolysis and release of Arf-1-GDP back into the cytosol. The Arf-1 construct that cannot bind to membrin (Arf-1-6-1) can still associate with the Golgi complex, possibly by direct interaction with an Arf-GEF such as BIG1 and 2, which are known to reside at the trans-Golgi (Fig. 9 B, II; Shinotsuka et al., 2002a,b; Zhao et al., 2002). Arf-1-6-1 colocalizes less with GBF1 (Fig. 8, A and B) and, during recovery from BFA, Arf-1-6-1 cannot associate with the peripheral, COPI-labeled, reforming Golgi structures (Fig. 7 A). Intriguingly, we observed a distinct difference between the FRAP kinetics of Arf-1 and Arf-1-6-1 (Fig. 9 A). Namely, that Arf-1-6-1-GFP had a much shorter recovery time after photobleaching (1/2 = 10 s) than did Arf-1-GFP (1/2 = 20 s). We speculate that the shorter residency time for Arf-1-6-1 could be due to interaction with trans-Golgi GEFs (BIG1 and 2) and GAPs. In contrast, the residency time of Arf-1 on the Golgi is longer and includes interaction of Arf-1 with membrin, GBF1 and ArfGAP1 at early Golgi. These differences in kinetic cycles may reflect the different GEFs and GAPs residing at the early and late Golgi (Fig. 9 B, I, II).

Functional relationship between Arf-1 and SNAREs

SNAREs have an essential role in regulating membrane fusion events throughout the secretory pathway (Hay, 2001; Bonifacino and Glick, 2004). SNAREs form cytoplasmic coiled-coil bundles that bridge two membranes about to undergo membrane fusion. Furthermore, as SNAREs are compartment specific and can engage in various SNARE pair conformations, they have the potential to serve as exquisite membrane receptors for cytosolic components such as COPI and COPII components whose regulated assembly controls vesicle formation.

Current models for transport in the early secretory pathway depict secretory cargo and the SNAREs syntaxin5, rbet1, and membrin being recruited into COPII vesicle budding from the ER (Fig. 9 B, I; Springer and Schekman, 1998). Our observations that Arf-1 cannot bind to membrin when it is in the ER or at ER exit sites, i.e., 30 min BFA (Fig. 7) suggest that the altered conformation of membrin in the ER or association with the COPII coat may prevent Arf-1 binding. The tethering protein p115 associates with these newly budded vesicles by binding directly to the SNAREs in a Rab1-dependent fashion (AlIan et al., 2000). At the Golgi, p115 and these SNAREs are believed to facilitate fusion of pre-Golgi structures to Golgi membranes or to other incoming pre-Golgi structures. GBF1 associates with p115 (Garcia-Mata and Sztul, 2003) and has been shown to be involved in COPI recruitment onto membranes (Claude et al., 1999; Kawamoto et al., 2002). Furthermore, GBF1 is essential for COPI recruitment to the transport intermediates bound for the Golgi (Garcia-Mata et al., 2003). These observations support the idea that p115 and membrin might coordinately recruit GBF1 and Arf-1-GDP onto the post-ER, transport structure, leading to Arf-1 activation and the recruitment of COPI (Fig. 9 B, I).

Materials and methods

Cells, antibodies and reagents

Cells were grown in DME supplemented with 10% FBS, 100 U/ml penicillin, and 100 μg/ml streptomycin at 37°C with 5% CO2. Rabbit anti–Arf-6 antibody that recognizes a carboxy-terminal peptide of the protein was used as described previously (Radhakrishna and Donaldson, 1997). Rabbit anti–BIG1 antibody was provided by C.L. Jackson [NIH; Yamaji et al., 2000]. Monoclonal antibodies against the HA epitope [16B12] and the myc epitope [9E10] were purchased from Covance and Zymed Laboratories, respectively. Monoclonal anti-GM130 and anti-GBF1 antibodies were purchased from BD Biosciences. Rabbit anti–p-8-COP antibody was purchased from Affinity BioReagents, Inc. Secondary antibodies (Alexa 594, Alexa 488, anti-mouse, and anti-rabbit) were purchased from Molecular Probes. Dithiobis(succinimidyl propionate) (DSP) was purchased from Pierce Chemical Co. E. coli containing a vector for GST-fusion proteins comprising VHS-OAT domain of human GGA3 was provided by J.S. Bonifacino [NIH; Dell’Angelica et al., 2000]. All other reagents were purchased from Sigma-Aldrich.

Plasmids and transient transfections

The chimeras of Arf-1 and Arf-6 were created by a two-step PCR procedure as described previously (Al-Awar et al., 2000). All other mutants of Arf-1 and Arf-6 were created using QuickChange site-directed mutagenesis kit (Stratagene). The cDNAs of untagged or carboxy-terminally HA-tagged wild-type and mutant Arf were subcloned into the modified pCDL-SHs expression vector (Takebe et al., 1998) or pEGFP-N1 vector (CLONTECH Laboratories, Inc.). Amino acids 101–116 of Arf1 were shuffled into pEGFP-C3 vector (CLONTECH Laboratories, Inc.). The plasmids for aminoterminal myc-tagged membrin, rbet1, sec22β, and HA-tagged syntaxin5 were created as described previously (Hay et al., 1996, 1997). The plasmids for GOLf-GFP and HA-tagged GBF1 were provided by J. Lipincott-Schwartz [NIH; Cole et al., 1996] and C.L. Jackson, respectively. Cells were grown on glass coverslips and transfected using FuGENE 6 (Roche) according to the manufacturer’s instructions. For FRAP experiments, HeLa cells were plated in Lab-Tek chambered coverglass (Nalge Nunc International).

Confocal microscopy

20 h after transfection, cells were treated as indicated, fixed, and subjected to immunofluorescence staining in the presence of 0.2% saponin as described previously (Radhakrishna and Donaldson, 1997). All fluorescence images were obtained with a confocal microscope (model LSM 510; Carl Zeiss Microlimaging, Inc.). Most images of fixed cells were captured using 63× 1.4 NA objective with a pinhole corresponding to a focal depth of 0.7 μm. To quantify Golgi-associated Arf-1-GFP, a 40× 0.7 NA objective was used with a pinhole corresponding to a focal depth of 12.4 μm. For FRAP experiments, cells were incubated in CO2-independent media [In Vitrogen], and imaged at 20°C on a confocal microscope (model LSM 510; Carl Zeiss Microlimaging, Inc.) using a 40× 0.7 NA objective with a pinhole corresponding to a focal depth of 2.5 μm. Image processing for figures was accomplished in Adobe Photoshop 5.5.

Analysis of colocalization

To quantify the level of colocalization for Golgi-associated Arfs with membrin, GBF1, and BIG1, 20 cells were randomly selected on the same coverslip. Levels for the laser power and detector amplification were optimized for each channel before starting the quantification. Images of the Golgi region were acquired at the same magnification and processed by Metamorph 4.6 (Universal Imaging Corp.).

In vitro binding experiments

To examine the interaction between Hs2-Arf-1 and membrin, HeLa cells overexpressing myc-membrin were lysed in binding buffer (25 mM Hepes, pH 7.5, 100 mM NaCl, 0.5 mM EDTA, 1 mM MgCl2, 1 mM DTT, 1 mM AEBSF, 3 μg/ml leupeptin, 3 μg/ml aprotinin, 3 μg/ml pepstatin A) containing 0.5% Triton X-100. Supernatants of the lysate were incubated with Hs2tagged Δ17Arf1 prebound to Ni-NTA beads (Qiagen) in the presence of 1 mM GDP for 3 h at 4°C and cross-linking reagent DSP was added at a final concentration of 1 mM. After incubation for 20 min at RT,
DSP activity was quenched by addition of 50 mM glycine. The beads were washed and the proteins bound to beads were subjected to SDS-PAGE and immunoblot analysis with anti-myc antibody.

Online supplemental material
Fig. S1 shows that Arf-1-6-1 and Arf-M110I, E113D when loaded with GTP-$\alpha$S could bind to GST-VPS-GAT as well as wild-type Arf-1. Also, measurement of CD spectra of these Arf-1 mutants demonstrated that the general conformation of Arf-1-6-1 and Arf-M110I, E113D is essentially identical to that of Arf-1. Fig. S2 shows that overexpressed GFP can activate Arf-1-6-1 in cells. Online supplemental material is available at http://www.jcb.org/cgi/content/full/jcb.2000409138/DC1.

We thank J. Lippincott-Schwartz, C.I. Jackson, and J.S. Bonifacino for reagents; and J. Lippincott-Schwartz, C.I. Jackson, F. Brown, R. Weigert, and E. Korn for comments on the manuscript. We also thank R.S. Lipstiz and N. Tjandra for support in measuring CD spectra.

A. Honda was supported by the JSPS Research Fellowships for Japanese Biomedical and Behavioral Researchers at NIH.

Submitted: 22 September 2004
Accepted: 16 February 2005

References


Randazzo, J.G., and P.A. Randazzo. 2002. ARAP1: a point of conver-


