There are two clathrin-coated vesicle adaptor complexes in the cell, one associated with the plasma membrane and one associated with the TGN. The subunit composition of the plasma membrane adaptor complex is \( \alpha \)-adaptin, \( \beta \)-adaptin, AP50, and AP17; while that of the TGN adaptor complex is \( \gamma \)-adaptin, \( \beta' \)-adaptin, AP47, and AP19. To search for adaptor targeting signals, we have constructed chimeras between \( \alpha \)-adaptin and \( \beta \)-adaptins within their NH2-terminal domains. We have identified stretches of sequence in the two proteins between amino acids \( \sim130 \) and \( 330-350 \) that are essential for targeting. Immuno-precipitation reveals that this region determines whether a construct coassembles with AP50 and AP17, or with AP47 and AP19. These observations suggest that these other subunits may play an important role in targeting. In contrast, \( \beta \) and \( \beta' \)-adaptins are clearly not involved in this event. Chimeras between the \( \alpha \) and \( \gamma \)-adaptin COOH-terminal domains reveal the presence of a second targeting signal. We have further investigated the interactions between the adaptor subunits using the yeast two-hybrid system. Interactions can be detected between the \( \beta/\beta' \)-adaptins and the \( \alpha/\gamma \)-adaptins, between the \( \beta/\beta' \)-adaptins and the AP50/AP47 subunits, between \( \alpha \)-adaptin and AP17, and between \( \gamma \)-adaptin and AP19. These results indicate that the adaptor subunits act in concert to target the complex to the appropriate membrane.

Both adaptor complexes are heterotetramers, consisting of two 100-kD subunits or adaptins, a medium chain of \( \sim50 \) kD, and a small chain of \( \sim20 \) kD. The plasma membrane adaptor complex is composed of \( \alpha \)-adaptin, \( \beta \)-adaptin, AP50, and AP17, while the TGN adaptor complex is composed of \( \gamma \)-adaptin, \( \beta' \)-adaptin, AP47, and AP19 (Keen, 1987; Ahle et al., 1988). Rotary shadowing of isolated adaptors shows that they consist of a brick-like core or “head” attached to two smaller appendages or “ears” by stalks that are thought to act as flexible hinges (Heuser and Keen, 1988). The ears correspond to the COOH-terminal domain of the two adaptins, while the head consists of the NH2-terminal domains of the adaptins together with the medium and small chains (Kirchhausen et al., 1989) (see the model in Fig. 1). But although the general organization of the complex is known, there is little information on exactly how the adaptor subunits interact with each other, or on what the function of each domain or subunit is. It is not known, for example, which part of the complex is responsible for targeting the adaptor to the correct membrane compartment.

It seems unlikely that the \( \beta \) and \( \beta' \)-adaptins are involved in adaptor targeting for several reasons. They are the most homologous of the four subunits (Kirchhausen et al., 1989; Ponnambalam et al., 1990); they have already been assigned a role in clathrin binding (Ahle and Unger-
wickell, 1989; Gallusser and Kirchhausen, 1993; and Cambridge and Pears (1994) have recently shown that when Drosophila β-adaptin (which shows homology to both β- and β′-adaptins) is transfected into mammalian cells, it localizes to both the TGN and the plasma membrane and assembles with both α- and γ-adaptin. The α- and γ-adaptins are better candidates for proteins containing targeting signals because they are the least homologous of the four subunits, and their ear domains in particular are completely unrelated (Robinson, 1990). In an earlier study we investigated the possibility that the α- and γ-adaptin ear domains might be responsible for targeting by constructing chimeras. A chimera consisting of the α-adaptin NH2-terminal domain, the γ-adaptin hinge, and the γ-adaptin ear (αγγ) was found to be localized to the plasma membrane (Robinson, 1993), suggesting that the γ-adaptin ear domain is not involved in targeting. However, a chimera consisting of the γ-adaptin NH2-terminal domain, the γ-adaptin hinge, and the α-adaptin ear (γγα) was found to be mainly associated with the TGN, but in some cells a fraction of the construct was localized to the plasma membrane. These results suggested that the ear may play a minor role in targeting, but that the major targeting signal is likely to be present in the adaptor head. Thus, any of the subunits with the possible exception of β/β′ could potentially be involved in adaptor localization.

The aim of the present study was to determine which part of the complex is responsible for targeting by making chimeras between the NH2-terminal domains of α- and γ-adaptin. Although there is no reason necessarily to assume that these domains contain the adaptor targeting signals, their localization within the complex suggests that they interact with the other adaptor subunits, and therefore the prediction was that some of the chimeras should assemble into complexes containing a mixture of plasma membrane and TGN adaptor subunits. Thus, this approach should allow us to test whether targeting can be correlated with the presence or absence of a particular subunit, while at the same time providing information about how the subunits interact with each other.

Materials and Methods

Construction of Plasmids

The adaptins have three domains: NH2-terminal (head), hinge, and ear. The NH2-terminal domain is defined as amino acids 1-619 in α-adaptin and 1-592 in γ-adaptin; the hinge is defined as amino acids 620-700 in α-adaptin and 594-703 in γ-adaptin; and the ear domain is defined as amino acids 701-938 in α-adaptin and 704-822 in γ-adaptin (see Robinson, 1989, 1993). Most of the constructs that were made contain the α-adaptin ear, and all have the bovine γ-adaptin hinge, which is required for recognition by the species-specific antibody mAb 100/3 (Robinson, 1993). The basic techniques used in making the constructs are described by Sambrook et al. (1989). The general strategy was first to identify stretches of identical or highly conserved protein sequence in the NH2-terminal domain where α- and γ-adaptin could be joined together. A naturally occurring restriction site was then sought in one DNA sequence and PCR was used to introduce the same site, in frame, into the other sequence. For example, Nv-NcI (the nomenclature refers to the NH2-terminal domain having γ-adaptin sequence up to amino acid residue 331) was made by introducing an ApaI site into γ-adaptin by PCR in the middle of a sequence that is conserved between the two adaptins. The α-adaptin naturally contains this restriction site so a three-way ligation of the following was performed: the γ-adaptin PCR product digested with NotI at the 5′ end and ApaI at the 3′ end (to give the first half of the chimera’s NH2-terminal sequence), α-adaptin digested with ApaI and ApaI (to provide the rest of the NH2-terminal sequence), and the expression vector encoding αγγ (Robinson, 1993) cut with NotI and ApaI (which releases the NH2-terminal domain of the construct, leaving the vector plus the bovine γ-adaptin hinge and α-adaptin ear). The digests were run on an agarose gel, the appropriate bands were isolated, the DNA was extracted using a GeneClean kit (BIO 101, Inc., Vista, CA), and the fragments were ligated together. In some cases no natural site could be exploited so restriction sites were introduced by PCR into both sequences. All of the joins between α- and γ-adaptin sequences and much of the PCR products were sequenced.

The following chimeras were constructed (see Fig. 2): Nv-NcI: introduced a NcoI site in one sequence; Nv-NcI: made use of the BanII site in γ-adaptin; Nv-NcI: made use of the NotI site in γ-adaptin; Nv-NcI: made use of the ApaI site in α-adaptin; Nv-NcI: made use of the SacI site in γ-adaptin; Nv-NcI: made use of the NsiI site in α-adaptin; Nv-NcI: made use of the DraIII site in α-adaptin; Nv-NcI: made use of the HindIII site in α-adaptin; Nv-NcI: introduced an EcoRV site into both sequences; Nv-NcI: made use of the BglII site in α-adaptin; Nv-NcI: made use of the SacI site in γ-adaptin.

Since alignment of the two sequences results in several gaps, the nomenclature does not always reflect the relationship between chimeras of the different series. For example, γ-adaptin residue 330 aligns with α-adaptin residue 330 (for alignment see Robinson, 1990), so that constructs Nv-NcI and Nv-NcI are actually joined within the same conserved stretch of sequence, but one consists of γ followed by α while the other consists of α followed by γ.

All of the chimeras were made using DNA from constructs αγγ in the expression vector pHKY53 (Robinson, 1993). However, because the NH2-terminal domain of the original γγγ construct was a chimera between mouse and cow, this construct was modified to obtain an NH2-terminal γ-adaptin sequence entirely derived from mouse using a similar strategy to that already described, making use of NotI, SacI, and ApaI sites. This facilitated the construction of other chimeras as the bovine NH2-terminal domain has not been entirely sequenced.

The ear swap constructs were made by digesting αγγ with NotI and ApaI to obtain an expression vector containing the hinge and ear domains only. The appropriate plasmid was digested with the same enzymes but in this case the NH2-terminal domain was isolated and ligated into the cut vector.

Transfection into Rat 1 Cells

Rat 1 fibroblasts maintained in DME containing 10% FCS (DME-FCS) were cotransfected with the various constructs and the G418-selectable plasmid prSVneo (Robinson, 1993) using one of the following protocols: (a) the calcium phosphate method as previously described (Robinson, 1990), (b) the DEAE Dextran method. Cells were grown in 25-cm2 flasks and washed in DME, and ~5 μg of construct DNA plus 1 μg of prSVneo in 0.5 ml of DME was added, followed by 0.5 ml of 1 mg/ml DEAE Dextran in TBS, pH 7.4. The cells were then incubated for 30 minutes at 37°C, after which the medium was replaced with DME-FCS containing 0.1 mg/ml chloroquine, and the cells were incubated in this solution for 3 hours at 37°C. The cells were then washed in DME-FCS and incubated overnight.

(c) Transfectam (Promega Corp., Madison WI). Cells grown in 25-cm2 flasks were washed and incubated in 0.5 ml DME. A solution of 10 μl Transfectam in 0.5 ml DME and a solution of DNA (5 μg of construct plus 1 μg of prSVneo) in 0.5 ml DME were mixed together and added to the cells, which were then incubated overnight at 37°C.

In all procedures the cells were trypsinized the next day and split into 3 dishes. They were left for two more days before G418 was added to the medium at a concentration of 0.5 mg/ml. After 2 wk, individual G418-resistant colonies were picked with a sterile yellow tip and transferred to a multiwell plate. Expression of the chimeras was assayed by immunofluorescence. Even after two rounds of cloning, some of the cell lines showed heterogeneity in their expression levels.

Immunofluorescence

Cells grown on multiwell slides were fixed in methanol and acetone as previously described (Robinson, 1990). Immunofluorescence was carried out using the mouse antibody mAb 100/3 (Ahle et al., 1988) which recognizes the bovine but not the rat γ-adaptin hinge. For some experiments the cells were double labeled either with the rabbit antibody C619-656, raised to the αC-adaptin hinge (amino acids 619-656) (Ball et al., 1995) or with an antibody raised against a β-adaptin fusion protein (see below).
Antibody incubations, labeling with secondary antibodies, and mounting and examination of the slides were carried out as previously described (Robinson, 1990).

Production of Monospecific Antibodies

To identify the adaptor subunits that coassemble with the various constructs, monospecific antibodies were raised. First, DNA encoding the subunits was amplified from rat liver cDNA (Clontech) by PCR and ligated into pBluescript, and the identity of the clones was confirmed by sequencing. A second PCR reaction was then used to amplify specific sequences and to introduce restriction sites compatible with pGEX3X. The sequences that were amplified encoded amino acids 583-619 for β-adaptin; amino acids 16-78 and 268-374 for AP50 (AP50-1 and AP50-2); amino acids 17-80 and 268-374 for AP47 (AP47-1 and AP47-2); amino acids 20-61 and 107-142 for AP17 (AP17-1 and AP17-2); and amino acids 20-61 and 107-158 for AP19 (AP19-1 and AP19-2). These sequences were chosen because they are where the two homologues show the most divergence (Kirchhausen et al., 1989, 1991; Ponnambalam et al., 1990; Nakayama et al., 1991). The PCR products were ligated into pGEX3X and transformed into MC1060 host cells for selection on GSH-Sepharose (Pharmacia LKB Biotechnology Inc., Piscataway, N J) according to the manufacturer's instructions. To purify the other seven fusion proteins, inclusion bodies were prepared (Bohmann and Tijian, 1989) and the proteins solubilized in sample buffer and subjected to preparative SDS PAGE. Up to 5 mg purified protein was obtained from each 100 ml culture. Rabbits were injected with 0.5 mg fusion protein in complete Freund's adjuvant, followed by boosts of 0.5 mg fusion protein in incomplete Freund's adjuvant at 2 and 8 wk after the primary injection. 10 d after the final injection, the rabbits were bled out and their sera tested on blots of purified adaptors. 7 of the 10 fusion proteins elicited a response against the appropriate adaptor subunit (the ones that did not were AP50-1, AP17-1, and AP19-1, and these were discarded). To ensure that the antibodies would be monospecific, and to improve the signal relative to background, the seven positive antisera were cross-absorbed and affinity purified. Each fusion protein was coupled to CNBr-activated Sepharose (Pharmacia), and 20 ml of each serum was absorbed over two nights at 4°C with resin containing 0.67 mg of the "wrong" fusion protein (e.g., anti-β was absorbed with β' and vice versa). The resin was then removed by centrifugation, and the sera were absorbed overnight at 4°C with resin containing 0.33 mg of the "right" fusion protein. Bound antibodies were eluted with 0.2 M glyc, pH 2.3, as previously described (Robinson and Pearse, 1986).

Immunoprecipitation and Western Blotting

The immunoprecipitation protocol was based on a method developed by B. Pearse that has previously been described (Robinson, 1993). Cells were lysed in 0.5% NP-40 and centrifuged at high speed to obtain a membrane pellet enriched in assembled adaptor complexes. The pellet was then extracted with 0.5M Na2CO3 to solubilize the membrane-associated adaptors, which were then immunoprecipitated using mAb 100/3, followed by rabbit anti-mouse IgG (Sigma Immunochemicals, St. Louis, MO) and protein A-Sepharose 4BFast (Sigma). After extensive washing (see Robinson, 1993), the pellets were resuspended in 2× sample buffer, boiled, and subjected to SDS PAGE. Gels were blotted onto nitrocellulose and labeled with the antibodies raised against the various adaptor subunits, followed by 125I-protein A (Amersham Corp., Arlington Heights, IL). For maximum resolution, the x-ray film was exposed at room temperature followed by 125I-protein A (Amersham Corp., Arlington Heights, IL). For maximum resolution, the x-ray film was exposed at room temperature followed by 125I-protein A (Amersham Corp., Arlington Heights, IL). For maximum resolution, the x-ray film was exposed at room temperature followed by 125I-protein A (Amersham Corp., Arlington Heights, IL). For maximum resolution, the x-ray film was exposed at room temperature followed by 125I-protein A (Amersham Corp., Arlington Heights, IL). For maximum resolution, the x-ray film was exposed at room temperature followed by 125I-protein A (Amersham Corp., Arlington Heights, IL). For maximum resolution, the x-ray film was exposed at room temperature followed by 125I-protein A (Amersham Corp., Arlington Heights, IL). For maximum resolution, the x-ray film was exposed at room temperature followed by 125I-protein A (Amersham Corp., Arlington Heights, IL).
Assembly of the Nγ Constructs

The immunofluorescence results suggest that a targeting signal may exist in the α- and γ-adaptins somewhere between amino acids 132 and 331. However, the α- and γ-adaptins are part of a complex, and an alternative explanation is that this stretch of sequence may be indirectly involved in targeting by binding to one or more of the other adaptor subunits. Thus, we carried out studies to determine whether there was any correlation between targeting and the presence of a particular subunit. For these experiments it was essential to be able to identify the other subunits unambiguously. To date, no antibodies against the medium and small chains have been described, and the two antibodies available that recognize the β subunits cross-react with both β-adaptin and β'-adaptin (Robinson, 1987; Ashle et al., 1988). In order to raise specific antibodies against each of the subunits, GST fusion proteins were constructed containing unique regions of β-adaptin, AP50, AP17, β'-adaptin, AP47, and AP19, and were used to immunize rabbits. The resulting antisera were tested on blots of purified plasma membrane and TGN adaptors. Fig. 4 shows that all six of the antibodies only recognize the subunit against which they were raised and do not cross-react with the homologous protein in the other complex.

To examine the composition of the adaptor complexes assembled from the chimeric adaptins, mAb 100/3 was used to immunoprecipitate each construct plus associated proteins from a carbonate-extracted high speed pellet of detergent-lysed transfected cells. Similar immunoprecipitates were prepared from cells expressing the constructs γγα and γγγ, and from nontransfected Rat 1 cells. The samples were subjected to SDS PAGE, blotted, and probed with antibodies against the plasma membrane and TGN adaptor subunits (Fig. 5). The antibodies against the adaptor medium chains produced some background labeling of the immunoglobulin heavy chain band, which can be seen in the control immunoprecipitates from the nontransfected cells as well as in the immunoprecipitates of the constructs. However, the specifically labeled adaptor medium chains can be clearly resolved from the immunoglobulin band: they run as much sharper bands just below it.

The αγ construct has been shown to localize to the plasma membrane (Robinson, 1993), and Fig. 5 demonstrates that this construct associates with the plasma membrane adaptor subunits β, AP50, and AP17, although there is also a small amount of β'-adaptin present. Complexes containing the chimeras Nγ-36 and Nγ-132, which are also targeted to the plasma membrane, were also found to contain β, AP50, and AP17. They, too, therefore associate with the subunits normally found in the plasma membrane adaptor complex. No other subunits could be detected in immunoprecipitates of Nγ-190; however, because this construct was found to be present in the high speed pellet in very small amounts, it is possible that the antibodies were not sensitive enough to detect them. The next two chimeras in the series, Nγ-331γ and Nγ-566γ, were found to be associated with β, AP47, and AP19. A small amount of β' could also be detected, suggesting that both β- and β'-adaptin can associate with these two chimeras. However, they appear to assemble preferentially with β-adaptin even though they are recruited to the TGN. A similar pattern was seen with the construct Nγ-331γ (see below). The γγα construct, which is targeted to the TGN (Robinson, 1993), associates with the normal subunits for the TGN adaptor complex, β'-adaptin, AP47, and AP19, although again some heterogeneity is observed for the β/β' subunits as there is a small amount of β-adaptin also present.

These results show a correlation between the presence of a particular medium and small chain and the targeting of the complex to a particular membrane. However, no correlation is seen for β- and β'-adaptin, indicating that the β subunits are not involved in this event. The results also show that unlike the medium and small chains, β- and β'-adaptins behave somewhat promiscuously: although all of the constructs appear to assemble preferentially with one of the two β subunits, small amounts of the other β subunit can also be detected.

Localization of the Nα Constructs

An Nα series of constructs was also made (see Fig. 2), in which α-adaptin sequence is followed by γ-adaptin sequence in the NH2-terminal domain, which is in turn followed by the bovine γ-adaptin hinge and the α-adaptin ear. This series was more difficult to study by immunoprecipitation because only small amounts of protein were
Figure 3. Immunofluorescence localization of the Ny series of constructs. Stably transfected cells were labeled with mAb 100/3, which recognizes the bovine γ hinge and thus only labels the chimeric protein and not endogenous α-adaptin (a–c, g, and h). The cells were double labeled with a rabbit antibody against the α-adaptin hinge, which only recognizes endogenous α-adaptin (d–f, i, and j). Ny-36 (a) and Ny-132 (b) are targeted to the plasma membrane, Ny-190 (c) is cytoplasmic, and Ny-331 (g) and Ny-566 (h) are targeted primarily to the TGN although some plasma membrane labeling can also be seen, particularly in the cells expressing Ny-331 (arrowheads). Bar, 15 μm.
Western blots of purified adaptors labeled with antibodies against the various subunits. Strips were cut from blots of either plasma membrane adaptors (left) or TGN adaptors (right) and probed with antibodies raised against nonhomologous stretches of sequence expressed as GST fusion proteins. The labeling shows that the antibodies are specific for the subunit against which they were raised. The lower molecular mass band labeled with the antibody against β-adaptin is presumably a breakdown product, since β-adaptin is known to be susceptible to proteolysis (Kirchhausen et al., 1989).

brought down, which appeared to be below the limit of detection for most of the antibodies. However, the immunofluorescence results shown in Fig. 6 reveal a very similar pattern to that seen for the Ny series.

Na-132 (Fig. 6, a) is localized to the TGN, with considerable cytoplasmic staining but no detectable plasma membrane staining (d). The next two chimeras in this series, Nα-171 (b) and Nα-265 (c), appear to be completely cytoplasmic with no recruitment to either the plasma membrane (e and f) or the TGN. The last three chimeras, Nα-350 (g), Nα-430 (h), and Nα-566 (i), are recruited to the plasma membrane as shown by their colocalization with endogenous α-adaptin (j–l). Thus, there is again a stretch of ~200 amino acids, between 132 and 350, which appears to be responsible for targeting the adaptors to the appropriate membrane, and chimeras made within this region do not associate with any membrane.

Although the chimeras Nα-350, Nα-430, and Nα-566 are recruited to the plasma membrane, they have a rather patchy distribution. Not every coated pit and vesicle detected with the antibody against endogenous α-adaptin contains the chimeric constructs, and the regions of colocalization generally occur at areas where linear arrays are observed rather than discrete dots. Furthermore, endogenous α-adaptin tends to be depleted from the patches containing the chimeras (Fig. 6, arrowheads). In particularly highly expressing cells, such as those shown in Fig. 7, a and c (small arrowheads), there often appears to be less endogenous α-adaptin in general than nonexpressing cells (large arrowheads). These observations suggest that the chimeras may be competing with endogenous α-adaptin for the other adaptor subunits and/or for docking sites on the membrane. The linear arrays containing the chimeras tend to be concentrated at the cell periphery (Fig. 7, b and d), suggesting that they might be associated with adhesion plaques. However, double labeling with anti-talin revealed only limited colocalization (not shown).

Effect of the Ear Domain on Targeting

The constructs in both the Ny series and the Nα series...
Figure 7. Immunofluorescence localization of the constructs Nct-350 and Na-566 from the Nct series, double labeled with mAb100/3 (a and b) and the rabbit antibody against the α-adaptin hinge (c and d). The constructs are generally found in linear arrays and tend to be concentrated at the cell periphery. In some of the highly expressing cells (small arrowheads), endogenous α-adaptin labeling appears to be less intense than in the nonexpressing cells (large arrowheads). Bar, 15 μm.

generally support the view that the adaptor head contains the major targeting signal. However, one of the constructs, Nγ-331, although primarily targeted to the TGN, also shows a substantial amount of labeling at the plasma membrane. To find out whether this plasma membrane localization is a result of the minor targeting signal in the α-adaptin ear, or whether there is another targeting signal between amino acid 331 and the hinge, an additional construct was made, Nγ-331γ, in which the α ear on Nγ-331 was replaced with the γ-adaptin ear. An equivalent construct was also made from the Nα series, Nα-350γ (see Fig. 2).

Unlike Nγ-331 with the α ear (Fig. 8, a and c; see also Fig. 3), Nγ-331γ is localized exclusively to the TGN (Fig. 8, b and d). This indicates that the presence of the α-adaptin ear is solely responsible for the fraction of Nγ-331 localized to the plasma membrane. The localization of the reverse construct, Nα-350, is also influenced by its ear domain. This construct has a patchy plasma membrane distribution when the α-adaptin ear is present (Fig. 8, e and g; see also Figs. 6 and 7). However, with the γ-adaptin ear, although much of the construct is cytoplasmic, some of it is recruited to the TGN and no plasma membrane localization can be seen (Fig. 8, f and h). Thus, the ear has a much stronger effect on targeting when placed on constructs containing a chimeric NH₂-terminal domain.

Figure 8. Effect of the ear domain on targeting. Cells expressing the constructs Nγ-331 (a) and Na-350 (e) with the α-adaptin ear, and cells expressing the same constructs but with the γ-adaptin ear, Nγ-331γ (b) and Nα-350γ (f), were double labeled with mAb 100/3 (a, b, e, and f) and the rabbit antibody against the α-adaptin hinge (c, d, g, and h). The presence of the γ-adaptin ear results in more TGN labeling relative to plasma membrane labeling. Bar, 15 μm.

Localization of β-Adaptin

Are the β subunits redistributed in cells expressing some of the chimeras? Because the antibody raised against β-adaptin was able to be used for immunofluorescence, it was possible to address this question by double labeling.
Some of the constructs in the N\textsubscript{y} series, including N\textsubscript{y}-566, were found to associate preferentially with \(\beta\)-adaptin although they are localized to the TGN, which suggests that some of the \(\beta\)-adaptin in these cells should also be detectable at the TGN. Fig. 9 shows a mixture of transfected and nontransfected cells double labeled for the construct (a) and for \(\beta\)-adaptin (b), and reveals that in the transfected cells, there is indeed a significant redistribution of \(\beta\)-adaptin to the TGN.

Another prediction is that by analogy with the N\textsubscript{y} series, constructs such as N\textsubscript{a}350 in the N\textsubscript{a} series should preferentially coassemble with \(\gamma\prime\)-adaptin rather than \(\beta\)-adaptin. Thus, since endogenous \(\alpha\)-adaptin is depleted from patches of coated pits containing the construct, \(\beta\)-adaptin should also be depleted. Fig. 9, c and d, shows that this is in fact the case. However, because as yet we have no evidence that the construct associates with \(\gamma\prime\)-adaptin, we cannot completely rule out the possibility that adaptor complexes assembled from this construct contain no \(\beta\) subunit of either type.

**Interactions between the Adaptor Subunits**

The results of the chimera experiments suggest that the \(\alpha\)- and \(\gamma\)-adaptns interact both with the \(\beta\)/\(\beta\prime\)-adaptns and with the medium and/or small chains. However, it is not possible using this method to show conclusively that two subunits bind to each other, because all of the adaptor subunits are coexpressed within the same cell and interactions could be indirect. To investigate interactions between defined pairs of subunits, we made use of the yeast two-hybrid system. cDNAs encoding the various subunits were inserted into the yeast vectors pGAD424 and pGBT9. pGAD424 directs the expression of a transcriptional activator fusion protein, while pGBT9 directs the expression of a GAL 4 DNA binding domain fusion protein. If the two fusion proteins interact, the transcriptional activator domain is brought to the correct location to allow production of \(\beta\)-galactosidase, which can be detected either by a plate assay or by a liquid culture assay.

Table I shows the results of coexpressing different adaptor subunits using this system. As predicted by the immunoprecipitation experiments, \(\beta\)- and \(\gamma\prime\)-adaptns were found to behave promiscuously, binding to subunits in both adaptor complexes. Thus, \(\beta\)-adaptin is able to interact not only with \(\alpha\gamma\alpha\) and with the plasma membrane adaptor medium chain AP50, but also with \(\gamma\)-adaptin (\(\gamma\gamma\alpha\) and \(\gamma\gamma\gamma\)) and with AP47. Similarly, \(\beta\prime\)-adaptin associates with both plasma membrane and TGN adaptor \(\alpha\gamma\gamma\) subunits and medium chains. No interactions could be detected between the \(\beta\) subunits and the adaptor small chains.

Constructs containing the \(\alpha\)- and \(\gamma\)-adaptin NH\textsubscript{2}-terminal domains, \(\alpha\gamma\alpha\) and \(\gamma\gamma\gamma\), were found to bind both to the

![Figure 9. Immunofluorescence localization of \(\beta\)-adaptin in cells expressing the N\textsubscript{a}350 (c and d) and N\textsubscript{y}566\textsubscript{y} (a and b) constructs. A mixture of transfected and nontransfected cells were double labeled with mAb100/3 (a and c) and an antibody against \(\beta\)-adaptin (b and d). Expression of the constructs causes a redistribution of \(\beta\)-adaptin. In the case of the N\textsubscript{a}350-expressing cells, \(\beta\)-adaptin is partially localized to the TGN region. In the case of the N\textsubscript{y}566\textsubscript{y}-expressing cells (small arrowheads), \(\beta\)-adaptin labeling is less intense, especially in regions containing the construct, than in nonexpressing cells (large arrowheads). Bar, 15 \(\mu\)m.](attachment:figure9.jpg)

**Table I. The \(\beta\)-Galactosidase Activities of Adaptor Subunits in the Two-Hybrid System**

| pGAD424 insert | pGBT9 insert | Colony color | \(\beta\)-Galactosidase units |
|----------------|-------------|--------------|-----------------------------|
| \(\beta\) | None | White | 0.00 |
| \(\beta\) | \(\alpha\gamma\alpha^*\) | Blue | 38.56 |
| \(\beta\) | \(\gamma\gamma\alpha\) | Blue | 0.37 |
| \(\beta\) | \(\gamma\gamma\gamma\) | Blue | 0.52 |
| \(\beta\) | AP50 | Blue | 102.00 |
| \(\beta\) | AP47 | Blue | 25.35 |
| \(\beta\) | AP17 | White | 0.00 |
| \(\beta\) | AP19 | White | 0.00 |
| \(\beta\) | None | White | 0.08 |
| \(\beta\) | \(\alpha\gamma\alpha^*\) | Blue | 22.29 |
| \(\beta\) | \(\gamma\gamma\alpha\) | Blue | 1.41 |
| \(\beta\) | \(\gamma\gamma\gamma\) | Blue | 1.45 |
| \(\beta\) | AP50 | Blue | 20.08 |
| \(\beta\) | AP47 | Blue | 18.65 |
| \(\beta\) | AP17 | White | 0.01 |
| \(\beta\) | AP19 | White | 0.03 |
| \(\alpha\gamma\alpha\) | None | White | 0.01 |
| \(\alpha\gamma\alpha\) | AP50 | White | 0.00 |
| \(\alpha\gamma\alpha\) | AP47 | White | 0.00 |
| \(\alpha\gamma\alpha\) | AP17 | Blue | 1.32 |
| \(\alpha\gamma\alpha\) | AP19 | White | 0.01 |
| \(\gamma\gamma\alpha\) | None | White | 0.01 |
| \(\gamma\gamma\alpha\) | AP50 | White | 0.02 |
| \(\gamma\gamma\alpha\) | AP47 | White | 0.00 |
| \(\gamma\gamma\alpha\) | AP17 | White | 0.00 |
| \(\gamma\gamma\alpha\) | AP19 | Blue | 12.35 |

Yeast strains were grown in SD media lacking leucine and tryptophan and \(\beta\)-galactosidase assays were performed on at least two independent colonies.* \(\alpha\gamma\alpha\) in the yeast vector pGBT9 produces a background \(\beta\)-galactosidase activity of 2.86 units.

Page and Robinson *Adaptor Targeting Signals and Subunit Interactions*
**Discussion**

Previous studies making use of α- and γ-adaptin chimeras have indicated that the major targeting determinant resides in the adaptor head rather than in the α and γ hinge or ear domains (Robinson, 1993). The present study reveals that a stretch of ~200 amino acids within the α- and γ-adaptin NH2-terminal domain is important for the targeting of adaptors to the appropriate membrane. In the first series of constructs, the chimera Nγ-132 was found to be recruited to the plasma membrane while Nγ-331 was directed primarily to the TGN, suggesting that residues 132 to 331 are involved in targeting, but not residues 1-132 and 331-600. A similar conclusion was reached from the reverse series of constructs, where a region between residues 132 and 350 was found to be important. Any chimera made with a join between α- and γ-adaptin within this 200 amino acid stretch resulted in a cytoplasmic distribution, suggesting that this disrupted the targeting signal.

However, these findings do not necessarily mean that the 200-amino acid stretch itself contains the targeting signal. The NH2-terminal domain of α- and γ-adaptin is the part of the protein that interacts with the other adaptor subunits, any one of which might contain targeting information, and an alternative explanation is that this stretch of sequence may be necessary for binding one or more of the other proteins. Thus, the subunit composition of the adaptor complexes assembled from the chimeric adaptins was determined. In the Nγ series, essentially all of the constructs were found to associate preferentially with β-adaptin rather than with β'-adaptin, including those with a TGN distribution. Previous studies suggested but did not prove that the β subunits are not involved in adaptor localization. The present findings provide definitive evidence that β- and β'-adaptin do not contain any targeting information.

In contrast, the medium and/or small chains are strong candidates for subunits containing targeting signals, since the chimeras Nγ-36 and Nγ-132, which are targeted to the plasma membrane, were found to associate with AP50 and AP17, while Nγ-331, Nγ-566, and Nγ-331γ, which are targeted either primarily or exclusively to the TGN, interact with AP47 and AP19. This correlation between the presence of a particular medium and small chain and recruitment onto a particular membrane suggests that one or both of these subunits are likely to be involved in targeting, although a role for α/γ-adaptin NH2-terminal sequence cannot be ruled out.

Although the major targeting determinant appears to reside in the adaptor head, the α- and γ-adaptin ears also contribute to targeting. This possibility was suggested by the original ear swap experiments, but the contribution of the ears is more striking in the present study where different ears were placed on NH2-terminal domain chimeras. Thus, Nγ-331 with the α ear is found at the plasma membrane as well as at the TGN, while Nγ-331 with the γ ear (Nγ-331γ) is found exclusively at the TGN; and Nα-350 with the α ear has a patchy plasma membrane distribution, while with the γ ear (Nα-350γ) the membrane-associated fraction is found at the TGN. One possible explanation for these observations is that the ears may play a passive role in targeting, promoting adaptor-adaptor interactions and thus causing chimeric adaptors to bind to a particular membrane through interactions with endogenous adaptors. However, although self-association has been observed for plasma membrane adaptors in vitro (Beck and Keen, 1991), it seems to involve the head rather than the ear domains, and no such self-association has been observed for TGN adaptors. Alternatively, the ear domain might contain a weak but active targeting signal that takes over when a more dominant targeting signal is destroyed or weakened. This second possibility is supported by the observation that most of the NH2-terminal domain chimeras appear to be impaired in their ability to interact with membranes, resulting in a more cytoplasmic distribution than that observed for either wild-type or ear-swapped adaptins. The fact that such chimeras, at least in the Nγ series, are still capable of interacting with the medium and small chains suggests that the α- and γ-adaptin NH2-terminal domains may contain intrinsic targeting information.

Although most of the chimeras showed at least some membrane association, those made with a join between amino acids ~130 and 330-350 appeared to be completely cytoplasmic. This suggests either that such constructs are missing a targeting signal in this region, or that they are unable to fold correctly and/or to coassemble with one or more of the other subunits. In the blot shown in Fig. 4 of the Nγ series, none of the other subunits could be detected in the immunoprecipitate of the cytoplasmic construct Nγ-190, but this result must be interpreted with caution since the precipitate also contained relatively little of the construct itself. Attempts to label blots of immunoprecipitates from the supernatant/ cytosol fraction rather than the pellet/membrane fraction generally resulted in very high background, but AP19 was clearly present (not shown), and our inability to detect any of the other subunits unambiguously may simply be a reflection of the quality of the antibodies (the adaptor subunits are very poor antigens and these are the first such antibodies so far described).

Three of the constructs in the Nα series, Nα-350, Nα-430, and Nα-356, had an unexpected distribution: they were found in only a subset of the plasma membrane coated pits, which tended to form linear arrays. This sort of linear pattern has also been observed in nontransfected cells, where the lines have been shown to correspond to stress fibers (Anderson et al., 1978), but in the transfected cells these linear arrays were often devoid of endogenous adaptors. The exclusion of endogenous adaptors from the coated pits containing the constructs suggests that some sort of competition might be occurring. For instance, the chimeric adaptors may compete with endogenous adaptors for a specific receptor or docking site, or they may preferentially self-associate. Alternatively, they may be impaired in their ability to cycle on and off the membrane...
and the coated pits containing the chimeras may be old pits unable to pinch off as coated vesicles and/or to uncoat. As well as providing information about targeting signals, the construction of chimeras has also extended our knowledge of how the adaptor subunits interact with each other. Thus, we have identified amino acids 132–331 as a sequence involved in the binding of the medium and/or small chains, since the construct Nγ-γ-132 associates with AP50 and AP17, while Nγ-331 associates with AP47 and AP19. We have also identified amino acids 566–594 as a sequence involved in the binding of the β subunit, since Nγ-566 preferentially associates with β-adaptin while γγγ preferentially associates with β'-adaptin. Interestingly, this sequence is immediately downstream from an 11-amino acid sequence that is identical in α- and γ-adaptin. Possibly the two sequences together constitute an important part of the β binding domain, the first sequence being involved in general binding and the second sequence providing some specificity. It is clear, however, that β- and β'-adaptin behave somewhat promiscuously. Immunoprecipitates not only of the NH2-terminal domain chimeras, but also of the constructs αγγ and γγγ, and even of wild-type α- and γ-adaptins in pig brain cytosol (not shown), show a certain amount of coprecipitation of the wrong β subunit.

The yeast two-hybrid approach has allowed us to investigate interactions between adaptor subunits more directly, using a more defined system. We were able to confirm that β- and β'-adaptin bind promiscuously, not only to α- and γ-adaptin but also to the adaptor medium chains. We were also able to demonstrate complex-specific interactions between the α/γ subunits and the adaptor small chains. Thus, we can now begin to refine the schematic model shown in Fig. 1 to include specific protein–protein interactions. An earlier study making use of reversible cross-linkers suggested that the 100-kD proteins (i.e., adaptins) interact with both the medium and the small chains, but at that time it was not possible to distinguish between the different adaptins (Virshup and Bennett, 1988). More recently a model has been proposed, based on relative sequence homologies, in which the β subunits bind to the small chains while the α/γ subunits bind to the medium chains (Nakayama et al., 1991). Our results show that in fact the opposite is the case. However, we cannot rule out the possibility that that there may be additional interactions that cannot be detected using the two-hybrid system due to conformational differences between isolated subunits and the adaptor complex as a whole. Indeed, it seems likely that the medium and small chains must interact with each other to account for our immunoprecipitation results, since AP50 was always found to be coincident with AP17, and AP47 with AP19.

In conclusion, our results show that there must be more than one targeting signal in the adaptor complex. The β subunits, which are to some extent interchangeable, can be ruled out; but the α- and γ-adaptin ears play more of a role in targeting than was previously suspected, and there is also a targeting signal in the head that is likely to involve the medium and/or small chains, and possibly also the NH2-terminal domains of the α- and γ-adaptins. These findings can be correlated with studies on adaptor targeting making use of in vitro reconstitution systems. It is clear from such studies that adaptor recruitment is not a simple binding event. Energy is required, and there is evidence that members of the ARF family of proteins are involved, possibly by activating the putative docking proteins (Robinson and Kreis, 1992; Traub et al., 1993; Stamnes and Rothman, 1993; Seaman et al., 1993). Membrane proteins known to be concentrated in clathrin-coated pits and vesicles, such as the mannose-6-phosphate receptor, are also likely to play a role (Le Borgne et al., 1993). Recent cross-linking experiments suggest that the docking proteins may consist of more than one subunit (Seaman, 1995; Seaman and Robinson, unpublished observations). Thus, it is possible that different targeting signals on the adaptor complexes interact with different components of the cellular machinery involved in adaptor recruitment. The yeast two-hybrid system has the potential to be used not only to investigate interactions between known proteins such as neighboring adaptor subunits, but also to look for unknown binding partners. We are currently using this method to try to identify novel proteins that interact with each of the adaptor subunits.

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