The Golgi-localization of Yeast Emp47p Depends on Its Di-lysine Motif But Is Not Affected by the retl-1 Mutation in α-COP

Stephan Schröder, Frauke Schimmöller, Birgit Singer-Krüger, and Howard Riezman
Department of Biochemistry, Biozentrum, University of Basel, CH-4056, Switzerland

Abstract. The Saccharomyces cerevisiae EMP47 gene encodes a nonessential type-I transmembrane protein with sequence homology to a class of intracellular lectins defined by ERGIC-53 and VIP36. The 12-amino acid COOH-terminal cytoplasmic tail of Emp47p ends in the sequence KTKLL, which conforms with the consensus for di-lysine-based ER-localization signals. Despite the presence of this motif, Emp47p was shown to be a Golgi protein at steady-state. The di-lysine motif of Emp47p was functional when transplanted onto Ste2p, a plasma membrane protein, conferring ER localization. Nevertheless, the di-lysine motif was required for Golgi-localization of Emp47p and showed the same charge-independent, position-dependent characteristics of other di-lysine motifs.

α-COP has been shown to be required for ER localization of di-lysine–tagged proteins. Consistent with this finding, the Ste2p-Emp47p hybrid protein was mislocalized to the cell surface in the α-COP mutant, retl-1. Surprisingly, the Golgi-localization of Emp47p was unaffected by the retl-1 mutation. To investigate whether Emp47p undergoes retrograde transport from the Golgi to the ER like other di-lysine–tagged proteins we developed an assay to measure this step after block of forward transport in a sec12 mutant. Under these conditions retrograde transport led to a specific redistribution of Emp47p from the Golgi to the ER. This recycling occurred from a Golgi subcompartment containing α,1,3 mannose-modified oligosaccharides suggesting that it originated from a medial- or later Golgi compartment. Thus Emp47p cycles between the Golgi apparatus and the ER and requires a di-lysine motif for its α-COP–independent, steady state localization in the Golgi.

The secretory pathway in eukaryotic cells is topologically separated into several distinct membrane-bound compartments performing different functions. Newly synthesized secretory proteins are transported through the compartments in a vectorial fashion. For some steps in this pathway specific positive signals have been identified that ensure proper delivery of a particular polypeptide to its final destination. Transport of secretory proteins from one compartment to the next is generally believed to be mediated by vesicles with characteristic coats, an increasing number of which are being characterized (Ladinsky et al., 1994; Narula and Stow, 1995).

The concept of secretory proteins passing through stable compartments must also account for the proper localization of those proteins that accomplish the specific functions characteristic for any given compartment. This localization problem for resident proteins can be solved by one or a combination of the following mechanisms: (a) passive retention because forward transport requires a signal, (b) active retention via some intermolecular interaction, and (c) retrieval/recycling after transport to another compartment. Proteins that function in sorting and transport between compartments will also have to be recycled if they are used for more than one round of transport.

For the localization of ER proteins two mechanisms conserved from yeast to mammalian cells have been uncovered in recent years, both belonging to class c as defined above. The first is the HDEL/KDEL retrieval system for ER-proteins. The COOH-terminal peptide sequence HDEL (Saccharomyces) or KDEL (mammalian cells) on luminal, but also on a few transmembrane proteins, is recognized by a specific receptor, Erd2p, present in the Golgi apparatus. Ligand transported out of the ER is bound by the receptor and the receptor/ligand complex then returns to the ER (Dean and Pelham, 1990; Lewis and Pelham, 1990, 1992; Lewis et al., 1990; Semenza et al., 1990). For transmembrane proteins of the ER another short COOH-terminal peptide sequence was identified that conferred ER localization (Pääbo et al., 1987; Nilsson et al., 1989; Jackson et al., 1990). This motif contains two critical lysine residues at either position -3,-4 or -3,-5 with respect to the COOH terminus of the protein. Using chimeric proteins, evidence was obtained in mammalian cells (Jackson et al., 1993) that the di-lysine motif, similarly to the
Abbreviations used in this paper: AL, anti-lumenal; AT, anti-tail; ER-GIC, ER-Golgi intermediate compartment.

HDEL/KDEL can mediate retrieval of proteins from post-ER compartments. Analyzing sugar modifications and the subcellular distribution of chimaeric proteins in yeast, Townsley and Pelham (1994) and Gaynor et al. (1994) provided convincing evidence for retrieval, possibly from the Golgi cisterna that is functionally defined by the presence of Ochlp. This glycosyltransferase adds the first O-glycosaccharides in yeast (Nakanishi-Shindo et al., 1994; Schweizer et al., 1990). ERGIC-53 and VIP36, a transmembrane protein from a monocytic cell line (Arar et al., 1995), were rediscovered as a major intracellular mannose-binding protein from a monocytic cell line (Arar et al., 1995).

In the present study we report the cloning and sequencing of a novel gene from Saccharomyces cerevisiae, EMP47, coding for a type I transmembrane protein with a di-lysine motif and with sequence homology to the ERGIC-53/VIP36 protein family. We characterized the distribution of Emp47p and showed that its steady-state Golgi localization requires its di-lysine motif, but is independent of α-COP, even though Emp47p cycles between the ER and the Golgi. We suggest models for Emp47p function based on its trafficking pattern.

Materials and Methods

Strains and Growth Conditions

Strains of Saccharomyces cerevisiae used in this study are listed in Table I. Unless otherwise mentioned, indicated strains were grown in complete medium (2% yeast extract, 2% peptone, 40 μg/ml uracil and adenine, and 2% glucose) to exponential phase (2×10^7 cells/ml) at 30°C. For cloning purposes Escherichia coli XL1 blue (Stratagene, La Jolla, CA) was used if not otherwise indicated.

Cloning of EMP47

Degenerate oligonucleotides deduced from the NH2-terminal sequence of p44 (NH2-HPLGDTSDAGKL; Singer-Krüger et al., 1993) were used to identify a clone designated 61 (Birgit Singer-Krtiger, 1993) from a yeast genomic library (Heitman et al., 1991). Clone 61 contained an insert of ~5.4 kb. The insert was mapped with respect to the site hybridizing with the degenerate oligonucleotides. A 2.3-kb EcoRI fragment was determined to comprise the whole gene. This fragment was subcloned into pBSK+ (Stratagene, La Jolla, CA). Restriction fragments of the EcoRI clone were sequenced using the dideoxynucleotide chain termination method (Sanger et al., 1977). Remaining gaps in the sequence were filled in by priming the sequencing reactions with specific oligonucleotides.

Table I. Strains of Saccharomyces cerevisiae Used in This Study

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1. Abbreviations used in this paper: AL, anti-lumenal; AT, anti-tail; ER-GIC, ER-Golgi intermediate compartment.
Biocomputing

All sequence analysis was performed on a VAX computer using the programs of the GCG-package (Genetics Computer Group, Madison, WI) and additional programs implemented by the Biozentrum Biocomputing Unit led by R. Doelz.

Construction of Deletion Disruption Mutants in EMP47

The 2.3-kB EcoRI fragment was subcloned into a pBSK-vector deleted for its single Sall site. The HincII fragment between nucleotides 469-1218 (numbering according to Fig. 1 A) was replaced with a 1.1-kb HindIII fragment blunt ended with Klenow enzyme and comprising URA3. Alternatively, the NsiI fragment between nucleotides 106-1375 was deleted, the ends blunt ended with T4 polymerase and the 4.2-kb Sall fragment of pBP6 (Fleig et al., 1986) comprising LYS2 was inserted. The resulting plasmid was cut with EcoRI and the digest transformed into RH1203, RH488, and RH732 using the LiAc-transformation method (Gietz et al., 1992) which was applied for all yeast transformations described in this work. Successful disruption was monitored by Western blotting with antisera AL (see below).

Recombinant EMP47 Variants

Myc-tagging: the 2.3-kB EcoRI fragment was partially digested with NsiI, the open sites were cut back to blunt ends and religated. A clone with the closed NsiI site at 1375 destroyed was opened at the remaining NsiI site at nucleotide 106. Annealed oligonucleotides coding for the 9E10 epitope (Evan et al., 1985) were introduced, reconstituting the NsiI site at the 3'-end of the epitope. The oligonucleotides introduced the sequence FQKLLSEEDLNEA at amino acid 9 of mature Emp47p. Introduction of an N-linked glycosylation site: the clone coding for the myc-tagged Emp47p was used to introduce two overlapping N-linked glycosylation consensus sites at position 49 and 50 (numbering of wild-type Emp47p as in Fig. 1 A) by PCR mutagenesis (Ho et al., 1989). The final PCR product was digested with DraII and NsiI, and the corresponding fragment cloned back into the plasmid coding for the myc-tagged Emp47p. Mutations of the COOH-terminal cytoplasmic tail of Emp47p were also created by PCR mutagenesis. The Sall(1218)/BamHI/J567 fragment (nucleotide numbers refer to Fig. 1 A) of the final PCR product was exchanged for the corresponding fragment of the wild-type sequence. All inserted sequences introduced from oligonucleotides or PCR mutagenesis were verified by sequencing. The recombinant EMP47 genes were transplanted into EcoRI or EcoRI/BamHI fragments into either Ylp1ac128 for integration at leu2 or into Ylp1ac204 for integration at trpl (Gietz and Sugino, 1988) after cutting the plasmids with BstXI.

Generation of Ste2p with the Cytosolic Tail of Emp47p: Ste2p-Emp47pTail

The plasmid pJR-320Bam-345Stop (Letourneur et al., 1994) was cut at the trpl locus. Recipient strains were MATA in which STE2 had been deleted by disruption using plasmid pUSTE203 (Nakayama et al., 1988).

Antibodies

Two antisera against Emp47p-specific sequences were raised in rabbits. The first, denoted AT (for anti-tail) was generated against a peptide (Neosystem Laboratoire, Strasbourg, France) comprising the 12 COOH-terminal amino acids of Emp47p and the stop codon were ligated into the BamHI site. The relevant region of the construct was sequenced. The construct was linearized with StuI for integration at the ara2 locus. Recipient strains were pGEMH15 (Matsuzawa et al., 1991) which was used in all cases where AT was used in this study. The second antiserum, called AL (for anti-lumenal) was raised against most of the luminal domain of Emp47p. The gene fragment ranging from the XbaI(197) site to the Sall (1218) site (nucleotide numbering according to Fig. 1 A) was cloned behind a 5'-6His-tag in the vector pOE11 (Kontron, Zürich, Switzerland). The recombinant protein was expressed in E. coli M15 and purified on a Ni2+-matrix. The purified protein was used for immunization of a rabbit and later, after coupling to CNBr-activated Sepharose 4B, for affinity purification of the serum. On Western blots, this antiserum recognized all recombinant variants of Emp47p described in this study. A glycinine/HC1, pH 2.5, eluate from the affinity-column was used. Antibodies against a13-linked mannose residues were generated according to Ballou (1970, 1976) using strain RSY918. The serum was absorbed as extract from RSY918 coimmobilized to CNBr-activated Sepharose 4B. A peptide antibody against Ste2p was described in Zanolari et al. (1992).

The following antibodies were used at the recommended dilutions: (A) polyclonal: Kar2p (kindly provided by R. Schekman, University of California, Berkeley, CA), Ochlp (kindly provided by Y. Jigami, National Chemical Laboratory for Industry, Tsukuba, Japan), Wbp1p (kindly provided by S. te Heesen, Eidgenössische Technische Hochschule, Zürich, Switzerland), alkaline phosphatase (kindly provided by D. Gallwitz, Max Planck Institute for Biophysical Chemistry, Göttingen, Germany); (B) monoclonal: 13Dll, directed against the 60-kD subunit of the vacuolar ATPase (kindly provided by T. Stevens, University of Oregon, Eugene, OR), 12CA5, directed against the HA-epitope (kindly provided by H. Rudolph, University of Stuttgart, Stuttgart, Germany), and 9E10, directed against the myc-epitope (kindly provided by R. Movva, Sandoz AG, Basel, Switzerland).

Indirect Immunofluorescence

Approximately 107 cells were sedimented for 1 h in a tabletop centrifuge and resuspended in fixative (PBS/3% paraformaldehyde/10% sorbitol). Prefixing the cells before spinning did not change the Emp47p pattern. After 1 h, cells were washed with PBS/10% sorbitol and the cell walls were digested for 1 h at 30°C (in 100 μl PBS/10% sorbitol with 0.14 μl β-mercaptoethanol) with an empirically determined amount of lyticase (Schen et al., 1991). Cells were washed with PBS/10% sorbitol and adsorbed to multiwell slides treated with poly-L-lysine. Quenching solution (PBS/10% sorbitol/1% BSA/1% Triton X-100) was added for 10 min at ambient temperature and then replaced by quenching solution containing the appropriate primary antibodies. The incubation at room temperature lasted for 1 h. The cells were then quickly washed five times with PBS/10% sorbitol. Fluorescently labeled secondary antibodies were added in quenching solution for 45 min at ambient temperature (Cy3-conjugated goat anti-rabbit IgG, Cy3-conjugated goat anti-mouse IgG; Jackson ImmunoResearch Laboratories, West Grove, PA; FITC-conjugated sheep anti-mouse IgG; Cappel Research Products, Durham, NC). Cells were then quickly rinsed five times, washed twice for 5 min, and three more times quickly with PBS/10% sorbitol. Embedding medium ( vectashield; Vector Laboratories, Burlingame, CA) supplemented with 0.1 μg/ml DAPI was added and slides covered with cover slips. Cells were viewed in a fluorescence microscope and documented by conventional photography or by storage of a digital image obtained with a video camera.

Enzymatic Assays

Kex2p was detected according to the method of Cunningham and Wicker (1989) with the modifications of Singer-Krüger et al. (1993). GDPase was measured as described by Abejon et al. (1989) and LeBel et al. (1978) with the modifications of Singer-Krüger et al. (1993).

Subcellular Fractionation by Velocity Sedimentation on Sucrose Density Gradients

The procedure was carried out with some modifications based on the protocol developed by Antebi and Fink (1992). Cells were spheroplasted in a volume of 2 ml as described previously (Schimmoller and Riezman, 1993) and then directly lysed by at least 10 passages through a 25-gauge needle after adding protease inhibitors to the final indicated concentrations: phenylmethylsulfonylfluoride (1 mM), leupeptin, aprotinin and pepstatin (5 μg/ml each). The lysate was cleared twice for 5 min at 500 × g in 2 ml reaction tubes. The supernatant (~1 ml) was confirmed by microscopy to be

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Cells were harvested and resuspended in fresh complete medium at ambient temperature at a density of 0.6 × 10³ cells/ml. Then 20 μg/ml cycloheximide was added. Within 5 min cells were split into aliquots of 0.6 × 10³ cells and transfected for 1 h to a shaking water bath set at either 24 or 35°C. After incubation, 10 mM Na₂SO₄ and 10 mM NaF (final concentration) were further disrupted with glass beads by shaking on an Eppendorf Mixer 5432 (Eppendorf, Hamburg, Germany) for 15 min. The samples were further processed for immunoprecipitation essentially as described above.

Results

EMP47 Is a Novel Gene Coding for a Transmembrane Protein

In previous work, partially purified endosomal fractions were prepared from Saccharomyces cerevisiae cells and a major Triton-X-114-soluble integral membrane protein in these fractions was named p44. NH₂-terminal sequencing of p44 yielded the sequence of the first 12 amino acids (Singer-Krüger et al., 1993). This sequence information was used to design degenerate oligonucleotides for the isolation of a genomic clone encoding p44. The clone was mapped and the sequence of a 2.3-kb EcoRI subfragment was determined (Fig. 1 A). An open reading frame of 1335 nucleotides is present on this fragment. 84 nucleotides downstream of the first ATG-initiation codon the open reading frame codes for the NH₂-terminal peptide of p44 (Fig. 1 A). Only a single amino acid difference at position 10 was noted between the NH₂-terminal peptide sequence (Gly) and the sequence derived from the DNA (Ser). The protein sequence upstream of the NH₂ terminus of the mature polypeptide is hydrophobic in nature (Fig. 1 B) and conforms with the rules for cleavable signal peptides (von Heijne, 1983). The mature polypeptide of 417 amino acids has one potential hydrophobic transmembrane domain (Fig. 1 B) ending only 12 amino acids before the COOH terminus. The presence of a cleaved signal peptide and the COOH-terminally located transmembrane domain imply that the protein adopts a type I-transmembrane orientation. This was verified by protease protection experiments (data not shown).

We named the gene EMP47 because the mature polypeptide has a calculated molecular weight of 47 K. We deleted one copy of EMP47 in the diploid strain RH1201 by replacing the internal HincII fragment (nucleotides 469–1218) with a 1.1-kb URA3 fragment. The disruption was verified by Southern analysis. After sporulation and dissection all spores within a tetrad grew equally well at temperatures from 15 to 37°C (data not shown). The disruptants still coded for a hypothetical truncated protein of 129 amino acids. However, haploid strains in which EMP47 was disrupted with LYS2 (see below) leaving only nine amino acids of the mature Emp47p were also viable from 15 to 37°C (data not shown).

Emp47p Is Homologous to the ERGIC-53/VIP36 Class of Intracellular Lectins

Database searches with the Emp47p sequence did not yield any obviously homologous proteins. We noticed, however, a significant homology between Emp47p and ERGIC-53 (Schindler et al., 1993) when directly comparing the two sequences. ERGIC-53 is a human type I transmembrane protein that has been shown to cycle between the ER, ERGIC, and the cis-Golgi and was defined as a marker protein for the ER to Golgi intermediate compartment (Schweizer et al., 1988). Fiedler and Simons (1994) have found homology between ERGIC-53 and VIP36. VIP36 is a type I transmembrane protein described in epithelial cells to be present in the Golgi, on the apical and basolateral surface and in transport vesicles directed towards them (Fiedler et al., 1994). Pairwise alignments between all three proteins with the program BESTFIT yielded significant homology scores. The scores were always more than five standard deviations higher than the mean score for alignments of the randomized sequences (Table II). The pairwise alignment scores for ERGIC-53 versus VIP36 are clearly better than those for the alignments with Emp-
47p, indicating that Emp47p is a more distant member of the family. Multiple alignment (Fig. 1, C and D) underscores, however, the observation that all three proteins are related to each other. This is most notable in the first 250 amino acids of the mature proteins (Fig. 1 C). The first 250 amino acids of VIP36 and ERGIC-53 were previously reported to display some homology with leguminous lectins. It was suggested that VIP36 and ERGIC-53 may function as intracellular lectins (Fiedler et al., 1994; Fiedler and Simons, 1994). Indeed very recently Arar et al. (1995) have isolated a mannose binding protein from myelomonocytic cells that proved to be identical to ERGIC-53.

The tertiary structures of both leguminous lectins and human galectins are mainly organized into antiparallel β-sheets (Sharon, 1993; Lobasnov et al., 1993). Emp47p has the same structural feature predicted for its first 250 amino acids (Fig. 1 B). The sequence homology with ERGIC-53 and VIP36 and the similar secondary structure predictions both qualify Emp47p as a putative intracellular lectin. The region of Emp47p from near amino acid 250 to the start of the transmembrane domain is predicted to have mainly α-helical (Fig. 1 B). In particular there is a probability of 0.78 (PEPCOIL, Lupas et al., 1991) to form coiled coil structures in the region from amino acid 336 to 364. This region may form a spacer separating the putative lectin domain from the membrane.

The short cytoplasmic tails of ERGIC-53, VIP36, and Emp47p also seem to be related to each other both in length and sequence (Fig. 1 D). In particular we noted the presence of a consensus ER-localization sequence of the KXXX type in Emp47p, corresponding to the KXXX type motif in ERGIC-53 (Jackson et al., 1990, 1993; Schindler et al., 1993). Although the COOH-terminal KRXX in VIP36 does not fit the di-lysine consensus and VIP36 was not reported to be present in the ER, the cytoplasmic domain of VIP36 is nevertheless overall remarkably similar to those of Emp47p and ERGIC-53.

**Emp47p Is Not an ER Protein but Colocalizes with a Golgi Marker**

Three yeast proteins with a di-lysine ER-localization consensus sequence have been identified so far. The first was the type I transmembrane protein Wbp1p, a subunit of the N-oligosaccharyl-transferase complex in the ER (t). However, it neither depends on its KXXX sequence for proper function nor does it seem to escape from the ER if the di-lysine is mutated (Gaynor et al., 1994). The second is Vma21p, required for the assembly of the vacuolar ATPase in the ER (Hill and Stevens, 1994). This protein was predicted to span the membrane twice with both NH2 and COOH terminus in the ER-lumen. Vma21p depends on its di-lysine motif for retention in the ER. The third protein is Gaa1p, a polytopic transmembrane protein that has a COOH-terminal sequence KXXXX (Hamburger et al., 1995). Gaa1p is an essential protein that is required in the ER for the attachment of glycosylphosphatidylinositol onto proteins. Its localization to the ER was determined upon overproduction. Mutating the COOH-terminal sequence in the overproduced Gaa1p allowed partial escape of the mutant protein from the ER (Hamburger, 1994).

We wondered therefore whether the COOH-terminal KXXXX sequence of Emp47p would convey a steady-state ER localization to the protein. To localize the protein an antibody against a peptide comprising the whole cytoplasmic tail (AT-antibody) was raised in rabbits. By immunofluorescence we showed that the Emp47p staining pattern was clearly distinct from that of the ER, visualized in the same strain by anti-Kar2p antibody. The ER-marker Kar2p (Normington et al., 1989; Rose et al., 1989) displayed the typical ring-like staining around the nucleus and subplasmamembrane staining (Fig. 2 A, right). In contrast the Emp47p AT-antibody produced a punctate staining (Fig. 2 B, left). The fluorescent structures, typically between 4 and 10 per mother cell, are often of elongated shape and vary in size and fluorescence intensity. We did not notice any accumulation in any particular region of either the mother or the daughter cell. Strains deleted for EMP47 did not stain with the anti tail antibody (data not shown).

The steady-state Emp47p immunofluorescence pattern is most reminiscent of that reported for Golgi proteins in yeast, such as the peripheral protein Sec7p and the transmembrane endoprotease Kex2p (Franzusoff et al., 1991; Redding et al., 1991). Another protein with a Golgi-like distribution in yeast is Pmr1p (Antebi and Fink, 1992). In a double immunofluorescence experiment we demonstrated that Emp47p and HA-Pmr1p (tagged with the influenza hemagglutinin-epitope, Antebi and Fink, 1992) exhibit 99 and 89% colocalization, respectively (Fig. 2 B, legend).**

**Emp47p Comigrates with Golgi Proteins during Subcellular Fractionation**

We used a second independent method to determine the steady-state localization of Emp47p in relation to other subcellular markers. Spheroplasts of cells transformed with an episomal plasmid expressing HA-Pmr1p were broken and the supernatant of a 500 g-spin was fractionated by sedimentation on a sucrose gradient (similar to Antebi and Fink, 1992). The gradient fractions were analyzed by the appropriate enzymatic assays or by immunoblotting. The results are shown in Fig. 3. In accordance with the immunofluorescence data (Fig. 2 B) Emp47p cofractionated with HA-Pmr1p. Both migrated together in the middle of the gradient. Emp47p separated almost completely from the ER marker Wbp1p (te Heesen et al., 1991), which occupied the bottom fractions of the gradient. The vacuoles hardly entered the gradient and also separated from Emp47p (Vacuolar ATPase, 60-kD subunit; and alkaline

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**Table II. Quality Scores of Pairwise Alignments Performed with the Program BESTFIT**

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</tbody>
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For each sequence comparison a mean random quality score and its standard deviation was obtained by performing 100 alignments with one sequence randomized (using default parameters). They were used to calculate the values given in parentheses: quality score of actual alignment minus mean score of random alignments divided by standard deviation of random alignments. Complete = comparison with the whole sequences.
Figure 1. Structure of Emp47p. (A) Nucleotide sequence and derived amino acid sequence of EMP47. Numbering of nucleotides begins at the start of the open reading frame. Numbering of amino acids begins at the first amino acid of the mature protein as determined by direct NH$_2$-terminal protein sequencing (dashed line). The putative transmembrane-domain is underlined. These sequence data are available from GenBank/EMBL/DDBJ under accession number X87622. (B) Biophysical parameters of Emp47p as determined with the program PEPTIDESTRUCTURE and PEPCOIL (GCG). Numbering starts with first amino acid translated from the open reading frame. Hydrophobicity calculated according to Kyte-Doolittle (1982), Turns (indicates t3-turns), a-helices and B-sheet predictions according to Garnier et al. (1978), coiled-coil probability according to Lupas et al. (1991). (C) Multiple alignment of the first 250 amino acids of the mature polypeptides of ERGIC-53, VIP36 (putative NH$_2$ terminus according to Fiedler et al., 1994) and Emp47p. The alignment was produced with PILEUP (GCG) using a gap weight of 2.4 and a gap length weight of 0.1 and plotted with the program PRETTYPLOT (GCG) using the default parameters. Homologous residues according to PILEUP are boxed. (D) Multiple alignment of
phosphatase, data not shown). Functionally the cis-most Golgi marker identified thus far is Ochlp (Nakanishi-Shindo et al., 1994; Gaynor et al., 1994). Ochlp consistently migrated in a very sharp peak displaced by at least one fraction from Emp47p. The overlap with other assayed Golgi markers was best for GDPase (Abeijon et al., 1989). The majority of GDPase is located cis of the transmost Golgi marker Kex2p and may be in all Golgi subcompartments that contain mannosyltransferases (Cunningham and Wickner, 1989; Bowser and Novick, 1991;
were positive for HA-Pmrlp only. This amounts to a colocalization of 99% between Emp47p and HA-Pmrlp and of 89% between HA-Pmrlp and Emp47p. Bar, 6 μm.

Two structures were positive for Emp47p only and 29 structures were used for quantitation of the colocalization. In these cells an HA-Pmrlp-signal comparable to the one seen in the figure was visualized with FITC-conjugated rabbit anti-mouse IgG and the anti-tail antibody with Cy3-conjugated goat anti-rabbit IgG. (B) Emp47p and Kar2p localization. (A) Emp47p staining is different from Kar2p staining representing ER. Fixed and permeabilized RH732 cells were incubated with Emp47p anti-tail antibody (left) or anti-Kar2p antibody (right). Primary antibodies were visualized using Cy3-conjugated goat-anti rabbit IgG. (B) Emp47p and HA-Pmrlp colocalize. RH448 cells transformed with pl161, coding for HA-Pmrlp (Antebi and Fink, 1992) were fixed, permeabilized, and then simultaneously incubated with 12CA5 (directed against the HA-Epitope of HA-Pmrlp) and AT-antibody. 12CA5 was visualized with FITC-conjugated rabbit anti-mouse IgG and the anti-tail antibody with Cy3-conjugated goat anti-rabbit IgG. Because pl161 is a multicopy-plasmid strong variance in HA-Pmrlp expression levels from cell to cell were seen. 57 cells with an HA-Pmrlp-signal comparable to the one seen in the figure were used for quantitation of the colocalization. In these cells a total of 224 structures positive for both markers were counted. Two structures were positive for Emp47p only and 29 structures were positive for HA-Pmrlp only. This amounts to a colocalization of 99% between Emp47p and HA-Pmrlp and of 89% between HA-Pmrlp and Emp47p. Bar, 6 μm.

Graham et al., 1994). Kex2p also migrated in the middle of the gradient, but its profile was different from that of Emp47p.

**Emp47p Has Access to the α1,3 Mannosyltransferase Containing Golgi Subcompartment**

Emp47p does not have any putative N-linked glycosylation sites. We wanted however to use the analysis of outer chain glycosylation as a further tool for collecting evidence about the localization of Emp47p. Therefore, we introduced two overlapping N-linked glycosylation consensus sites (NX/T/S) at position 49 and 50 of the mature protein. This was achieved by mutating amino acids Q50 to N and N51 to T, creating the sequence NNTS. The mutant Emp47p was also tagged with a c-myc epitope immediately after the signal-peptidase cleavage site at amino acid 9. We integrated myc-glyco-EMP47 into the genome of a haploid strain in which EMP47 was deleted (nucleotides 106–1375 replaced with LYS2, see Materials and Methods). In a pulse-chase experiment, we radiolabeled cells with [35S]methionine and cysteine for 5 min at 30°C and then chased for 0 min or 30 min at the same temperature. Cell extracts were prepared, first precipitated with the AT-antibody and reprecipitated with either the same antibody or a polyclonal antibody against α1,3-linked mannose. The precipitates of the second round of precipitation were then analyzed by SDS-PAGE followed by autoradiography (Fig. 4 A). An isogenic strain expressing myc-tagged Emp47p was treated the same way in a parallel experiment. After the 5-min pulse the AT-antibody precipitated one sharp band ~49 K corresponding to myc-Emp47p (the weak extra band at ~62 K is not related to Emp47p as it is also present in a delete strain, data not shown). Myc-Emp47p was stable during the chase period. 76% of the signal precipitated by the AT-antibody immediately after the pulse was recovered after the 30-min chase (quantification by PhosphoImager). In the case of the myc-glyco-Emp47p a prominent band of slightly higher molecular mass was precipitated, probably corresponding to the core glycosylated protein. In addition the autoradiogram revealed a broad smear of radioactivity ranging in apparent molecular mass up to >100 kD. This is typical of glycoproteins with extensive α1,6-, α1,2-, and α1,3-linked mannose outer chain modifications. 54% of the total myc-glyco-Emp47p had received outer chain modifications after the pulse and 89% after the chase. The core-glycosylated myc-glyco-Emp47p had largely disappeared after the chase (only 16% remained) while the high molecular smear slightly increased in intensity (106% of the 0 min chase value). After the chase we further noted the appearance of a new band at slightly lower mobility than that of the core-glycosylated myc-glyco-Emp47p.

In yeast outer chain modifications of N-linked glycans have been allocated to functionally successive steps corresponding to different Golgi cisternae. Only recently it was found that the first α1,6-linked mannose is added to the core oligosaccharide by ochlp (Nakanishi-Shindo et al., 1994). Ochlp also operationally defines a new cis-Golgi compartment (Gaynor et al., 1994). It is separated from the elongating α1,6 mannosyltransferase and the α1,3 mannosyltransferase that had previously been defined as cis and medial-Golgi markers, respectively (Graham and Emr, 1991). To study whether Emp47p can be modified by the α1,3 mannosyltransferase we precipitated the newly synthesized myc-glyco-Emp47p with the anti-α1,3 serum. As can be seen in Fig. 4, immediately after the pulse, 63% of the high molecular mass smear that was precipitated with the AT-antibody could be precipitated by the anti-α1,3 serum as well. After 30 min of chase the intensity of the anti-α1,3 mannose precipitate reached 95% of the intensity of the total smear. Thus almost complete α1,3 mannoside modification of the N-linked carbohydrates was observed within 30 min. As expected myc-Emp47p was not precipitated by the anti-α1,3 serum. This also provided an internal control for the complete inactivation of the AT-antibody from the first round of precipitation. The experiment supports the view that Emp47p rapidly reaches a medial-Golgi compartment as defined by the α1,3 mannosyltransferase.

Visualization of myc-glyco-Emp47p by immunofluorescence (Fig. 4 B, top) revealed a pattern similar to that of
Emp47p (compare Figs. 2 A and 5, top), indicating that introducing the tags did not cause a mislocalization of the protein. This was confirmed by coexpressing HA-Pmr1p and performing double-immunofluorescence (Fig. 4 B, middle and bottom). Quantification (see Fig. 4 B, legend) yielded a colocalization between myc-glyco-Emp47p and HA-Pmr1p of 98%.

Steady-state Golgi Localization Depends on COOH-terminal KXXKX Sequence

We next determined whether the COOH-terminal KTKLL sequence plays a role in the steady-state localization of Emp47p. For that purpose we created a set of site-directed mutations affecting the consensus features of di-lysine-based signals. All constructs were tagged with a myc-epitope at amino acid 9 of the mature protein because our AT-antibody was not expected to recognize the mutated tails. As it is possible that Emp47p forms higher order complexes, we integrated the mutant genes into the genome of a haploid pep4 strain in which EMP47 was deleted (nucleotides 106–1375 replaced with LYS2, see Materials and Methods). The pep4 mutation, which alleviates the problem of vacuolar proteolysis, was used because we had preliminary indications that some tail-mutant proteins were rapidly degraded.

The immunofluorescence analysis of some key constructs is shown in Fig. 5, while the results with the other constructs are summarized in Table III. The c-myc tagged but otherwise unchanged Emp47p yielded the wild-type
Figure 4. Glycosylation and localization of an Emp47p variant. (A) Cultures of strains RH3046 (myc-glyco-Emp47p) and RH-3047 (myc-Emp47p) were grown at 24°C, radiolabeled for 5 min at 30°C, and then chased at the same temperature for 0 min or 30 min as indicated. Cell extracts were prepared and precipitated first with AT-antibody. Precipitates were reprecipitated with either AT-antibody or with antisera against α,3 linked mannose as denoted. The final precipitates were separated by 8% SDS-PAGE (migration of molecular weight standards of 45, 66, and 97 K is indicated) and the gels were analyzed by exposure to film and Phospholmager-plates. (B) (Top) Immunofluorescence labeling of myc-glyco-Emp47p in RH3046 using 9El0 anti-myc antibody; (middle and bottom) double-immunofluorescence on RH3046 transformed with p1161, stained for myc-glyco-Emp47p with AT-antibody (middle) and HA-Pmr1p with HA-antibody (bottom). The images of these cells were recorded with a video equipment, adjusted to similar background and brightness with the shadow/highlight tool of the image editor PSP (JASC Inc., Minnetonka, MN) and printed on a 600 dpi printer. 20 cells with an HA-Pmr1-signal comparable to the one seen the figure were used for quantitation of the colocalization. In these cells a total of 81 structures positive for both markers were counted. Two structures were positive for Emp47p only and one structure was positive for HA-Pmr1p only, yielding a colocalization of 98% between Emp47p and HA-Pmr1p and of 99% between HA-Pmr1p and Emp47p. Bar, 6 μm.

Figure 5. Influence of the COOH-terminal KXXX motif of Emp47p on its intracellular steady-state localization. Constructs encoding myc-tagged Emp47p with a wild-type or mutated di-lysine motif were expressed in RH2825 (deleted for EMP47). Each construct is denoted by its last five COOH-terminal amino acids. KTKLLS4 indicates the construct in which the wild-type sequence was tailed with four serines. The left panels show the immunofluorescence patterns detected with the 9El0 antibody directed against the myc-epitope. The right panels show the corresponding Nomarski image with the vacuoles appearing as indentations. Bar, 6 μm.

however led to a complete redistribution of the mutant protein to the vacuolar membrane. This is obvious from comparing the immunofluorescence with the corresponding Nomarski image (Fig. 5, KTKLL). As summarized in Table III, changing lysine −5 or both lysines also resulted in vacuolar staining. The same was true for the deletion of the KTKLL sequence. Like for other di-lysine motifs, arginines replacing the lysines resulted in loss of function and the mutant Emp47p was found in the vacuole (Fig. 5, RTRL1). Furthermore, the sequence KTKLL displayed a position dependence. Adding four serines at the COOH-terminus of Emp47p also resulted in a vacuolar staining pattern (Fig. 5, KTKLSS4). Thus the KTKLL sequence in Emp47 displays all the hallmarks of a di-lysine ER-localization motif. The Emp47p-tail is also sufficient to confer ER-localization to the plasma membrane protein Ste2p.

punctate pattern (Fig. 5, top). Moving the lysine at position −5 to position −4 did not change the pattern, demonstrating the equivalence of KXXX and KXXX in this case (Fig. 5, TKKLL). Changing lysine −3 to glutamine
Table III. Summary of the Qualitative Immunofluorescence Pattern of myc-tagged Emp47p Tail Mutants Expressed in an emp47Δ Strain (RH2825)

<table>
<thead>
<tr>
<th>COOH-terminal sequence</th>
<th>IF pattern</th>
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<tbody>
<tr>
<td></td>
<td>Punctate</td>
</tr>
<tr>
<td>wt: ..RIRQEIIKTKLL</td>
<td>+</td>
</tr>
<tr>
<td>..RIRQEIIQTKLL</td>
<td></td>
</tr>
<tr>
<td>..RIRQEIIQTQLL</td>
<td></td>
</tr>
<tr>
<td>..RIRQEIIKAA</td>
<td>+</td>
</tr>
<tr>
<td>..RIRLAIIKTKLL</td>
<td></td>
</tr>
</tbody>
</table>

Site-directed mutations are indicated in bold type. For comparison the wild-type sequence of the cytoplasmic tail of Emp47p (wt) is given as well.

upon transplantation (see below). Therefore Emp47p is the first known protein in which a functional di-lysine motif is essential for a Golgi localization.

Mutating two other features that are conserved in the cytoplasmic tails of Emp47p, ERGIC-53, and VIP36 (Fig. 1 C) did not change the wild-type distribution. Those mutations (Table III) are the exchange of the two COOH-terminal leucines (consensus: large hydrophobic) with alanine and the exchange of the strictly conserved hydrophilic/charged amino acids QE for LA (hydrophobic/neutral).

**Emp47p Can Recycle to the ER**

Di-lysine ER-localization motifs can bring about a steady-state ER-localization by recycling (see Introduction and Discussion). To test whether Emp47p could also follow a recycling pathway to the ER we made use of the sec12 mutant. In sec12 secretion is blocked before the budding of transport vesicles from the ER at nonpermissive temperature (Nakano et al., 1988; Barlowe and Schekman, 1993). If recycling still occurs under these conditions and if Emp47p follows this pathway it should be possible to re-distribute Emp47p to the ER, thus depleting the Golgi pool at the same time.

![Figure 6. Indirect immunofluorescence analysis of the dynamics of intracellular distribution of Emp47p and Pmr1p in sec12 cells. sec12 cells expressing either myc-EMP47 integrated at the leu2 locus (sec12, middle) or HA-PMR1 from the 2μ-plasmid pL161 (bottom) were incubated for 1 h in the presence of 20 μg/ml cycloheximide at either permissive (24°C) or nonpermissive temperature (35°C). The wild-type strain RH448 (wt, top) was treated the same way in parallel. Emp47p in RH448 was detected with AT-antibody. The images of the latter cells were recorded with a video equipment and printed on a 600 dpi printer. myc-Emp47p was detected with 9El0 antibody. HA-Pmr1p was detected with 12CA5. Bar, 6 μm.](https://jcb.rupress.org/content/152/3/890/F6)
Wild type or sec12 cells (in some cases transformed to express a particular marker-protein) were grown at the permissive temperature (24°C). Cycloheximide was added to avoid a contribution of newly synthesized Emp47p. Then aliquots were put at either 24 or 35°C (nonpermissive) for 1 h. Cells were then fixed and processed for immunofluorescence. Fig. 6 shows that wild-type cells still displayed a punctate pattern after incubation at both temperatures (top). sec12 cells expressing myc-Emp47p in addition to the endogenous Emp47p also retained a punctate pattern after incubation at permissive temperature (Fig. 6, sec12, 24°C). At restrictive temperature, however, the immunofluorescence pattern in sec12 cells changed qualitatively. The punctate structures disappeared and a ring around the nucleus (compare corresponding DAPI stain) and some staining in the periphery of the cell became visible. This pattern is equivalent to ER-staining in yeast as exemplified by the Kar2p-immunofluorescence in Fig. 2 A. The comparatively low intensity of the Emp47p immunofluorescence signal after recycling was most likely due to the distribution of the antigen over a much larger surface area.

The change in the immunofluorescence pattern of Emp47p is consistent with the interpretation that Emp47p redistributed from the Golgi to the ER upon imposing the sec12 block. Importantly, Pmr1p, with which Emp47p colocalizes under normal growth conditions, does not qualitatively change its punctate appearance in immunofluorescence when the sec12 block is imposed (Fig. 6, bottom). Therefore, the redistribution seen for Emp47p was not simply due to a change of morphology of the Emp47p compartment nor to a general merging of the Golgi with the ER.

We also applied the sucrose gradient analysis to monitor the changes in intracellular distribution of Emp47p after a sec12 block. sec12 cells were incubated in the presence of cycloheximide at permissive or nonpermissive temperature. They were then spheroplasted and lysed. The cleared lysates were fractionated on sucrose-gradients as described in Materials and Methods. The immunoblot-quantification of the gradient fractions is shown in Fig. 7 A. It provides quantitative evidence for the recycling of Emp47p that is complementary to the immunofluorescence analysis. 1 h after imposing the sec12 block, Emp47p was redistributed from its steady-state position in the middle of the gradient to the bottom of the gradient (Fig. 7 A, top), where the ER marker Wbp1p migrated under both sec12 permissive and nonpermissive conditions (Fig. 7 A, middle). The cis-most Golgi marker, Och1p, did not change its migration properties after the sec12 block (Fig. 7 A, bottom). This is similar to what we had observed for the HA-Pmr1p localization in the immunofluorescence experiment (Fig. 6, bottom) and provides additional evidence that the Golgi apparatus is still present. A quantification of the kinetics of the redistribution process is shown in Fig. 7 B. We added NaF and NaN3 at various times after shift to the sec12 nonpermissive temperature (37°C). One cell aliquot was kept at the permissive temperature (24°C) throughout the duration of the experiment. Golgi and ER fractions were then separated on sucrose gradients as above. Significant redistribution of Emp47p took place only at 37°C and it was time and energy dependent with a half time of retrograde transport of ~30 min.

Figure 7. Dynamic intracellular redistribution of Emp47p in sec12 cells observed by velocity sedimentation on sucrose gradients. RH1491 (sec12) cells were incubated for the indicated times at either permissive (24°C) or nonpermissive (35 or 37°C) temperature in the presence of 20 μg/ml cycloheximide before spheroplasting and homogenization. Lysates cleared by a spin at
**α1,3 Mannose-modified Emp47p Can Recycle to the ER**

The myc-glyco-Emp47p provided a tool to address the question from which Golgi subcompartment recycling can occur. We radiolabeled sec12 cells stably expressing the myc-glyco-Emp47p. Labeling was performed at 24°C for 15 min followed by a 10-min chase at the same temperature. We then added cycloheximide and incubated aliquots at either 24 or 35°C. Cells were spheroplasted, broken, and then the lysate was spun at 500 g. Supernatants of that spin were separated on sucrose gradients as described in Materials and Methods. The gradient fractions were first immunoprecipitated with AT-antibody. The precipitates were then split into aliquots and reprecipitated with either AT-antibody or with antiserum against α1,3-linked mannose. Fig. 8 shows the PhosphoImager quantification of the endogenous Emp47p and the high molecular weight “smear” precipitated by the antiserum against α1,3 linked mannose. It can be seen that both the nonglycosylated Emp47p and the α1,3 mannose modified Emp47p variant qualitatively behaved in the same way. At the permissive temperature for sec12 the majority of the radioactivity was found in the middle of the gradient. After shift to 35°C for 1 h the Golgi-signal decreased in size and the signal from the ER fractions increased. Therefore we conclude that myc-glyco-Emp47 can recycle from an α1,3 mannosyltransferase containing Golgi compartment to the ER.

**Steady-state Localization of Emp47p Is Unchanged in a ret 1-1 Mutant Cell**

Letourneur et al. (1994) isolated a mutant in α-COP (ret1-1) that was deficient in the intracellular retention of an α-factor receptor (Ste2p) chimera bearing the cytosolic, COOH-terminal di-lysine motif of Wbp1p. To determine whether the di-lysine motif of Emp47p would also be recognized by α-COP and whether Emp47p would depend on α-COP for its steady-state Golgi-localization, we fused the 12-amino acid tail of Emp47p to Ste2p and expressed the construct together with myc-Emp47p in MATa cells that were deleted for the endogenous STE2 and were either wild type or ret1-1. The cells were grown at 30°C, conditions under which ret1-1 is deficient for the retention of Ste2p-Wbp1ptail (Letourneur et al., 1994). We then examined the intracellular distribution of myc-Emp47p and Ste2p-Emp47ptail by immunofluorescence. The results are shown in Fig. 9 A. Clearly Ste2p-Emp47ptail was retained in the ER in RET1 cells (compare DAPI staining of the nucleus). In ret1-1 mutant cells, however, the staining around the nucleus was abolished, and staining at the perimeter of the cells was observed. This is the pattern also observed for the wild type plasma membrane protein Ste2p in the parental strains (Fig. 9 B). Thus the cytoplasmic tail of Emp47p controlled the intracellular distribution of the Ste2p fusion protein in very much the same way as the Wbp1p-tail (Letourneur et al., 1994). Surprisingly, Emp47p distribution was apparently unaffected by the ret1-1 mutation (Fig. 9 A, top). This held true when we visualized Emp47p by immunofluorescence in ret1-1 pep4Δ.
**Table IV. The Influence of RET1, PEP4 and the Di-lysine Signal on the Turnover of Emp47p**

<table>
<thead>
<tr>
<th>Strain</th>
<th>Relevant genotype</th>
<th>Half-time for degradation (hrs)</th>
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<tbody>
<tr>
<td>RH3193</td>
<td>RET1, PEP4, EMP47</td>
<td>5.1</td>
</tr>
<tr>
<td>RH3187</td>
<td>ret1-1, PEP4, EMP47</td>
<td>5.0</td>
</tr>
<tr>
<td>RH3274</td>
<td>ret1-1, pep4A, EMP47</td>
<td>5.0</td>
</tr>
<tr>
<td>RH3275</td>
<td>RET1, PEP4, emp4A, myc-EMP47-QTQLL</td>
<td>0.8</td>
</tr>
<tr>
<td>RH2830</td>
<td>RET1, pep4A, emp4A, myc-EMP47-QTQLL</td>
<td>5.0</td>
</tr>
</tbody>
</table>

After a 15-min pulse with $^{35}$S protein-labeling mix at 30°C at least five chase time points were taken in duplicate for each strain, covering 60 min for RH3275 and 4.5-6 h for the other strains. Cell extracts were prepared (see Materials and Methods) and precipitated with AT-serum, which also recognizes the QTQLL mutant tail. Average values of each timepoint were obtained by Phospholmager-analysis. The values were fitted with a linear equation from which the half-time was determined (rounded to the nearest tenth of an hour). Correlation coefficients of the optimal curve-fits were in the range of $R = 0.928$ to $R = 0.995$.

**Discussion**

**The Steady-state Localization of Emp47p**

We have cloned and sequenced a gene coding for a novel type I transmembrane protein, Emp47p. This protein has sequence homology to ERGIC-53 and to VIP36, a newly defined class of putative intracellular lectins (Fiedler and Simons, 1994; Arar et al., 1995). Emp47p carries a COOH-terminal di-lysine motif typically found on resident ER-membrane proteins, but is nevertheless found in the Golgi under steady-state conditions. Golgi localization was demonstrated by a combination of subcellular fractionation on sucrose gradients and immunofluorescence that showed that Emp47p is not localized to the ER, to the plasma membrane, nor the vacuole. On the other hand, Emp47p colocalized with Pmr1p and overlapped with GDPase, two presumed Golgi markers.
Although recent progress has been made in the ultrastructural characterization of the Golgi in *Saccharomyces* (Preuss et al., 1992), analysis of the subcompartimentalization of this organelle still rests on the biochemical analysis of Golgi-specific processing events and the characterization of some proteins involved in these events. The framework was established by looking at the successive glycosylation and proteolytic processing of proteins on the biosynthetic route (Graham and Emr, 1991; Gaynor et al., 1994) and can be summarized as follows. The first and perhaps cis-most Golgi-specific modification is the addition of an α-1,6 mannose by Ochlp (Nakanishi-Shindo et al., 1994), followed by elongation with additional α-1,6 mannose residues, followed by addition of α-1,3 mannose residues, followed by the proteolytic cleavage by Kex2p in perhaps the trans-most Golgi compartment. This would define four Golgi subcompartments. One would predict that GDPase, which is required for import of GDP mannose into the Golgi lumen, would be present in the first three Golgi subcompartments. This is consistent with its fractionation pattern and overlap with Ochlp. Other Golgi markers have been placed partially within this framework by means of subcellular fractionation and/or immunofluorescence (Abeijon et al., 1989; Bowser and Novick, 1991; Cleves et al., 1991; Cunningham and Wickner, 1989; Franzusoff et al., 1991; Segev et al., 1988; Stearns et al., 1990).

A more precise Golgi localization of Emp47p can be inferred from the virtually complete colocalization with the Ca$^{2+}$ ATPase, Pmr1p, both in sucrose density gradient fractionation and in immunofluorescence, and from the glycosylation pattern of the Emp47p variant. In a *pmr1Δ* strain Golgi-specific sugar modifications of invertase are abolished (Abeijon et al., 1993) and heterologous proteins are secreted in a core-glycosylated form. The growth lesion of *ypt1-1* is alleviated. *Ypt1p* is a peripheral Golgi GTPase that was shown to be required for ER to Golgi and early intra-Golgi transport steps (reviewed by Segev, 1994). Furthermore *pmr1Δ* interacts with several sec alleles (Rudolph et al., 1989; Antebi and Fink, 1992). It will be interesting to see if one of the functions of Pmr1p is to provide Ca$^{2+}$ for the putative lectin-activity of Emp47p (see below).

Antebi and Fink (1992) found that on sucrose density gradients Pmr1p migrated in a profile widely overlapping though not congruent with the trans-most Golgi-marker Kex2p, a result we confirmed in the present study. In immunofluorescence studies on Pmr1p only a modest colocalization with Kex2p (27%) was observed. An even lower degree of colocalization was found with Sec7p (17%), a peripheral Golgi-membrane protein which itself colocalizes to a large extent with Kex2p (reviewed by Franzusoff, 1994). Thus Pmr1p and Emp47p are at least not extensively associated with the trans-most Golgi subcompartment.

Additional information as to which Golgi subcompartments Emp47p is accessible, comes from studies of an N-glycosylated version of the protein. We could show that its glycans are largely modified by α-1,3 linked mannose within 5 min. This rapid acquisition of α-1,3 mannose linkages corresponds to the time required for similar modifications on carboxypeptidase Y and α-factor, suggesting that Emp47p is not retained for any significant amount of time in the ER (Graham and Emr, 1991; Klionsky et al., 1988). The access of tagged Emp47p to the α-1,3 mannosyltransferase compartment did not reflect aberrant targeting due to N-glycosylation by three criteria. First, the steady-state localization of the tagged Emp47p was not changed compared to the WT-protein as judged by colocalization with HA-Pmr1p. Second, we noted a similar stability of Emp47p and its glycosylated version. This argues against the possibility that we visualized the glycosylated Emp47p in transit to the vacuole, where mutant Emp47p with an impaired localization signal is targeted (see below). Third, we obtained evidence for a similar recycling to the ER of wild type Emp47p and its glycosylated version (see below). In conclusion, from the subcellular fractionation and the glycan-analysis the steady-state localization of Emp47p must be after the Ochlp subcompartment (cis-most Golgi) and before the Kex2p (trans-most Golgi) subcompartment.

### The Di-lysine Signal Is Required for the Steady-state Localization of Emp47p

As mentioned before, functional di-lysine signals have been demonstrated for proteins located at the ER at steady-state. ERGIC-53 is the only nonchimeric protein with a di-lysine motif that is known to reside partially downstream of the ER at steady-state, in the ER-Golgi intermediate compartment, and to a minor extent in the cis-Golgi (Schweizer et al., 1988). Emp47p is the first protein that is dependent on a di-lysine signal for its steady-state distribution in the Golgi. This adds the di-lysine motif to signals involved in Golgi protein localization (Machamer, 1993; Nilsson and Warren, 1994; Wulfsbch and Payne, 1993).

The change of any conserved feature within the di-lysine motif abolished the normal Golgi localization of Emp47p. Mutant Emp47p accumulated in the vacuole of *pep4* strains and was rapidly degraded in strains not deficient in vacuolar proteolysis (data not shown). We have not investigated the itinerary of the mutant Emp47p to the vacuole, but it is likely to occur by the proposed default pathway (Roberts et al., 1992; Gaynor et al., 1994). The di-lysine motif of Emp47p complied with all the tests developed so far for the identification of functional ER-localization signals (Jackson et al., 1990; Nilsson et al., 1989). The lysine at position −5 can be moved to −4 without apparent effect, the lysines can not be replaced by arginine, and the lysines have to be in the right position with respect to the COOH-terminus of the protein. Furthermore the cytoplasmic tail of Emp47p is sufficient to confer ER-localization to Ste2p, which normally resides at the plasma membrane. What features of Emp47p could then determine a post-ER localization?

The transmembrane domain of Emp47p has one peculiarity in that it contains a proline at position 392 (Fig. 1 A). Proline residues have been implicated in structural and dynamic aspects of transmembrane domains and their interactions (Williams and Deber, 1991). Mutating proline 392 to leucine in Emp47p did not change the apparent steady-state distribution of the protein (data not shown). The luminal domain could also contribute to the steady-state distribution of Emp47p in a post-ER compartment. If the luminal domain has lectin function it is conceivable
that the putative interaction with glycans would provide a targeting signal (see below).

Recycling of Emp47p

To date, di-lysine motifs have been found to function in ER localization of proteins. The underlying mechanism, retrieval from a post-ER compartment, was indirectly deduced from the presence of Golgi-modified forms of these proteins in the ER (Gaynor et al., 1994; Jackson et al., 1993; Townsley and Pelham, 1994). For the first time we were able to directly investigate retrograde transport of a di-lysine protein from the Golgi complex to the ER. Furthermore, we examined a protein that was not overexpressed nor chimeric. To study the kinetics and quantity of recycling we developed an assay making use of the sec12 mutation. Sec12p is required for the formation of ER-derived, COP II-coated transport vesicles (Barlowe et al., 1994). Thus, in the absence of Sec12p, transport out of the ER was abolished and material that recycled to the ER accumulated there. We found recycling to be almost quantitative within 1 h. This is a long time compared to the rate of secretion, transport to the vacuole (see above) and the forward transport of Emp47p itself. However, it should be noted that the cells were incubated in the presence of a protein synthesis inhibitor and forward transport was blocked during the recycling assay. We were surprised that the redistribution of Emp47p to the ER was almost complete. This indicates that either there are no factors that have to be reexported to the Golgi to sustain multiple rounds of retrograde transport or that a SEC12-independent forward transport pathway exists that enables the export of these hypothetical components. In any event, it is clear from our results that the retrograde pathway is independent of SEC12, suggesting that COP-II-coated vesicles are not required for this step. This novel transport assay should allow us to investigate the in vivo role of other gene products in retrograde traffic.

The appearance of Golgi-modified di-lysine proteins in the ER has been well documented (Gaynor et al., 1994; Jackson et al., 1993; Townsley and Pelham, 1994). There is less information however about the Golgi subcompartment(s) from which recycling of di-lysine proteins can occur. Gaynor et al. (1994) demonstrated for an invertase-Wbp1p fusion protein that it did not receive sugar modifications beyond the addition of the first α,1,6 mannos by Och1p. Therefore, the cis-most Golgi subcompartment seems to be the salvage compartment for this particular hybrid protein. We present evidence that Emp47p with α,1,3 mannose-modified glycans redistributed on gradients from a Golgi-position to an ER-position. The redistribution was as extensive as that of the wild-type Emp47p under the same conditions. This suggests that Emp47p can recycle to the ER from the α,1,3 mannosyltransferase compartment or beyond. It remains to be shown whether this recycling is a one step process or occurs step by step backwards through the secretory pathway.

We have no evidence that Emp47p which returned to the ER can be reexported to the Golgi. Yet our data about the trafficking of Emp47p and the knowledge about the transport of other di-lysine proteins suggest that their distribution in the cell reflects a steady-state equilibrium between forward and retrograde transport. The steady-state position of different di-lysine proteins must therefore depend upon additional targeting information. For some proteins such targeting information can exist in the fine-tuning of the di-lysine signal by flanking amino acids (Jackson et al., 1990, 1993; Gaynor et al., 1994). In the case of Emp47p forward transport information is likely to reside in the lumenal domain, as we could not find any other determinants in the tail, and the tail itself was sufficient to confer ER-localization to Ste2p.

The Role of COP I

Di-lysines signals have been shown to bind coatomer in vitro (Cosson and Letourneur, 1994). Even more importantly, several subunits of yeast coatomer are required for the intracellular retention of a di-lysine–tagged Ste2p (Letourneur et al., 1994). Letourneur et al. therefore discussed the possibility that coatomer may function in retrograde transport of di-lysine proteins. Emp47p could be an important tool to test the potential involvement of coatomer in recycling. Our results showed that retl-1 cells, mutated in α-COP, were not able to correctly localize the Ste2p-Emp47p tail to the ER. However, the Golgi localization of Emp47p itself was unaffected in the mutant. It could be that other alleles of retl would affect Emp47p localization, but we consider this unlikely. First, the di-lysine motif of Emp47p is definitely required for its Golgi localization. Second, coatomer in the retl-1 cells has lost the ability to bind di-lysine motifs in vitro (Letourneur et al., 1994). It could be that retrograde transport from cis-Golgi to the ER is blocked in retl-1 cells, but that this transport step is not required for Emp47p localization. Alternatively, it could be that retrograde transport from Golgi compartments distal to the cis-Golgi does not require RET1, but a different coat. By analogy to the clathrin adaptor complexes (Keen, 1993) perhaps different, compartment-specific coatomers exist that recognize similar signals. RET1 could affect a cis-Golgi/ER coatomer. Emp47p would reach later Golgi subcompartments due to forward targeting and therefore only interact with a medial-Golgi–specific coatomer. We attempted to clarify this issue using our retrograde transport assay in a sec12/retl-1 double mutant. Unfortunately the double mutants did not yield reproducible results (data not shown) perhaps due to indirect effects of the simultaneous presence of the two mutations in the cells.

The Lectin-like Domain

Emp47p shows significant homology in its lumenal domain to two mammalian proteins located in the secretory pathway, ERGIC-53 and VIP36, the former of which has been shown to have lectin activity (Arar et al., 1995). There is another sugar-binding, membrane protein of the secretory pathway that does not display any sequence homology with the aforementioned lectins, the ER protein calnexin. It retains incompletely folded glycoproteins by recognition of GlcMα,Manα,GlcNAcα–oligosaccharides (Ou et al., 1993; Ware et al., 1995). In the case of ERGIC-53, VIP36 and Emp47p it is impossible to predict substrate specificity from the sequence homologies. Sugar-specificities would
probably be different, given the divergent intracellular distributions and sources of the proteins.

Although Emp47p is not essential, a putative function in glycoprotein-processing and/or sorting could manifest itself in differences in glycosylation-patterns or kinetics of transport of glycoproteins. We have looked at the biosynthesis of three glycoproteins: invertase, carboxypeptidase Y, and the glycosylphosphatidylinositol-anchored protein Gas1p. All three were apparently processed normally and transported with wild-type kinetics in the emp47 mutant cells (data not shown). The effect of Emp47p could however be restricted to particular glycoproteins or involve nonprotein substrates. Therefore, based on the steady-state and dynamic localization of Emp47p and the glycosylation events that occur in yeast we propose three principal scenarios for a lectin-function of Emp47p. First, Emp47p could function in the Golgi as a membrane bound, compartment-specific cofactor for glycosylation. Due to the Emp47p steady-state distribution beyond the Ochlp-compartment-specific cofactor for glycosylation. Due to the Emp47p steady-state and dynamic localization of Emp47p and the glycosylation change factor essential for transport vesicle budding from the ER. Nature (Lond.). 365:347-349.


Received for publication 30 May 1995 and in revised form 15 August 1995.

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