Guanosine Diphosphatase Is Required for Protein and Sphingolipid Glycosylation in the Golgi Lumen of *Saccharomyces cerevisiae*

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**Abstract.** Current models for nucleotide sugar use in the Golgi apparatus predict a critical role for the luminal nucleoside diphosphatase. After transfer of sugars to endogenous macromolecular acceptors, the enzyme converts nucleoside diphosphates to nucleoside monophosphates which in turn exit the Golgi lumen in a coupled antiporter reaction, allowing entry of additional nucleotide sugar from the cytosol. To test this model, we cloned the gene for the *S. cerevisiae* guanosine diphosphatase and constructed a null mutation. This mutation should reduce the concentrations of GDP-mannose and GMP and increase the concentration of GDP in the Golgi lumen. The alterations should in turn decrease mannosylation of proteins and lipids in this compartment. In fact, we found a partial block in O- and N-glycosylation of proteins such as chitinase and carboxypeptidase Y and underglycosylation of invertase. In addition, mannosylinositolphosphorylceramide levels were drastically reduced.

The lumen of the Golgi apparatus is the subcellular organelle where proteins and lipids become terminally glycosylated. In mammalian cells, nucleotide sugars are transported from the cytosol, their site of synthesis, into the lumen of the Golgi apparatus, via specific carrier proteins. After transport into the lumen and transfer of the sugars to the appropriate macromolecular acceptors, nucleoside diphosphates, the other reaction products are presumably substrates for a nucleoside diphosphatase, which converts them to nucleoside monophosphates. These exit the lumen of the Golgi in a coupled, equimolar, exchange with additional, cytosolic, nucleotide sugar (Hirschberg and Snider, 1987). Nucleoside diphosphates are inhibitors of glycosyltransferases while the monophosphates are not (Khatra et al., 1974; Kuhn and White, 1977; Brandan and Fleischer, 1982). The Golgi membrane transporters for nucleotide sugars appear to be of physiological significance: mutant CHO and MDCK cells have been described in which a specific defect in nucleotide sugar transport leads to the corresponding defect in glycosylation of proteins and lipids in vivo (Hirschberg and Snider, 1987).

*S. cerevisiae* contains heavily mannosylated proteins, and a highly specific guanosine diphosphatase (GDPase)1 has been described and purified to homogeneity (Yanagisawa et al., 1990). This enzyme appears to be localized in the lumen of Golgi vesicles (Abeijon et al., 1989). Addition of mannose to outer chains of N- and O-linked oligosaccharides in glycoproteins as well as mannosylation of inositolphosphorylceramides (IPC) occurs in this compartment (Kukuruzinska et al., 1987; Puoti et al., 1991). In all these reactions, GDP-mannose, the mannosyl donor, is synthesized in the cytosol and translocated into the Golgi lumen via a specific membrane carrier (Abeijon et al., 1989). After GDP-mannose entry into the lumen and mannosylation of endogenous protein and lipid acceptors, GDP, is converted, presumably by the above GDPase, to GMP which, by analogy to the mammalian system, is the nucleotide which exits the Golgi lumen and allows entry of additional cytosolic GDP-mannose. In the absence of GDPase, a decrease of GMP, the putative antipporter, should lead to a decrease of GDP-mannose in the Golgi lumen and therefore to substantially reduced Golgi mannosylation.

To determine the in vivo role for the above described *S. cerevisiae* Golgi GDPase, its gene (*GDA1*) was cloned and a null mutation was constructed. The recovered strain was viable and showed no in vitro membrane-bound GDPase ac-

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1. Abbreviations used in this paper: CPY, carboxypeptidase Y; GDPase, guanosine diphosphatase; IPC, inositolphosphorylceramides; MIPC, mannosylinositolphosphorylceramide; M(IP)2C, mannosylphosphorylinositolceramide; ORF, open reading frame; PI, phosphatidylinositol.

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tivity. As predicted, the null strain showed a block of O- and N-mannosylation of proteins such as chitinase and carboxypeptidase Y and underglycosylation of external invertase. In addition, a significant impairment of mannosylation of IPC was also found.

**Materials and Methods**

Restriction endonucleases and DNA-modifying enzymes were purchased from New England Biolabs (Beverly, MA) or GIBCO BRL (Gaithersburg, MD). pUC13, Small cut, and phosphatase treated was from Pharmacia LKB Biotechnology Inc. (Piscataway, NJ). Radiochemicals: [2-3H]Mannose, 14 Ci/mmol (American Radiolabeled Chemicals, Inc., St. Louis, MO); Tran3S-labeling mixture (ICN Biomedicals, Inc., Costa Mesa, CA). Radiochemicals: [2-3H]Mannose, 14 Ci/mmol (American Radiolabeled Chemicals, Inc., St. Louis, MO); Tran3S-labeling mixture (ICN Biomedicals, Inc., Costa Mesa, CA). Radiochemicals: [2-3H]Mannose, 14 Ci/mmol (American Radiolabeled Chemicals, Inc., St. Louis, MO); Tran3S-labeling mixture (ICN Biomedicals, Inc., Costa Mesa, CA).

**Materials and Methods**

**Strains and Growth Conditions**

*S. cerevisiae* strains were grown in YEPD or SD medium supplemented with the required amino acids (Sherman et al., 1986). Cells were grown at 30°C. Solid media was made by adding 2% agar to the liquid stock. Sporulation and tetrad dissection were carried out according to published procedures (Sherman et al., 1986). *E. coli* DH5α and DH5α FIIQ (GIBCO BRL) were used in the cloning experiments. The *E. coli* strains were grown in LB medium (Maniatis et al., 1982). Ampicillin (50 μg/ml) was added when needed. All nucleic acid manipulations and bacterial transformations were carried out according to Maniatis et al. (1982). Yeast transformations were carried out by the lithium acetate method of Ito et al. (1983).

**Peptide Sequence Analysis**

Approximately 80 μg of highly purified GDPase obtained after the second Mono Q column (Yanagisawa et al., 1990; see Fig. 5 a, lane 5) was subjected to SDS-PAGE, electroblotted to nitrocellulose, and stained with Ponse's amido black. Portions of the nitrocellulose were cut out and subjected to peptide sequencing, as described in detail by Aebersold et al. (1987). Digestion of the 48-kD GDPase with trypsin was performed in situ according to Aebersold et al. (1987), omitting the NaOH wash, and subjected to HPLC fractionation. Peptides were separated by a narrow-bore reverse phase HPLC (Hewlett-Packard 1090 HPLC equipped with a 1040 iodide assay detector, using a VyDAC 2.1 × 150 mm C18 column as described by Camirand et al., 1991). While monitoring absorbance at 210 nm, fractions were collected manually by peak and stored at −20°C. Some peptides were then selected for sequencing by automated Edman degradation on a model 470 sequenator (Appl. Biosystems Inc., Foster City, CA). Tryptic digests, HPLC, and peptide sequencing were done by William S. Lane (Harvard Microchemistry Facility, Harvard University, Cambridge, MA).

**Synthetic Oligonucleotide Design and PCR**

Regions of least degeneracy were selected in two of the internal peptides of the GDPase for the design of oligonucleotides (See Table I). Sense and antisense 26-mers were designed for each peptide according to Moremen (1989). All oligonucleotides were designed with mixed bases (64–128-fold mixtures overall for oligonucleotides Is/la and 2s/2a, respectively), and contained deoxyinososine residues (3 and 4 residues in oligonucleotides Is/la and 2s/2a, respectively) at positions of degeneracy. Oligonucleotides were synthesized on an Applied Biosystems model 380 B DNA synthesizer.

For the PCR experiments, every sense-antisense primer combination was tested [3 μM each] using genomic DNA of *S. cerevisiae* PRY123 as template (0.1–0.2 μg) in 25 μl reactions. 35 cycles were conducted as follows: 1 min at 92°C, 1 min at 50°C and 3 min at 72°C, and extensions of 5 min at 72°C were carried out after the last cycle. Primers Is and 2a (Table I) gave a 140-bp amplification product. This product was phosphorylated with T4 polynucleotide kinase, blunted with T4 polymerase, and cloned into the Small site of pUC13. The insert was then cloned into M13 and sequenced. The authenticity of the product was confirmed by the presence of coding sequence for amino acids E and S (Table I, peptide 2) left out of the primer design for confirmation purposes. The PCR amplification product was labeled by extension of the 1s and 2a primers with [α-32P]dCTP (New En-

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**S. Cerevisiae Strains Used**

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<th>Source</th>
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gland Nuclear) and Klenow fragment of DNA polymerase I. The labeled product was used as a probe for screening a S. cerevisiae genomic library in YEp3 plasmid.

**Screening of S. cerevisiae Genomic Library and Overexpression of the GDA I Gene**

The S. cerevisiae genomic library in YEp3 was plated on nitrocellulose filters on LB-ampicillin plates (~20,000 clones were screened). Two sets of replicas were prepared on nitrocellulose membranes (Schleicher and Schuell, Inc., Keene, NH). Both sets were prehybridized and hybridized according to Maniatis et al. (1982). The labeled PCR product was used as a positive control. Positive clones were picked, purified, and plasmids isolated and subjected to restriction analysis. Southern hybridizations confirmed the presence of PCR product sequences in the isolated plasmids.

Five independent clones were isolated and used to transform S. cerevisiae PRY223 strain. Cells containing YEp3 vector without insert were used as controls. Independent transformants were grown to early logarithmic phase and a crude membrane extract (Orlean et al., 1988) was tested for overexpression of GPDase activity.

**Subcloning, Plasmid Construction, and DNA Sequence Analysis**

Restriction analysis of the five independent YEp3 clones showed that four had a 3.7 kb Xhol fragment in common, which hybridized with the PCR amplification product. This 3.7 kb Xhol fragment was subcloned in the Sal site of the vector YEp352 (Hill et al., 1986) to generate p3X (see Fig. 1).

The other YEp3 clone had a 3.5 kb HindIII fragment hybridizing with the PCR probe; it was cloned into the multiple cloning site of the vector YEp32 to generate p3H (see Fig. 1). This 3.5 kb HindIII fragment was also cloned into the vector pBlueScript to generate p3HB, needed in the construction of the plasmid used in the gene disruption experiments (see below). A 3 kb PstI-Xhol genomic fragment was cloned into the PstI-Xbal sites at the multiple cloning site of the vector YEp32 to generate p3 PX (see Fig. 1).

Plasmid p3X, p3H, p3PX, and YEp352 without insert were used to transform S. cerevisiae PRY223 and overexpression of GPDase activity was tested as described in the previous section. Based on these results, a 2.2 kb HindIII-Nhel genomic fragment (see Fig. 1) was selected for sequencing and cloned in both orientations into M13 mp19. Sequencing overlapped deletions were introduced on the M13 clones with T4 polymerase using the Cycler biosystem kit (International Biotechnology, Inc., New Haven, CT). Sequence was obtained by the "ideoxy" chain termination method (Sanger et al., 1977), using deoxyosineo triphosphate in place of GDP and the sequence analysis showed 2:2 segregation of the LEU2 marker on every case. Transformants from strains PRY225 are called G1-G8, and transformants from strain PRY238 are called G9 through G16.

Strains G2-9, G2-10, G2-11, and G2-12 represent one tetrad from the G2 diploid and strains G1-5, G1-6, G1-7, and G1-8 represent one tetrad from the G11 diploid. These strains were used throughout this study.

**Guanosine Diphosphatase Assay**

GDPase activity was assayed essentially as described previously (Yanagisawa et al., 1990). Briefly, incubation mixtures contained in a final volume of 0.1 ml, enzyme (10-50 µg of total membrane extract, Orlean et al., 1988), CaCl2 (1 mM), Triton X-100 (100 µg), GDP (0.2 µmol), and imidazole-HCl buffer pH 7.5, (20 µmol). For UDPase and ADPase assays, GDP was replaced by UDP or ADP at the same concentration. Incubations were done for 5 min at 30°C.

**Protein concentration was determined using the BCA protein assay agent as described by the manufacturer (Pierce, Rockford, IL).**

**Radio labeling of S. cerevisiae Cells for the Analysis of O-linked Carbohydrates**

Exponentially growing cultures (YEP 2% Sucrose) with an initial OD600 = 1, were used. 30 min before labeling, 2 OD600 of cells were harvested and suspended in 1 ml of YEP 0.5% sucrose. Labeling was done with [2-3H]mannose (specific activity 14 Ci/mmol); 25 µCi/ml were used when total membrane fraction was isolated and 1 mCi/ml when labeled chitinase was isolated. Cells were labeled during 60 min.

**O-linked Carbohydrate Analyses**

The method of Haslebeck and Tanner (1983) was followed for the isolation of total O-linked carbohydrates from radiolabeled cells. The degradation was achieved in 0.1 M NaOH for 24 h at room temperature after which the reaction was stopped by addition of HCl to a final concentration of 0.15 M and the protein was removed by centrifugation. Radiolabeled species in the supernatant were subjected to paper chromatography (Whatman 1 paper) in ethyl acetate/butanol/acetic acid/water (3:4:2.5:4, by vol) during 24 h, or thin layer chromatography on silica gel 60 plates with two ascents in butanol-ethanol-water (5:3:2, by vol). The standard sugar mixture contained mannose, maltose, and raffinose which was detected by silver staining and hybridization with a probe for the actin message.

**Disruption of the GDA1 Gene**

**Construction of pGDA1.** The pGDA1 plasmid contains the GDA1 gene, with 128 codons in the center of the GDA1 coding region were deleted and replaced by the LEU2 gene (see Fig. 1). It was constructed in three steps for technical reasons. (Step 1) The 1,550-bp Psbl-NheI fragment of p3 HB (containing part of the GDA1-ORF) was cloned into the Psbl and XbaI sites of pUC18 to give plasmid A. (Step 2) The 650-bp HindIII-PstI fragment of p3 HB (containing part of the GDA1-ORF) was cloned into the multiple cloning site of p3H-L1 to obtain plasmid B. P3H-L1 has a 3-kb, BglII fragment from the GDA1-ORF. (Step 3) A 3.7-kb Hind II-Xmal segment of plasmid B (containing the first 172 codons of the GDA1-ORF and the entire LEU2 gene) was cloned into plasmid A cut with HindIII and Hpal to produce pGDA1 (Fig. 1).

**Construction of G2 and G11 Strains.** The heterozygous gda1::LEU2/ GDA1 strains G2 and G11 were made via one-step gene replacement (Rothstein, 1983) by transforming the parent strains PRY225 and PRY238, respectively, with a 4.8-kb HindIII-BamHI fragment from pGDA1 containing the LEU2 marked gda1 deletion. Leu + transformants were selected and allele replacement was confirmed by Southern analysis (Maniatis, 1982).

**GDPase activity was assayed essentially as described previously (Yanagisawa et al., 1990). Briefly, incubation mixtures contained in a final volume of 0.1 ml, enzyme (10-50 µg of total membrane extract, Orlean et al., 1988), CaCl2 (1 mM), Triton X-100 (100 µg), GDP (0.2 µmol), and imidazole-HCl buffer pH 7.5, (20 µmol). For UDPase and ADPase assays, GDP was replaced by UDP or ADP at the same concentration. Incubations were done for 5 min at 30°C.**

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**Isolation of Chitinase from Culture Media by Chitin Binding**

Native chitinase was isolated from saturated S. cerevisiae cultures grown in YEPD basically as described by Kuranda and Robbins (1991). Chitinase from 10 ml of media from a saturated culture was allowed to bind ~30 mg of purified chitin (Sigma Chem. Co., St Louis, MO) for 4 h at 4°C. Chitin was then pelleted by centrifugation and washed three times with PBS. The washed pellet was suspended on 1 ml of SDS sample buffer (2% SDS, 5% β-mercaptoethanol, 10% glycerol) heated to 100°C for 10 min, and analyzed by SDS-PAGE on 6% resolving gels with the discontinuous buffer system described by Laemmli (1970). The gel was then stained with Coomassie brilliant blue.

Radiolabeled chitinase was isolated from 1 ml of [2-3H]mannose la-
beled cells as described by Orlean (1990). The material was then subjected to β-elimination and paper chromatography as described in the O-linked carbohydrate analysis section.

**Immunoprecipitation of Carboxypeptidase Y**

The method described by Orlean (1990) was followed. Briefly, logarithmically growing cultures (OD 600~0) in methionine-free minimal medium and 2% glucose were used as starting material. Between 2 and 4, OD600 of cells were harvested and suspended in 1 ml of the same medium. Labeling was done for 30 min with 100 μCi/ml Trans 35S-labeling mix. After labeling, the cells were washed and suspended on 200 μl PBS with 1% SDS, and broken with glass beads. Triton X-100 was added to give a final concentration of 0.4%. Samples were precleared with preimmune serum and protein A-Sepharose (2 h at 4°C), and then immunoprecipitated with 5 μl of anti-CPY serum (a gift from F. Schechmann, University of California, Berkeley, CA) overnight at 4°C. Protein A conjugates were washed and boiled for 10 min in SDS-sample buffer, and run on SDS-PAGE. Acrylamide concentration was 10% on the resolving gel; the discontinuous system described by Laemmli (1970) was used. The gel was then treated with ENHANCE (New England Nuclear) and exposed to Kodak X-OMAT x-ray film at ~80°C.

**Analysis of External Invertase**

Preparation of the invertase extracts, native PAGE of the external invertase, and activity staining were done as described by Ballou (1990) with minor modifications. Five OD600 of cells growing logarithmically on YEPD (2% glucose) were harvested and suspended in 3 ml of YEP containing 0.5% glucose to induce invertase during 4 h at 30°C. Further treatment was as described (Ballou, 1990) and 10 μl of total lysate was loaded on the gel. The crude extracts were heated to 50°C for 30 min before loading onto the native gel in order to convert the invertase to a single oligomeric form (Esmon et al., 1987). The concentration of acrylamide was raised to 8% and 30-cm long slabs were run for 10 h at 10 mA constant current. These changes were introduced in order to better resolve the highly glycosylated forms of invertase.

**Partial Purification of Invertase**

To increase the production of invertase, wild-type (G2-9) and gda 1 null cells G2-11 were transformed with the plasmid pRD58 containing the SUC2 gene (Carlson and Botstein, 1982). After transformation, the strains produced 4–5 times more invertase than the parents. Invertase was induced by growing cells for 3 h in YPD medium containing 0.1% glucose. Cells were harvested (80 g) and broken with a Bead Beater (Bio Spec Products, Inc., Bartlesville, OK) using 0.5-mm, acid washed, glass beads. Invertase purification was done as described previously by Verostek et al. (1991) up to the DE 52 cellulose column step. Invertase activity was measured as previously described by Goldstein and Lampen (1975).

**SDS-PAGE and Western Blotting of Purified Invertase**

Active fractions (0.5 U) of enzyme from wild-type and gda 1 null strains from the DE 52 cellulose column were combined into three pools and subjected to SDS-PAGE on 11% gels with the discontinuous buffer system described by Laemmli (1970). After electrophoresis, samples were blotted to PVDF membranes with CAPS buffer, pH 11. Equivalent membranes were probed with affinity-purified rabbit IgG antibodies against invertase core protein and against ε1,6 and ε1,3 mannose linkages (antibodies were a generous gift of Dr. Randy Schekman, University of California, Berkeley). Final visualization was obtained with anti-rabbit IgG conjugated with alkaline phosphatase and development with the stabilized substrate for alkaline phosphatase Western Blue (Promega). Tran 35S-labeling mix. After centrifugation, the pellet was extracted two more times with chloroform/methanol/water, 60 plates (Merck Sharpe & Dohme/isotopes, St. Louis, MO) using CHCl3/CH3OH/0.22% KCl in water (55:45:10) as solvent system. Approximately 200,000 cpm per lane were applied. The developed TLC plates were sprayed with ENHANCE (New England Nuclear) and fluorograms were obtained after exposure of Kodak X-OMAT film for 3 d at ~80°C. When quantitation was required, it was done as described for the O-linked carbohydrate analyses. Identification of the lipids was based on (a) reported Rf; (b) comigration with authentic standards (PI and lyso PI); (c) sensitivity to mild alkaline hydrolysis; and (d) analysis of head groups (Puotli et al., 1991).

**Results**

**Cloning of the Luminal Golgi Guanosine Diphosphatase GDAI Gene**

In S. cerevisiae, GDP-mannose is the sugar nucleotide used for all known Golgi glycosylation reactions (Kukuruzinska et al., 1987; Puotli et al., 1991). A luminal, highly specific GDPase was previously found associated with this subcellular compartment (Abeljon et al., 1989). The Golgi GDPase was purified to homogeneity (Yanagisawa et al., 1990) and tryptic peptides derived from the deglycosylated 48-kD enzyme were used to obtain amino acid sequence (Table I). Degenerate synthetic oligonucleotides corresponding to peptides 1 and 2 were designed in sense and antisense orientations because the relative positions of the peptides in the GDPase

**Table I. Amino Acid Sequence of Tryptic Peptides from GDAp and PCR Primer Design**

<table>
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<tr>
<th>Peptide</th>
<th>Primer</th>
<th>aa Position in the protein</th>
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<td>1</td>
<td>F L T D E I L N K</td>
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<tr>
<td>2</td>
<td>E S N D I Y I F S Y F Y D R</td>
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<tr>
<td>3</td>
<td>L P T K V P L G G C T T O V Y E P</td>
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<tr>
<td>4</td>
<td>F G D E N Y</td>
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</table>

Amino acid sequence of tryptic peptides from purified GDPase was obtained as described in Materials and Methods. Peptides 3i and 3ii were obtained from the sequencing of a complex peak; boxes represent positions where primary/secondary identifications were not possible; ( ) indicate tentative identification of amino acids. f, inosine; s, sense; a, antisense.
Overexpression of GDPase activity

Figure 1. Restriction endonuclease cleavage pattern of S. cerevisiae genomic DNA isolated from the YEpl3 genomic library. The 140-bp amplification product of the PCR reaction is indicated with a hatched bar. Restriction fragments were subcloned into YEpl3 to generate pl3X, pl3H, and pl3PX. Their ability to overexpress GDPase activity is shown. The 2.2-kb HindIII-NheI fragment was sequenced, and the GDA1-ORF is denoted as a black box flanked by ATG and TGA-codons. Disruption of GDA1-ORF was performed using the HindIII-BamHI fragment of pGDA1, which contains a LEU2 insertion and deletion of the PstI-HpaI (381 bp) fragment of the GDA1-ORF. The HpaI/SmaI ligation and the NheI/XbaI ligation in pGDAA1 did not regenerate either of the restriction sites.

The 140-bp PCR product was labeled by primer extension and used to screen a S. cerevisiae genomic library in YEpl3. A total of 20,000 clones were screened from which five positive colonies were isolated. These clones contained 7-9-kb inserts. Restriction endonuclease cleavage showed that a 3.7-kb XhoI piece and a 3.5-kb HindIII fragment hybridized with the PCR probe. Both of these fragments and a smaller PstI-XhoI piece (also hybridizing with the PCR probe) were subcloned into YEpl3 giving plasmids pl3X, pl3H, and pl3PX (Fig. 1).

Since YEpl3 is a 2μm type vector which replicates with high copy number in S. cerevisiae, “overexpression” of GDPase was measured upon transformation of strain PRY223 with pl3X, pl3H, and pl3PX. Both pl3X and pl3H gave 6-8-fold overexpression of GDPase activity. This result showed that the 0.6-kb Hind III–PstI fragment missing in pl3PX (Fig. 1) was required for activity. Based on this information, a 2.2-kb HindIII–NheI fragment, which hybridized with the PCR probe, was selected for sequencing.

Sequence of the GDA1 Gene

Sequence information was obtained from both DNA strands for the complete 2.2-kb HindIII–NheI fragment. A 1,557 bp ORF was found starting at a methionine residue 133 bp downstream of the HindIII cloning site (Fig. 2 A). The predicted protein contains the sequence corresponding to all the peptides obtained from the GDPase protein (Fig. 2 A). No NH2-terminal protein sequence was obtained. The hydrophobicity plot of the predicted protein shows a single putative membrane-spanning region of 15 amino acids, starting 9 amino acids after the first methionine (Fig. 2 B). Although this putative transmembrane domain is short, Adams and Rose (1985) demonstrated that mutants of vesicular stomatitis virus glycoprotein G containing 14 or more amino acids of the original 20-amino acid transmembrane domain assumed a transmembrane orientation and were correctly targeted. The deduced protein sequence of the GDA1 gene encodes a 519-amino acid polypeptide with a calculated molecular weight of 56,817 D. Three potential N-glycosylation sites are present within the coding region (Fig. 2 A).

These results are in agreement with the observation that GDPase was purified as a luminal Golgi glycoprotein. The hydrophobic plot suggests a typical type II membrane protein with a single hydrophobic stretch acting as an uncleaved signal sequence and anchor to the membrane (Parks and Lamb, 1991) preceded by a short hydrophilic, cytosolic tail (Fig. 2 B). Most mammalian (Paulson and Colley, 1989; Moremen
Table II. Guanosine Diphosphatase Activity after Disruption of GDA1 ORF

<table>
<thead>
<tr>
<th>Strain</th>
<th>Relevant genotype</th>
<th>GDPase (U*/mg protein)</th>
<th>UDPase (U*/mg protein)</th>
</tr>
</thead>
<tbody>
<tr>
<td>G2-9</td>
<td>GDA1</td>
<td>1.68</td>
<td>0.12</td>
</tr>
<tr>
<td>G2-10</td>
<td>GDA1</td>
<td>1.46</td>
<td>0.12</td>
</tr>
<tr>
<td>G2-11</td>
<td>gda1::LEU2</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>G2-12</td>
<td>gda1::LEU2</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

Total membrane fractions were assayed for their ability to hydrolyze GDP, ADP, and UDP. GDPase and UDPase activity are defined as GDPase or UDPase minus ADPase. ADPase activity was 0.22 U/mg protein for every fraction. Results are the average of three independent determinations.

* One unit is the amount of enzyme that releases 1 μmol of inorganic phosphate per min under the standard assay conditions described in Materials and Methods.

and Robbins, 1991) and some yeast (Carmirand et al., 1991) glycosyltransferases and glycosidases sequenced to date share this characteristic; the bulk of the globular carboxy-terminal domain, with the potential N-glycosylation sites and catalytic activity, face the lumen of the organelle. The GDPase is known to be a "high mannose" glycoprotein since it binds to Con A and is deglycosylated by endo H (Yanagisawa et al., 1990). The discrepancy in the apparent MW of the purified, deglycosylated GDPase (48 kD on SDS-PAGE) and that predicted based from the ORF (57 kD) is probably the result of proteolytic cleavage of the enzyme during purification.

GDA1 Is Not Essential for Cell Viability and Growth

The GDPase gene (GDA1) was disrupted by replacing the 381 bp Pst-HpaI fragment in the center of the coding region with a fragment encoding LEU2 (Fig. 1). A linear 4.8-kb HindIII-BamHI fragment containing the gda1::LEU2 allele was used for transformation of PRY225 and PRY238. A schematic representation of the disrupted allele is shown in Fig. 1. Eight independent diploid transformants from each background were sporulated and 12 asci each from 4 of them were dissected. Viable colonies could be generated from each of the tetrad spores, indicating that the GDA1 gene is not essential for viability. Tetrad analysis showed that Leu⁺:Leu⁻ segregated 2:2 in all cases. One tetrad from each genetic background was analyzed in more detail. Southern analyses confirmed the correct replacement of the GDA1 gene by the gda1::LEU2 allele (data not shown).

Assays of GDPase confirmed the loss of this activity in the Leu⁺ strains. Table II shows the result of a typical experiment. GDPase activity is not detected in membranes derived from the disrupted strains. All values are corrected for production of inorganic phosphate from ADP, which is not a substrate for the enzyme (Yanagisawa et al., 1990). ADPase values were constant in the four samples from each tetrad (see legend of Table II).

GDA1 Is Required to Complete the O-Glycosylation of Proteins

Analysis of the O-linked carbohydrate chains was performed by labeling cells in vivo with [2-3H]mannose for 60 min. Total O-linked carbohydrates were then released by β-elimination and radiolabeled carbohydrate chains were resolved by either paper or thin layer chromatography. The oligosaccharide pattern from the wild-type strains agreed with those previously published (Häusler et al., 1992; Haselbeck and Tanner, 1983) and showed five species (Man₃M₃; Man₄, mannobiose; Man₅, mannotriose; Man₆, mannotetraose; and Man₇, mannopentose).

Figure 3. O-glycosylation: total alkali releasable saccharides. Total base sensitive oligosaccharides from various strains radiolabeled with [2-3H]mannose were separated on thin layer chromatography (butanol, ethanol, water-5:3:2) and subjected to autoradiography. Lanes 1 and 3 are strains G11-6 and G11-8, both wild type for GDA1; lanes 2 and 4 are strains G11-5 and G11-7 in which the GDA1-ORF is disrupted. Lane 5 is strain CGY2333 in which the PMR1-ORF is disrupted; lane 6 is strain CGY2332, the corresponding wild type. Approximately 100,000 cpm β-eliminated from 15 to 30 μg of protein were loaded on lanes 1–4, and 6. On lane 5, 160,000 cpm β-eliminated from 90 μg of protein were loaded. M₁, mannose; M₂, mannobiose; M₅, mannotriose; M₆, mannotetraose; and M₇, mannopentose.
was an almost complete absence of chains with 3, 4, and 5 mannose residues (Fig. 3, lanes 2 and 4). To extend these findings, four tetrads from each genetic background were subjected to the same labeling protocol, total O-linked sugar chains were released, resolved by paper chromatography, and labeled M1–M5 species quantitated. We found a three-fold increase of M1 and a 1.2-fold increase of M2 in the gdalΔ strains from both genetic backgrounds (not shown). The decrease in O-linked sugar chains with 3, 4, in 5 mannose residues was more pronounced in gdalΔ strains originated from the G2 diploid that in those originated from the G11 diploid strain. In the G2 derived disrupted strains, we detected a decrease of 4-5-fold in M1, 10-fold in M4, and 6-10-fold in the M5 species. The decline was 2-3-fold in M1 species, 4-5 in M4, and 3-5 in M5 species in the G11 derived disrupted strains (not shown). The wild-type strains corresponding to tetrads from both genetic backgrounds were indistinguishable (not shown).

Mutations in PMR1, a member of the Ca++ ATPase family, have been reported to perturb the secretory pathway and Golgi N-glycosylation in yeast (Rudolph et al., 1989). The O-glycosylation phenotype of this mutant has not been reported. As with the gdalΔ deletion, we found that the pmr1::LEU2 mutants cannot complete the O-linked sugar chains; species with 4 and 5 mannoses were not found (Fig. 3, lane 5). We measured a 2.4-fold increase in the amount of M1, a 1.3-fold increase in M2, and 20% decrease of M3 in the pmr1Δ. The almost normal amounts of M3 in pmr1Δ are a significant difference from gdalΔ, where almost none was found.

Secreted, O-Mannosylated Chitinase Is Underglycosylated in gdal Mutants

*S. cerevisiae* chitinase is secreted into the growth medium and is extensively and exclusively O-mannosylated (Orlean et al., 1986; Kuranda and Robbins, 1991). The enzyme can be purified from culture media by chitin binding and its mobility on SDS-PAGE depends on the amount and length of the O-linked attached sugar chains (Kuranda and Robbins, 1991). As seen in Fig. 4, lanes 1 and 2 vs lanes 3 and 4, similar amounts of chitinase were isolated by chitin binding from the medium of saturated cultures of wild-type and gdalΔ strains indicating that mutant cells do not have a defect in

![Figure 4](http://rupress.org/jcb/article-pdf/122/2/307/1258105/307.pdf)
secretion. The mobility on SDS-PAGE was greater for the chitinase produced by the gdalA strains (Fig. 4, lanes 1 and 3 vs lanes 2 and 4). A smaller difference was observed when comparing chitinase produced by the pmrlΔ strain to the wild-type enzyme (Fig. 4, lane 6 vs lane 6).

To further substantiate the assumption that differences in apparent mobility of chitinase produced by wild-type and mutant strains were the result of differences in glycosylation, cells were labeled in vivo with [2-3H]mannose, chitinase was isolated by chitin binding, sugar chains were isolated by β-elimination and separated by paper chromatography (Orlean et al., 1991). The pattern seen in the O-linked chains released from wild-type chitinase was similar to that previously published (Hausler et al., 1992; Kuranda and Robbins, 1991; Orlean et al., 1991) (Fig. 5, A and B). Chitinase produced by the gdalΔ strains contained 35% of the radiolabel in the M1 species (relative to total M species); M1 was almost completely absent in chitinase from the wild-type. M2 had the remaining 65% of the radiolabel released from gdalΔ chitinase while M1, M4, and M5 were absent (Fig. 5 A). Chitinase produced by the pmrlΔ strain also showed a significant accumulation of the M1 species; M2 and M3 were also present, but in this case only M4 and M5 were absent (Fig. 5 B).

gdal Mutants Cannot Synthesize the Golgi p2 Form of Carboxypeptidase Y

The vacuolar enzyme Carboxypeptidase Y (CPY) has been extensively studied; it is a glycoprotein with four N-linked carbohydrate chains (Stevens et al., 1982). Three forms of the enzyme have been identified: the mature (proteolytically processed) vacuolar form, the core glycosylated ER form of the proenzyme (pl), and the more extensively glycosylated p2 form which is found in the Golgi (Stevens et al., 1982).

The three forms were immunoprecipitated from wild-type extracts (Fig. 6, lanes 3 and 5); the GDA1 disrupted strain, however, showed only the ER precursor pl, and a smaller than wild-type mature form, while the Golgi modified p2 was not detected (Fig. 6, lanes 2 and 4). It had previously been shown that the conversion of pl to p2 is solely the result of further mannosylation of the N-linked core in the Golgi, and is not required for accurate proteolytic processing and targeting (Stevens et al., 1982). Thus, the mature form of CPY made by the gdalΔ strain lacks the additional carbohydrates normally added in the Golgi. The core protein of gdal::LEU2 was not significantly altered because immunoprecipitation of CPY from wild-type and gdalΔ strains followed by treatment with endo H and electrophoresis showed that proteins from both strains migrated equally (not shown).

To further support this finding we immunoprecipitated CPY from wild-type and gdalΔ strains and subjected the samples to SDS-PAGE and autoradiography. As expected, the wild-type strain showed a strong signal for p2 (Fig. 6, lane 3), while the gdalΔ strain showed only a weak signal for p2 (Fig. 6, lane 4). The pl form was not detected in either sample, confirming the results of the previous experiment.

Figure 5. O-linked sugar chains released from secreted chitinase. Paper chromatography of mannoligosaccharides β-eliminated from secreted chitinase isolated by chitin binding from the medium of the experiment shown in Fig. 3. The solvent system was ethyl acetate/butanol/acetic acid/water (3:4:2.5:4). 1-cm strips were cut and subjected to liquid scintillation counting. (A) (closed circles) wild type, values represent the average from strains G11-6 and G11-8; (open circles) gdalΔ, represents the average from strains G11-6 and G11-8; (open triangles) pmrlΔ, represents the average from strains G11-6 and G11-8. (B) (closed triangles) wild type, values represent the average from strains G11-6 and G11-8; (open triangles) pmrlΔ, represents the average from strains G11-6 and G11-8. Strains are described in the legend of Fig. 3.

Figure 6. N-glycosylation of CPY: effect of GDA1 disruption. Cells were labeled with 35SO4 for 60 min followed by immunoprecipitation, SDS-PAGE, and radioautography. (Lane 1) represents strain PRY 304; (lane 2) strain G11-5; (lane 3) strain G11-6; (lane 4) strain G11-7, and (lane 5) strain G11-8. Strains are described on the legend to Fig. 3. pl (precursor 1) and p2 (precursor 2) refer to the ER and Golgi forms of CPY, respectively. Mature CPY originates by proteolytic cleavage of p2.
from mnnl, mnnl0. The structure of the oligosaccharides of CPY from this strain has been reported (Ballou et al., 1990) and lacks outer chain α-3 linked mannoses which are added by the mannosyltransferase encoded by the MNN1 gene (Nakajima and Ballou, 1975). The enzyme has been localized to an intermediate Golgi compartment (Graham and Emr, 1991). The electrophoretic pattern obtained from this strain, with an apparently normal pl form, a mature CPY smaller than wild type, and no observable p2 form, appears identical to that obtained for the gda1Δ strain (Fig. 6, lane 1 vs lanes 2 and 4).

**Invertase Is Underglycosylated in gda1 Mutants**

Invertase is a highly glycosylated protein whose rate of migration on a native gel depends on the number and size of the N-linked oligosaccharide chains (Ballou, 1990). Moreover, the crude extracts were heated to 50°C for 30 min before loading on to the native gels in order to convert the invertase to a single oligomeric form (Esmon et al., 1987). Fully glycosylated external invertase from wild-type strains migrated as a diffuse band in the upper third of the gel (Fig. 7, lanes 2, 3, and 7) as reported by Ballou (1990). Invertase produced by pmrlΔ strains has been shown to migrate faster, at a rate similar to invertase from strains carrying the mnn9 mutation (Rudolph et al., 1989) consistent with the absence of outer mannan chains. This behavior was confirmed by the present study (Fig. 7, lanes 1 and 6). Invertase produced by the gda1Δ strains showed an intermediate phenotype (Fig. 7, lanes 4 and 5, vs lanes 1 and 6 and lanes 2, 3, and 7); it clearly is underglycosylated, but not completely devoid of outer mannan chains. This result was independent of the genetic background in which the null mutations were made (not shown).

To further determine the degree of underglycosylation of invertase, wild-type and gda1 null cells were transformed with a multicopy plasmid carrying the external invertase gene (SUC2). The enzyme was partially purified from these overproducing strains. Invertase from the wild-type strain eluted from the DEAE cellulose column as a sharp peak with maximum activity at 90–100 mM NaCl (Fig. 8 A). Invertase from the gda1 null mutant was more heterogeneous eluting from the DEAE column as a broad peak with maximum activity between 95 and 130 mM NaCl (Fig. 8 A). This behavior is consistent with either underglycosylation, hyperphosphorylation, or both. Internal nonglycosylated invertase binds very tightly to DEAE, requiring 2 M NaCl for elution (Fig. 8 A). Fractions across the activity peak of each strain were divided into three pools (P1, P2, and P3 for wild-type enzyme and P4, P5, and P6 for gda1 null mutant enzyme; Fig. 8 A) and subjected to SDS-PAGE followed by blotting to PVDF membranes as described in Materials and Methods. One membrane was stained with antiinvertase antibody (Fig. 8 B). Invertase from the wild-type strain migrated as a broad band with an apparent mobility of 100–150 kD (Fig. 8, lanes 1, 2, and 3); this is similar to the previously described behavior of invertase by Trimble et al. (1991). The mobility of the invertase from the gda1 null mutant strain was clearly more heterogeneous, appearing as a diffused ladder of species migrating between 80 and 130 kD (Fig. 8 B, lanes 4, 5, and 6). Moreover, invertase which elutes later from the DEAE column (lane 6) was of the size range of invertase from Pichia pastoris and S. cerevisiae pmr1 mutant strains (Fig. 8, lanes 7 and 8; B). Preparations of invertase from Pichia pastoris have been shown on SDS-PAGE as a ladder of species of the same size (85–95 kD) as the ER form of invertase from S. cerevisiae Sec 18 mutants.

![Image](https://example.com/image.png)
Figure 8. N-glycosylation of invertase II: chromatographic behavior and analyses of mannose linkages. The wild-type strain (G2-9) and gda 1 null strain (G2-11) were transformed with pRD 58 containing the \textit{SUC2} gene; cultures were derepressed for invertase production and the enzyme was purified as described in Materials and Methods. (A) Profile from the DEAE-cellulose column. \(P_1\), pooled fractions 16–18; \(P_2\), pooled fractions 19–21; \(P_3\), pooled fraction 22–24, all from wild-type invertase; \(P_4\), pooled fraction 18–20; \(P_5\), pooled fractions 21–23; and \(P_6\), pooled fractions 24–26 all from gda 1 null mutants. Pooled fractions (0.5 U of activity) were resolved on 11% SDS-PAGE, Western blotted with rabbit anti-invertase antibodies (B) or rabbit anti-\(\alpha1,3\) linked mannose antibodies (C), and visualized with alkaline phosphatase conjugated to anti-rabbit IgG. In B and C, lanes 1, 2, and 3 are \(P_1\), \(P_2\), and \(P_3\) from wild-type invertase; lanes 4, 5, and 6 are \(P_4\), \(P_5\), and \(P_6\) from gda 1 null invertase; lane 7 is invertase from pmr 1 null strain (CGY 2333); lane 8 is invertase from \textit{Pichia pastoris} strain GS115.

at 37°C (Trimble et al., 1991). Chromatography of \textit{P. pastoris} oligosaccharides released by endo H showed that over 90% of the species were Man\(_{10-12}\) GlcNac (Trimble et al., 1991). Invertase produced by pmr 1 mutants have also been shown to be devoid of outer mannan chains.

All the invertase fractions from the wild-type and gda 1 null mutant strains showed reactivity with antibodies against the \(\alpha1,6\)-mannose linkage. Staining for the presence of terminal \(\alpha1,3\) linked mannose showed that this linkage occurred, as expected, in the wild-type invertase (Fig. 8 C, lanes 1, 2, and 3). Invertase secreted by the gda 1 null mutants showed a wide range of reactivity varying in amounts similar from wild-type (Fig. 8 C, lane 4) to very reduced levels (lane 6), further supporting the heterogeneity of this enzyme's mannan chains. Invertase from \textit{P. pastoris} (lane 8) does not contain such linkage in agreement with previous biochemical studies (Trimble et al., 1991).

The Cell Wall Is Altered in gda1 Mutants

The \textit{MNT1} gene (Häusler et al., 1992) is identical to \textit{KRE2} (Hill et al., 1992), a gene isolated based on resistance of \textit{S. cerevisiae} to killer toxin \(K_1\). Wild-type \textit{S. cerevisiae} strains are sensitive to \(K_1\), while gda1 mutants were partially resistant (Bussey, H., personal communication) indicating a structural alteration of the cell wall. Although \(\beta1,6\) glucans are components of the \(K_1\) killer toxin receptor on the cell
wall (Boone et al., 1990), other components must play a role since the structure and amounts of β-1,6 glucan is normal in mnt l/kr2 null mutants (Hill et al., 1992). β-glucans are known to be crosslinked with mannoproteins in the S. cerevisiae cell wall. Perhaps the basis for toxin resistance is a reduced number of attachments between these two types of chains.

**Biosynthesis of Mannosylinositolphosphorylceramides Is Severely Impaired in gdal Mutants**

About one third of S. cerevisiae lipids contain inositol; of these, 60% is phosphatidylinositol (PI) which is essential for cell viability and growth ( Culbertson and Henry, 1975; Henry, 1982; Nikawa et al., 1982). The remaining 40% consists of three classes of related inositolphosphate-containing sphingolipids, they are: (a) IPC containing a single inositolphosphate; (b) mannosylinositolphosphorylceramides (MIPC), containing a single inositolphosphate with a mannose attached; and (c) the major sphingolipid, mannosyl-diphosphorylinositolceramide (M[IP]2C) which contains a second inositolphosphate attached to the mannose of MIPC (Steiner et al., 1969; Smith and Lester, 1974). Diversity in the types of sphingoid bases and in the degree of hydroxyl and chain lengths of the fatty acids gives rise to many molecular species of these three lipid classes (Smith and Lester, 1974).

Yeast membranes contain activities which transfer (a) inositolphosphate from PI onto endogenous ceramides yielding IPC, and (b) mannose, from GDP-mannose, onto IPC to yield MIPC (Becker and Lester, 1980). It is also known that the biosynthesis of mannosylinositolphosphorylceramides (MIPC) is dependent on genes controlling the flow of secretory vesicles from the ER to the Golgi apparatus (Puoti et al., 1991). Previous results suggest that IPC is the critical substrate transported between ER and Golgi vesicles, because ER blocked mutants like sec17 and sec18 accumulate IPC and cannot synthesize MIPC at the restricted temperature (Puoti et al., 1991).

From knowledge that MIPC is likely to be made in the Golgi, that GDP-mannose is the mannosyl donor, and that MIPC and M(IP)2C are normally found in the plasma membrane facing the periplasmic space, we speculated that mannosylation of IPC probably occurs in the Golgi lumen for completion of glycosylation. Anti sec7p IgG blocks ER to Golgi transport in vitro (Antebi, 1991). A null mutation in PMI1 exhibits pleiotropic Golgi dysfunctions (Antebi, 1991).

We shall briefly review the current status of S. cerevisiae Golgi subcompartmentation before interpreting the phenotype of gdal strains in relation to this Golgi structure. The complexity of the S. cerevisiae Golgi is just unravelling; few genes have been cloned whose products are specific markers of this compartment. Among these are integral membrane proteins responsible for Golgi functions, such as (a) mntlp, an α,2 mannosyltransferase involved in O-glycosylation (Häusler and Robbins, 1992; Häusler et al., 1992); (b) kex2p, an endoproteinase that processes α-factor in a late Golgi compartment (Redding et al., 1991); and (c) pmrlp, a P-type ATPase, homologous to mammalian Ca ++ pumps (Rudolph et al., 1989; Antebi, 1991). A null mutation in PMIRI exhibits pleiotropic Golgi dysfunctions (Antebi, 1991).

Other specific Golgi markers are peripheral membrane proteins such as sec7lp involved in vesicle-mediated protein sorting and traffic through the Golgi segment of the secretory pathway. Anti sec7lp IgG blocks ER to Golgi transport in vitro (Frazinouzoff et al., 1992) and conditional sec7 mutants accumulate Golgi-like structures (Novick et al., 1981). Other peripheral Golgi membrane proteins include small (20–25 kD) ras-like GTP-binding proteins such as arflp and yptlp. These are localized on the cytosolic surface of the Golgi complex and function in protein transport to and/or within the organelle (Stearns et al., 1990; Segev et al., 1988). Sec14p is a peripheral membrane and cytosolic protein which cofractionates with the putative late Golgi marker kex2p and has PI/PC transfer (exchange) activity; cond-

**Discussion**

We have shown in the gdal null mutant that, (a) elongation of O-linked carbohydrate chains is blocked at the mannobiose step in bulk cell mannanoproteins and in secreted chitinase; (b) N-linked carbohydrates of CPY are not elongated beyond the pl (ER) stage; (c) invertase is underglycosylated; and (d) biosynthesis of MIPC is severely impaired. All these processes have in common a requirement for GDP-mannose in the Golgi lumen for completion of glycosylation. GDA1 is the structural gene for a GDPase, previously localized by subcellular fractionation, to a Golgi-like compartment (Abejion et al., 1989). GDA1 deletion was not expected to be lethal because mutants which can only complete glycosylation in the ER (like mnln9) are viable (Ballou, 1990).
Figure 9. Effect of \( GDA1 \) disruption on the biosynthesis of MIPC. Wild-type (G2-10 strain, lanes 1 and 3) and \( gdalA \) (G2-12 strain, lanes 2 and 4) cells were incubated with \([\text{3H}]\text{myoinositol}\) for 10 min, followed by addition of high concentration of unlabeled myoinositol and further incubation for 10 min (lanes 1 and 2) or 90 min (lanes 3 and 4). Labeled lipids, PI, IPC, MIPC, M(\( \text{IP}\)\(_2\))C were extracted and analyzed by thin layer chromatography (CHCl\(_3/\)CH\(_3\)OH/0.22\% aqueous KCl, 55:45:10) and fluorography. Quantitation is presented in Table III.

Table III. Effect of \( gdalA \) on the Biosynthesis of Inositol-containing Phospholipids

<table>
<thead>
<tr>
<th>Inositol phospholipid</th>
<th>Wild-type</th>
<th>( gdalA )</th>
<th>( gdalA/\text{wt} )</th>
</tr>
</thead>
<tbody>
<tr>
<td>PI</td>
<td>42,700</td>
<td>47,700</td>
<td>1.12</td>
</tr>
<tr>
<td>IPC</td>
<td>10,000</td>
<td>15,500</td>
<td>1.55</td>
</tr>
<tr>
<td>MIPC</td>
<td>10,600</td>
<td>4,300</td>
<td>0.40</td>
</tr>
<tr>
<td>M(( \text{IP})(_2))C</td>
<td>3,400</td>
<td>1,800</td>
<td>0.53</td>
</tr>
</tbody>
</table>

Ratios of radioactivity of inositol-containing phospholipids

<table>
<thead>
<tr>
<th></th>
<th>Wild-type</th>
<th>( gdalA )</th>
</tr>
</thead>
<tbody>
<tr>
<td>IPC/PI</td>
<td>0.23</td>
<td>0.32</td>
</tr>
<tr>
<td>MIPC/IPC</td>
<td>1.06</td>
<td>0.28</td>
</tr>
<tr>
<td>M(( \text{IP})(_2))C/IPC</td>
<td>0.34</td>
<td>0.12</td>
</tr>
<tr>
<td>M(( \text{IP})(_2))C/MIPC</td>
<td>0.32</td>
<td>0.42</td>
</tr>
</tbody>
</table>

Results were taken from the 90-min time point of the experiment described in Fig. 8.

Abeljion et al. *S. cerevisiae* Golgi GDPase
α,6-mannosyltransferase, (b) α,3-mannosyltransferase, and (c) kex2 endopeptidase (Graham and Emr, 1991). S. cerevisiae strains which lack clathrin heavy chains mislocalized Golgi proteases involved in α factor maturation like kex2p and dipetidylaminopeptidase A to the cell surface, while other Golgi integral membrane proteins such as GDPase were not affected (Seeger and Payne, 1992).

Recently, improved ultrastructural EM analyses with per-manganese staining and serial sectioning, showed that wild-type S. cerevisiae cells contain ~30 Golgi-like structures (Preuss et al., 1992) slightly concave disks, typically observed as single isolated cisternae (60% of cases). Occasionally two (30% of cases) or up to three (10% of cases) of these structures are in parallel stacks, often associated with nearby 50-nm vesicles. Golgi structures are always discrete, not contiguous with ER or other organelles. The yeast Golgi compartments are equidistant from the nucleus and the cell wall (Preuss et al., 1992), and different from the mammalian Golgi complexes which are near the nucleus as a consequence of their association with the microtubule organizing center (Kreis, 1990). Permanganate staining in S. cerevisiae revealed morphological features and structures similar to the cisternae and vesicles labeled with antibodies against yptlp, sec7p, and α,6-mannose residues (Preuss et al., 1992) the latter recognizing proteins which have gained access to the Golgi (Ballou, 1982). Unfortunately, no colocalization of these antigens was done in this EM study.

The above ultrastructural studies agree with previous immunofluorescent experiments which showed yeast Golgi associated antigens dispersed in many locations within the cell, but not overlapping with other organelles. By immunofluorescence sec7p colocalizes with kex2p in most instances (60–80%) (Franzusoff et al., 1991). Kex2p is thought to occupy a late Golgi subcompartment whereas sec7 appears to be associated with several Golgi subcompartments (Franzusoff et al., 1991; Franzusoff and Schekman, 1989). PMR may be in another subcompartment because indirect immunofluorescence showed a punctate pattern resembling Golgi staining, but double-labeling experiments in wild-type cells (Antebi, 1991) revealed only a small degree of congruence (although in close juxtaposition) between pmr1p and sec7p (17%) or pmr1p and kex2p (26%); pmr1p accumulated in aberrant Golgi-like structures that occur in sec7 mutants.

How does knowledge of the above Golgi subcompartments relate to the phenotype of gdal null mutants and our current hypothesis of the Golgi localization and function of the gdalp? Current models of nucleotide sugar transport into the Golgi lumen predict a critical role for gdalp in those luminal reactions requiring GDP-mannose as substrates: after mannosylation of proteins and lipids, GDP, a reaction product, is converted by gdalp to GMP which can exit the Golgi lumen in an exchange coupled to entry of additional GDP-mannose from the cytosol. In the absence of gdalp, transport of GDP-mannose into the Golgi lumen should be diminished, leading to reduced availability of the nucleotide sugar and inhibition of those mannosylation reactions occurring in this compartment.

Upon examining total O-glycosylation of proteins we found a threefold increase in the amount of base sensitive monosaccharide in the gdal strains compared to wild type, strongly suggesting that O-linked sugar chains were normally initiated by the addition of a single mannose residue. Gdalp is not expected to play a role in this initiation step, because it is well established that the biosynthesis of O-linked carbohydrate chains starts in the ER, with the first sugar being transferred to serine or threonine residues of the protein from dolichol-P-mannose (Haselbeck and Tanner, 1983, Orlean, 1990). Dolichol-P-mannose synthase has its active site towards the cytosol (Beck, P. J., C. Albright, P. Orlean, P. W. Robbins, M. J. Gething, and J. F. Sambrook. 1990. J. Cell Biol. 111:37a), and transport of GDP-mannose into a lumenal compartment is not required for this reaction. It has been proposed that dol-P-mannose can catalyze the translocation of the mannosylated dol-P-mann from the cytosolic to the luminal side of the ER (Haselbeck and Tanner, 1982), where the sugar becomes attached to the Ser/Thr of the proteins by a recently purified protein O-mannosyltransferase (Sharma et al., 1991).

GDP-mannose is probably the direct donor of the second to fifth O-mannoses which are added stepwise to complete the O-linked mannosyl chains (Haselbeck and Tanner, 1983). These reactions probably occur in the lumen of the Golgi apparatus. Analyses of bulk cell mannoproteins of gdal null mutants showed a virtual complete absence of O-linked mannose chains with 3, 4, or 5 sugars though, unexpectedly, mannobiose was similar to wild type. Because the second O-linked mannosyl is thought to be added in the Golgi lumen, we were initially surprised by the amount of O-linked mannobiose found in gdal mutants. However, Kuranda and Robbins (1991) reported that intracellular chitinase from secl8 labeled at the restrictive temperature contained more than half of the sugars as mannobiose, the remaining being mannose. Significant amounts of mannobiose, in addition to mannose, were also detected in cell wall mannans of secl8 (Haselbeck and Tanner, 1983). Recent studies have shown that secl8 (together with secl7 and 22) belongs to a subset of sec mutants blocked in ER to Golgi transport (class II), in which 50-nm vesicles and enlarged ER structures accumulate (Kaiser and Schekman, 1990). These mutants are believed to be blocked in fusion of these vesicles to the target compartment while class I mutants (secl2, 14, 16, and 23), which accumulate only ER structures appear to be blocked earlier in secretion, during the budding stage (Kaiser and Schekman, 1990). It will be important to determine the length of the O-linked mannose chains synthesized by these mutants.

The α,1,2 mannosyltransferase (mntlp) responsible for the addition of the third O-linked mannose has been localized by subcellular fractionation to the Golgi, and colocalizes with the GDPase activity (Abeijon et al., 1989). This α,1,2 mannosyltransferase activity is inhibited in the gdal mutant; thus the O-glycosylation phenotype of gdal is very similar to that of mntl null mutants (Hausler et al., 1992). This provides independent evidence for both activities occurring in the same subcellular compartment.

Bulk mannoproteins and secreted chitinase from pmrl strains contained almost normal amounts of O-linked M₃ species and thus appear to be blocked in O-mannosylation later than gdal mutants. Subcompartmentation may play a role in the differential effects of these mutations on Golgi processing, since gdalp and pmr1p would be thought to alter Golgi glycosylation in a general, non-specific fashion.

The vacuolar serine protease CPY has been used to detect...
alterations in Golgi N-glycosylation since conversion of the core glycosylated 61 kD, ER, form of the proenzyme (pICPY) to the 69 kD precursor 2 (p2CPY) is solely due to the addition in the Golgi of five mannoses to each of the four N-linked core units present in the proenzyme (Hasilik and Tanner 1978a). This precursor is converted by proteolytic cleavage to a mature, 61-kD form in the vacuole. Glycosylation is not required for correct targeting and processing of CPY (Hasilik and Tanner, 1978b). As predicted, gdal mutants could not synthetize p2CPY and the mature form migrated faster than wild-type on SDS-PAGE. These differences were solely due to glycosylation because mutant and wild-type CPY showed equal SDS-PAGE migration after endo H treatment.

External invertase synthesized by wild-type strains has long outer mannan chain added to core-N-linked oligosaccharides (Ballou, 1990), while that secreted by gdal mutants was underglycosylated but not completely lacking outer mannan chains. Invertase secreted by the mutants is more heterogeneous than that by wild type and partially lacks the terminal α1, 3 linked mannoside units added in the Golgi apparatus. A substantial portion of it showed only core oligosaccharides which are added in the ER. Even though the glycosylation defect observed in invertase is less pronounced than that of CPY and chitinase, four different reasons can explain why a severe decrease in the availability of GDP-mannose in the Golgi lumen of gda 1 mutants may differentially affect individual glycosylation reactions: (a) Different mannosyltransferases have distinct Kms for GDP-mannose (Nakajima and Ballou, 1975). Thus, low concentrations of the nucleotide sugar may affect mannosylations of different substrates to a different extent. (b) Different mannosyltransferases most likely also have different Ki for GDP and thereby selectively affect the synthesis of different glycosylated products. (c) The Golgi apparatus of S. cerevisiae is a subcompartmentalized organelle based on structural (Preuss et al., 1992) and functional evidence (Franzusoff and Schekman, 1989). The various subcompartments most likely have different local substrate concentrations. (d) Invertase has mannose phosphate on the outer chains, the donor of which is also GDP mannose, although the reaction product in this case is GMP, and not GDP. The transfer of mannose phosphate is a luminal reaction and can generate the putative antipporter, GMP, independently of gdalp. GMP present in the Golgi lumen could in turn facilitate the entry of additional cytosolic GDP-mannose, causing the glycosylation defects induced by the gdal mutation to be less severe in those subcompartments where addition of mannose phosphate occurs. This hypothesis can be tested in a double mutant gdal, mnn6 (defective in phosphomannan formation [Ballou, 1990]) where invertase may only be core glycosylated. In more general terms, we recognize that the antipporter activity required to sustain the level of mannosylation found in the deletion strain may be derived from GMP generated by enzymes other than gdalp or from weak antipporter activity of GDP. Mutations in peripheral Golgi proteins arfl and yptl lead to a glycosylation phenotype of invertase very similar to gdal (Stearns et al., 1990). Although CPY also contains mannose-phosphate, the addition probably occurs at a different subcellular site than for invertase (Stevens et al., 1982). Sec18 showed almost no phosphate radiolabeled invertase while CPY phosphate content was normal. In addition, conversion of pICPY to p2CPY did not result in additional phosphate incorporation (Stevens et al., 1982). The gdal and pml1 mutations, which have quantitatively different effects on N-glycosylation of CPY and invertase, provide another example of disparity between secretory and vacuolar proteins routed through the yeast Golgi.

Sphingolipids are ubiquitous eukaryotic plasma membrane constituents that contain a common hydrophobic portion (ceramide) which is anchored in the membrane, and a variable hydrophilic region which in S. cerevisiae has mannosylinositol phosphate exposed to the cell surface (Patton and Lester, 1992). In higher eukaryotes they may act as mediators of signal transduction and cellular regulation (Hakomori, 1990; Hamm and Bell, 1989). Our results with gda1 strains provide direct evidence that the biosynthesis of the mannosyl-sphingolipids occurs in the lumen of the S. cerevisiae Golgi apparatus, supporting previous studies which suggest that GDP-mannose is the direct mannose donor in the formation of MIPC (Becker and Lester, 1980) and that these reactions probably occur in the Golgi apparatus (Puoti et al., 1991). The severe decrease of the above lipids in the gdal mutant strains opens the possibility of studying their influence on membrane activities in vivo. Studies in vitro have shown that H* ATPase, a major protein of the S. cerevisiae plasma membrane is stimulated by sphingolipids (Patton and Lester, 1992).

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